

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2002, 08:28:56 ; Search time 1704.01 Seconds  
(without alignments)  
6154.385 Million cell updates/sec

Title: US-09-826-212-1\_COPY\_183\_959

Perfect score: 777  
Sequence: 1 atggccggatccccaagac.....tgctctgattgtgtgtgt

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: em\_estdb:\*
- 2: em\_esthum:\*
- 3: em\_estin:\*
- 4: em\_estnu:\*
- 5: em\_estov:\*
- 6: em\_estpl:\*
- 7: em\_estro:\*
- 8: em\_hic:\*
- 9: gb\_est1:\*
- 10: gb\_est2:\*
- 11: gb\_hic:\*
- 12: gb\_gss:\*
- 13: em\_gss\_hum:\*
- 14: em\_gss\_inv:\*
- 15: em\_gss\_pln:\*
- 16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	766	98.6	1034	11	BC017852 Homo sapi
2	450.4	58.0	452	9	AA861474
3	375.2	48.3	769	10	BG545631
4	368.8	47.5	923	10	BM045988
5	353	45.4	454	9	AA150541
6	336.2	43.3	428	10	BF899559
7	334.4	43.0	737	10	BM046590
8	329.2	42.4	365	9	BE175577
9	315.4	40.6	538	9	BE175577
10	307.4	39.6	826	10	BM048564
11	292.2	37.6	546	9	AT821105
12	262.8	33.8	598	9	AA150849
13	260	33.7	462	9	AL603419
14	262	33.5	484	10	BI020428
15	236.4	30.4	408	10	BI019989
16	232.2	29.9	258	9	AW372179
17	227.2	29.2	768	10	BI753417

18	222.2	28.6	770	10	BI825012
19	216.6	27.9	824	10	BE548028
20	213.4	27.5	821	10	BM049457
21	203.4	26.2	720	10	BG681978
22	201.8	26.0	536	9	AA453916
23	197.2	25.4	917	9	AL529460
24	193.4	24.9	1208	10	BM478250
25	186.6	24.0	787	10	BE745635
26	185.8	23.9	786	10	BI818469
27	184.6	23.8	222	10	BI025710
28	184	23.7	1156	10	BG250320
29	181.8	23.4	352	10	T71406
30	178.2	22.9	848	10	BE546076
31	175	22.5	676	9	BG436729
32	173.2	22.3	858	9	AL515088
33	172.2	22.2	209	10	BF056044
34	170.4	21.9	1073	10	BG325647
35	169.4	21.8	753	10	BE780380
36	168	21.6	492	9	AW298308
37	146.2	18.8	469	9	AA223122
38	129.8	16.7	997	10	BE563253
39	125.2	16.1	346	10	BF762329
40	125	16.1	343	9	AA031883
41	123.2	15.9	339	10	BF762292
42	120.2	15.5	790	10	BF038233
43	118.6	15.3	524	12	AO539831
44	118.6	15.3	838	12	AO748776
45	118	15.2	916	10	BM043896

# ALIGNMENTS

RESULT 1  
LOCUS BC017852  
DEFINITION Homo sapiens, tumor necrosis factor receptor superfamily, member 10C, decoy without an intracellular domain, clone IMAGE:4700855,  
mRNA.

ACCESSION BC017852  
VERSION BC017852.1  
KEYWORDS GI:17389657  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1034)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (03-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: http://mgc.ncl.nih.gov  
COMMENT Contact: MGC help desk  
Email: g9aps-r@mail.nih.gov

Tissue Procurement: CLONTECH  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LULM)  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: http://www.shgc.stanford.edu  
Contact: (Dickson, Mark) mcd@paxil.stanford.edu  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/HLN at: http://image.llnl.gov  
Series: IRAL Plate: 36 Row: P Column: 3  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10835042  
This clone has the following problem: frame shifted.  
Location/Qualifiers

# FEATURES





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Db      212 ATGAACACGACCCGGGAGACTCTGCCCCAGCTGCTGAAGACATGATGAACACCGAGCCCA 153
QY      562 gggactctctgccccagctgtctgaagagagacaatgacacccagccgggagactcctgccccca 621
      152 GGGACTCTCTGCCCCAGCTGCTGAAGAGACATGACACACGCGGGAGACTCTGCCCCCA 93
QY      622 gctgtctgaagagacaatgacacccagccgggagactcctgccccagctgtctgaagagaca 681
      92 GCTGCTGAAGAGACATGACACACGCGGAGACTCTGCCCCAGCTGCTGAAGAGACA 33
QY      682 atgaccacacagccgggagactcctgtctcttc 713
      32 ATGACACACGACCCGGGAGACTCTGCTCTTC 1

RESULT  3
BG545631 769 bp mRNA linear EST 04-APR-2001
LOCUS     602572889F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4700855 5'
DEFINITION mRNA sequence.
ACCESSION BG545631
VERSION    BG545631.1 GI:13544296
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 769)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: L1CM1535 row: b column: 24
            High quality sequence stop: 617.
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        /clone_1ib="NIH_MGC_77"
        /lab_host="DH10B (T1 phage-resistant)"
        /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site:1:
        SfiI (ggcgctcgcc); Site:2: SfiI (ggcattatggcc); 5' and
        3' adaptors were used in cloning as follows: 5' adaptor
        sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
        5'-ATTCTAGAGCCGAGGCGCGGACATG-dt(30)BN-3' (where B = A,
        C, or G and N = A, C, G, or T). Average insert size 1.9
        kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
        by PCR. This library was enriched for full-length clones
        and was constructed by Clontech Laboratories (Palo Alto,
        CA). Note: this is a NIH_MGC Library."
BASE COUNT 203 a 207 c 220 g 139 t
ORIGIN
Query Match 48.3%; Score 375.2; DB 10; Length 769;
Best Local Similarity 94.5%; Pred. No. 1.6e-95;
Matches 497; Conservative 0; Mismatches 18; Indels 11; Gaps 10;
QY 1 atggcccgatccccaagacccaataaagtctgtcatcgtcgctgctctgtgcca 60
      |||||||
Db 199 ATGGCCCGGATCCCGAAGACCCCTTAAGTCTCTGTCATCGTCGCGTCTCTGTCGA 258
      |||||||
QY 61 gtctagcttactctgcacacactgcccgagagagaaagtccccaagacagtggcc 120
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Db      259 GTCCTAGCTTACTTGCCACCATCTGCCGCGAGAGAGAACTTCCCAAGACAGACTGGCC 318
QY      121 ccacaagcaacagagacagcttcaaggaggagagtgctcagacagatctcctatagatca 180
      319 CCACAGCAACAGAGGACACAGCTTCAAGGGGAGAGAGTGTCCAGCAGGATCTCATAGATCA 378
QY      181 gaacatactgagcctgtaaccg-tgcacagaggg-tgtgatatcac-caacgcttc 237
      379 GAACATATGAGGCTGTGAACCCGTTGCACAGAGAGGTGTGTGATTACACAAAGCTTCC 438
QY      238 aacaaatgaaccttctgtt-cccatgtacagttgttaaatcagatcaaaaac-ataaaa 295
      439 AACAAATGAACCTCTTGCTTCCCATGTACAGTTGTTAAATCAAGATCAAAAACGATATAA 498
QY      296 gtctctgacacataccagagacacagtgctgtctgtgtaagaagagcaaccttcgggaatg 355
      499 GTTCTCGACCATATACAGACACAGAGTGTGTAAGAAAGGACCTTCCGGAATG 558
QY      356 aaactcccccagagatgtgccggaagtgaagcagt-g-cctagtggggaagtcacagt- 413
      559 GAAACTCCCCAGAGATGTGCCGGAAGTGTACAGAGTACCTTATTGGGGAAGTCCAAATC 618
QY      414 cagtaattgtacgtcct-ggagatgatatcagtgctgtgaagaattgtgtccaatgcca 472
      619 CAGGAATCTGTACTGTGGGATGATATCCAAAGTAGCGAAGATTGGTGCCAAATGCCA 678
QY      473 ctgtggaacccagctgtctgaagagacaatgaacacccagccgg 518
      679 CTGTGGAAA-CCCAAGATGCTGA--AGAAATGACACCCAGCGGG 721
Db      679 CTGTGGAAA-CCCAAGATGCTGA--AGAAATGACACCCAGCGGG 721

RESULT  4
BM045988 923 bp mRNA linear EST 07-NOV-2001
LOCUS     603625140F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:3451897 5'
DEFINITION mRNA sequence.
ACCESSION BM045988
VERSION    BM045988.1 GI:16775255
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 923)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: DCRD/DRP
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.llnl.gov
            Plate: L1CM1942 row: p column: 10
            High quality sequence stop: 757.
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        /clone_1ib="NIH_MGC_40"
        /tissue_type="carcinoma, cell line"
        /lab_host="DH10B (phage-resistant)"
        /note="Organ: prostate; Vector: pDR7; Site:1: XhoI;
        Site:2: EcoRI; cDNA made by oligo-dT priming.
        directionally cloned into EcoRI/XhoI sites using the
        following 5' adaptor: GGCACGAG(G). Library constructed by
        Ling Hong in the laboratory of Gerald M. Rubin (University
        of California, Berkeley) using ZAP-cDNA synthesis kit
        (Stratagene) and Superscript II RT (Life Technologies)."

```



KEYWORDS	EST
SOURCE	human
ORGANISM	human: Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 428) Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Birones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar. 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/ICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4*MF0201-1-031200-002-c07&t3=2000-12-03&t4=1) Seq primer: puc18 forward High quality sequence stop: 427. Location/Qualifiers 1..428 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="MF0201" /dex_stage="Adult" /note="Organ: marrow; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT	119 a 122 c 109 g 78 t
ORIGIN	
Query Match	43.3%; Score 336.2; DB 10; Length 428;
Best Local Similarity	96.1%; Pred. NO. 1.5e-84;
Matches 366; Conservative 0; Mismatches 13; Indels 2; Gaps 2;	
QY	1 atgagccgagatccccaaagacctaaagttcgcgtcatcagctgagcgtctgtgcca 60
Db	46 ATGGCCCGGATGCCCAAGACCTTAAAGTTTCGTGCTGATGTCGCG-GTCTGTGGCA 104
QY	61 gtctagcttactctctgcaccacactgtcccgcgacagagagaagttccccaagacagatggcc 120
Db	105 GTCTAGCTTACTCTGTCACCACTGGCCGGAGAGGAAGAAATGCCCCACAGACAGTGGCC 164
QY	121 ccacagcaacagagagacagatctcaaggaggagagagtgctcaagcagatctcatagatca 180
Db	165 CCACGCAACAGAGGACACAGCTTCAGAGGGGAGAGTGATCTCAGACGAGATCTCATGAGATCA 224
QY	181 gaacatactggagacctgttaacccgtgcacacagagagtgctggattacaacaagccttcaac 240
Db	225 GAACATACTGCAAGCCTGTAAACCCGTGCACAGAGGGTGATTTACACCAACCTTCCAAC 284
QY	241 aatgaaccttctgtctccatgltacagttgtttaataagatcaaaaacataaaagttcc 300
Db	285 AATGAACCTTCTGTGCTTCCCATGTACAGTTGTTAAATCAGATCAAAACATTAAGTTCC 344
QY	301 tgcaccatgacccagagacacagtgctgtcagtgt-aaagaagcaccttcgggaatgaa 359

DB	345	TCGACCATGACCAGACACACTGTGTCACTGTATAAAGAGAGACACTTCGGGAATGAAAA	404
QY	360	ctccccagagatgttcccgaa	380
DB	405	CTCCCCAGAGATGTCCGGAA	425
RESULT	7		
BM046590			
LOCUS			
DEFINITION	BM046590	737 bp	mRNA linear EST 07-NOV-2001
ACCESSION	603626666p1	NIH_MGC_40	Homo sapiens cDNA clone IMAGE:5453129 5',
VERSION	BM046590		mRNA sequence.
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 737)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapds-remail.nih.gov		
	Tissue procurement: DCTD/DTF		
	cDNA Library Preparation: Ling Hong/Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.lnl.gov		
	Plate: LNCM1946 row: c column: 18		
	High quality sequence stop: 737.		
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	/tissue_type="carcinoma, cell line"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;		
	Site_2: EcoRI; cDNA made by oligo-dT priming.		
	Directionally cloned into EcoRI/XhoI sites using the		
	following 5' adaptor: GGCAGAG(G). library constructed by		
	Ling Hong in the Laboratory of Gerald M. Rubin (University		
	of California, Berkeley) using ZAP-cDNA synthesis kit		
	(Stratagene) and Superscript II RT (Life Technologies).		
	Note: this is a NIH_MGC Library."		
BASE COUNT	182 a	209 c	196 g 150 t
ORIGIN			
Query Match	43.0%; Score 334.4; DB 10; Length 737;		
Best Local Similarity	83.9%; Pred. No. 6,1e-84;		
Matches	426; Conservative	0; Mismatches	76; Indels 6; Gaps 4;
QY	6	ccgagatcccaagaccctaaagttcgtcgtcgtcgcagtcgctcgtcgtccagtcct	65
DB	181	CCTGCACTCCCAAGATCTTAAGTTGTCGTCTTCATCTCGCGGTTCTGTCGCCGTCCG	240
QY	66	agcttacctccacacctatgcctccgagagagaaattcccaagacagatgagccca	125
DB	241	GTTTACTCTGCTCCACCAATCCCGGACAGAGACAAATTCCACGACGAGAGTGCCCA	300
QY	126	gcaacagagacacagcttcaaggggagagatgttcacagcagatcctcatagacaga	185
DB	301	GCAACAGAGGGCGACGCTCAAGAGAGAGAGTGTCCACAGAGATCTCATATACAGATA	360
QY	186	tactggacctgttaacccgtgtcacagaggtgttgatttaaccacagcttccaacatga	245
DB	361	TACTGGACCTGTTAACCCGTGTACAGAGAGAGTGTGATTATACCAATTGCTTCAACCAATTT	420

BASE COUNT	ORIGIN
136 a	154 c 141 g 100 t 7 others







Search completed: August 13, 2002, 10:49:52  
 Job time: 8456 sec

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LOCUS      BI019989              408 bp    mRNA    linear    EST 14-JUN-2001
DEFINITION CM3-MT0292-110101-625-f09 MT0292 Homo sapiens CDNA, mRNA sequence.
ACCESSION  BI019989
VERSION     BI019989.1  GI:14426619
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 408)
AUTHORS     Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Bionesi,M.R.,
             Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
             Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
             Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
             ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
             Simpson,A.J.
TITLE       Shotgun sequencing of the human transcriptome with ORF expressed
             sequence tags
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE    20202663
COMMENT     Contact: Simpson A.J.G.
             Laboratory of Cancer Genetics
             Ludwig Institute for Cancer Research
             Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
             Brazil
             Tel: +55-11-2704922
             Fax: +55-11-2707001
             Email: asimpson@ludwig.org.br
             This sequence was derived from the FAPESP/LICR Human Cancer Genome
             Project. This entry can be seen in the following URL
             (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-MT0292-
             110101-625-f09&t3=2001-01-11&t4=1)
             Seq primer: puc 18 forward
             High quality sequence start: 31
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                 /clone_lib="MT0292"
                 /dev_stage="Adult"
                 /note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2:
                 SmaI; A mini-library was made by cloning products derived
                 from ORESTES PCR (U.S. Letters Patent application No. 196
                 ,716 - Ludwig Institute for Cancer Research) profiles
                 into the puc 18 vector. Reverse transcription of tissue
                 mRNA and cDNA amplification were performed under low
                 stringency conditions."
BASE COUNT  112 a      105 c      94 g      97 t
ORIGIN
Query Match      30.4%; Score 236.4; DB 10; Length 408;
Best local Similarity 99.6%; Pred. No. 3,1e-56;
Matches 237; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 164 Caggatcctagatcagacatacttgagcctgtaaccgtgcacagagggtgtgatt 223
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Db 171 CAGGATCTCATAGATCAGACATGCTGAGCGCTTAACCCGTGCACAGAGGCTGTGATT 230
QY 224 acacacagcttccaaacagacactctgtctcccatgacaggtttgttaacagatc 283
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Db 231 ACACCAAGGCTCCACAAATGAACCTTCTGCTCCATGTCATGTTGTAATCAGATC 290
QY 284 aaaaacataaaagtctctgaccatgacacagagacagtggtcagtgtaaaagagca 343
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Db 291 AAAAAACATTAAGTCTTGACCATGACACAGACACAGTGTGTACAGTAAAGCAAGCA 350
QY 344 ccttcggaaatgaacatcccccagagatgtgcccggaaagttagcaggtgcccctagtgg 401
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Db 351 CCTTCGGAATGAAGAACTCCCAAGAGATGTGCCGGAAGTGTAGCAGGTGCCCTAGTGG 408

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GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: August 13, 2002, 08:35:06 ; Search time 13.5 Seconds  
(without alignments)  
421.568 Million cell updates/sec

Title: US-09-826-212-2\_COPY\_27\_259

Perfect score: 233

Sequence: 1

1 TTARQEEVPOQTVAPOQORH.....YLSCTIVGIVLVIVFV 233

Scoring table:

Gapop 60.0 , Gapect 60.0

Searched:

Word size : 5

Total number of hits satisfying chosen parameters: 2406

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/backfile1.pep:\*

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	233	100.0	259	US-09-006-353A-2	Sequence 2, Appl1
2	233	100.0	259	US-09-153-927-3	Sequence 3, Appl1
3	14	6.0	386	US-09-086-483A-2	Sequence 2, Appl1
4	8	3.4	303	US-09-333-593A-4	Sequence 4, Appl1
5	8	3.4	411	US-09-329-633A-2	Sequence 2, Appl1
6	8	3.4	411	US-09-079-029-1	Sequence 1, Appl1
7	8	3.4	412	US-09-333-593A-2	Sequence 2, Appl1
8	8	3.4	424	US-09-333-593A-8	Sequence 8, Appl1
9	8	3.4	440	US-08-883-036A-2	Sequence 2, Appl1
10	8	3.0	61	US-08-465-380-61	Sequence 61, Appl1
11	8	3.0	61	US-08-486-397-61	Sequence 61, Appl1
12	8	3.0	61	US-08-486-399-61	Sequence 61, Appl1
13	8	3.0	61	US-08-461-965-61	Sequence 61, Appl1
14	8	3.0	61	US-08-634-641-61	Sequence 61, Appl1
15	8	3.0	61	US-09-249-471-61	Sequence 61, Appl1
16	8	3.0	61	US-09-249-472-61	Sequence 61, Appl1
17	8	3.0	61	US-09-249-451-61	Sequence 61, Appl1
18	8	3.0	61	US-08-809-455-61	Sequence 61, Appl1
19	8	3.0	61	US-09-249-461-61	Sequence 61, Appl1
20	8	3.0	61	US-09-249-448-61	Sequence 61, Appl1
21	8	3.0	93	US-08-118-270-335	Sequence 335, App
22	8	3.0	93	PCT-US93-08528-335	Sequence 335, App
23	8	3.0	219	US-08-928-213B-60	Sequence 142, Appl
24	8	3.0	257	US-08-818-112-142	Sequence 137, App
25	8	3.0	257	US-08-818-111-137	Sequence 142, App
26	8	3.0	265	US-09-056-556-142	Sequence 9, Appl1
27	8	3.0	365	US-08-467-559B-9	Sequence 9, Appl1

28	7	3.0	377	US-08-118-270-14	Sequence 14, Appl1
29	7	3.0	377	PCT-US93-08528-14	Sequence 14, Appl1
30	7	3.0	401	PCT-US96-09848-13	Sequence 31, Appl1
31	7	3.0	407	PCT-US96-09848-15	Sequence 15, Appl1
32	7	3.0	467	US-09-086-483A-6	Sequence 6, Appl1
33	7	3.0	468	US-08-390-000A-7	Sequence 7, Appl1
34	7	3.0	468	US-09-013-895A-2	Sequence 2, Appl1
35	7	3.0	472	US-08-194-338-6	Sequence 6, Appl1
36	7	3.0	477	US-08-087-772A-16	Sequence 16, Appl1
37	7	3.0	1835	US-09-404-650-5	Sequence 5, Appl1
38	7	3.0	3739	US-09-320-878-2	Sequence 2, Appl1
39	7	3.0	3739	US-09-105-537-33	Sequence 33, Appl1
40	7	3.0	11877	US-09-105-537-6	Sequence 6, Appl1
41	6	2.6	14	US-08-630-915A-145	Sequence 145, App
42	6	2.6	18	US-08-792-832A-39	Sequence 39, Appl1
43	6	2.6	24	US-08-792-832A-33	Sequence 33, Appl1
44	6	2.6	25	US-09-023-339-5	Sequence 5, Appl1
45	6	2.6	32	US-08-477-877B-56	Sequence 56, Appl1
46	6	2.6	32	US-08-472-281A-56	Sequence 56, Appl1
47	6	2.6	34	US-08-792-832A-56	Sequence 56, Appl1
48	6	2.6	36	US-08-050-319B-30	Sequence 30, Appl1
49	6	2.6	36	US-08-465-982-30	Sequence 30, Appl1
50	6	2.6	39	US-08-792-832A-53	Sequence 53, Appl1
51	6	2.6	39	US-08-465-982-30	Sequence 30, Appl1
52	6	2.6	101	US-08-199-637A-399	Sequence 39, App
53	6	2.6	117	US-08-478-039-97	Sequence 97, Appl
54	6	2.6	117	US-08-476-349A-97	Sequence 97, Appl
55	6	2.6	97	US-08-290-592E-16	Sequence 16, Appl1
56	6	2.6	97	PCT-US95-10053-13	Sequence 13, Appl1
57	6	2.6	97	PCT-US96-09448-16	Sequence 16, Appl1
58	6	2.6	101	US-08-199-637A-399	Sequence 39, App
59	6	2.6	117	US-08-478-039-97	Sequence 97, Appl
60	6	2.6	117	US-08-290-592E-17	Sequence 17, Appl
61	6	2.6	117	US-08-545-809A-90	Sequence 90, Appl1
62	6	2.6	117	US-08-545-809A-128	Sequence 128, App
63	6	2.6	117	US-09-025-769B-22	Sequence 22, Appl
64	6	2.6	117	PCT-US95-10053-14	Sequence 14, Appl
65	6	2.6	117	PCT-US96-09448-17	Sequence 17, Appl
66	6	2.6	119	US-08-983-607-34	Sequence 34, Appl1
67	6	2.6	120	US-09-025-769B-36	Sequence 36, Appl1
68	6	2.6	120	US-09-025-769B-59	Sequence 59, Appl1
69	6	2.6	123	US-08-477-877B-94	Sequence 94, Appl1
70	6	2.6	123	US-08-472-281A-94	Sequence 94, Appl1
71	6	2.6	123	US-08-477-889B-94	Sequence 94, Appl1
72	6	2.6	125	US-08-905-223-320	Sequence 320, App
73	6	2.6	133	US-08-468-560C-8	Sequence 8, Appl1
74	6	2.6	139	US-08-219-237B-8	Sequence 8, Appl1
75	6	2.6	140	US-08-477-347-17	Sequence 17, Appl1
76	6	2.6	140	US-08-476-862-8	Sequence 8, Appl1
77	6	2.6	145	US-08-997-362-55	Sequence 55, Appl1
78	6	2.6	145	US-08-997-362-55	Sequence 55, Appl1
79	6	2.6	145	US-08-873-970-55	Sequence 55, Appl1
80	6	2.6	145	US-09-095-855-55	Sequence 55, Appl1
81	6	2.6	145	US-08-705-347A-55	Sequence 55, Appl1
82	6	2.6	145	US-09-324-542-55	Sequence 55, Appl1
83	6	2.6	192	US-08-086-428B-58	Sequence 58, Appl1
84	6	2.6	192	US-08-086-428B-62	Sequence 62, Appl1
85	6	2.6	192	US-08-086-428B-74	Sequence 74, Appl1
86	6	2.6	192	US-08-086-428B-76	Sequence 76, Appl1
87	6	2.6	192	US-08-468-570-58	Sequence 58, Appl1
88	6	2.6	192	US-08-468-570-62	Sequence 62, Appl1
89	6	2.6	192	US-08-468-570-74	Sequence 74, Appl1
90	6	2.6	192	US-08-468-570-76	Sequence 76, Appl1
91	6	2.6	192	US-08-290-665A-58	Sequence 58, Appl1
92	6	2.6	192	US-08-290-665A-62	Sequence 62, Appl1
93	6	2.6	192	US-08-290-665A-74	Sequence 74, Appl1
94	6	2.6	192	US-08-290-665A-76	Sequence 76, Appl1
95	6	2.6	192	PCT-US95-10398-62	Sequence 62, Appl1
96	6	2.6	192	PCT-US95-10398-68	Sequence 68, Appl1
97	6	2.6	192	PCT-US95-10398-74	Sequence 74, Appl1
98	6	2.6	192	PCT-US95-10398-76	Sequence 76, Appl1
99	6	2.6	202	US-08-793-229-37	Sequence 27, Appl1
100	6	2.6	202		

101	6	2.6	202	3	US-09-285-957-27	Sequence 27, Appl	174	6	2.6	613	4	US-09-232-201-7	Sequence 7, Appl1
102	6	2.6	205	3	US-08-974-022-51	Sequence 51, Appl	175	6	2.6	613	4	US-09-232-201-94	Sequence 94, Appl
103	6	2.6	205	4	US-08-795-445A-51	Sequence 51, Appl	176	6	2.6	635	4	US-07-832-855-2	Sequence 2, Appl1
104	6	2.6	205	4	US-08-795-447A-51	Sequence 51, Appl	177	6	2.6	676	3	US-08-947-165-71	Sequence 71, Appl
105	6	2.6	205	4	US-08-974-186-51	Sequence 51, Appl	178	6	2.6	707	2	US-08-576-165-4	Sequence 4, Appl1
106	6	2.6	205	4	US-08-795-446B-51	Sequence 51, Appl	179	6	2.6	708	2	US-08-576-165-2	Sequence 2, Appl1
107	6	2.6	273	2	US-08-997-080-75	Sequence 75, Appl	180	6	2.6	764	1	US-08-424-567-2	Sequence 2, Appl1
108	6	2.6	273	3	US-08-997-362-75	Sequence 75, Appl	181	6	2.6	764	1	US-08-711-928-2	Sequence 2, Appl1
109	6	2.6	273	3	US-08-873-970-75	Sequence 75, Appl	182	6	2.6	764	4	US-09-184-937-2	Sequence 2, Appl1
110	6	2.6	273	4	US-09-095-855-75	Sequence 75, Appl	183	6	2.6	764	4	US-07-741-453A-54	Sequence 54, Appl
111	6	2.6	273	1	US-09-324-542-75	Sequence 75, Appl	184	6	2.6	764	4	US-07-741-453A-60	Sequence 60, Appl
112	6	2.6	275	1	US-07-611-528A-2	Sequence 2, Appl1	185	6	2.6	783	6	US-08-836-325-8	Sequence 8, Appl1
113	6	2.6	275	1	US-08-083-946-2	Sequence 2, Appl1	186	6	2.6	816	1	US-07-711-157A-4	Sequence 4, Appl1
114	6	2.6	275	3	US-08-452-915-2	Sequence 9, Appl1	187	6	2.6	816	1	US-08-229-444B-2	Sequence 2, Appl1
115	6	2.6	281	2	US-08-405-175A-9	Sequence 9, Appl1	188	6	2.6	827	4	US-08-541-780-4	Sequence 4, Appl1
116	6	2.6	313	3	US-08-926-842B-62	Sequence 62, Appl	189	6	2.6	827	4	US-08-660-286-11	Sequence 11, Appl
117	6	2.6	344	4	US-09-147-236-11	Sequence 11, Appl	190	6	2.6	827	4	US-08-469-253-11	Sequence 11, Appl
118	6	2.6	347	3	US-09-059-369-2	Sequence 2, Appl1	191	6	2.6	827	4	US-09-642-146-11	Sequence 11, Appl
119	6	2.6	350	1	US-08-458-067-2	Sequence 2, Appl1	192	6	2.6	827	4	US-08-042-747A-8	Sequence 8, Appl1
120	6	2.6	350	5	PCT-US96-07795-2	Sequence 2, Appl1	193	6	2.6	885	3	US-08-804-439A-23	Sequence 23, Appl
121	6	2.6	350	5	PCT-US96-07796-2	Sequence 2, Appl1	194	6	2.6	885	3	US-08-720-229-23	Sequence 23, Appl
122	6	2.6	366	2	US-08-804-699-2	Sequence 2, Appl1	195	6	2.6	1088	4	US-09-082-059-2	Sequence 2, Appl1
123	6	2.6	370	2	US-08-997-080-194	Sequence 194, App	196	6	2.6	1099	3	US-08-442-100-2	Sequence 2, Appl1
124	6	2.6	370	2	US-08-997-362-194	Sequence 194, App	197	6	2.6	1477	3	US-08-452-459-10	Sequence 10, Appl
125	6	2.6	370	4	US-09-035-855-194	Sequence 194, App	198	6	2.6	1477	3	US-08-423-752-10	Sequence 10, Appl
126	6	2.6	375	1	US-09-324-542-194	Sequence 194, App	199	6	2.6	1477	3	US-08-945-994-3	Sequence 3, Appl1
127	6	2.6	388	4	US-08-742-621-1	Sequence 1, Appl1	200	6	2.6	1477	4	US-08-716-873-24	Sequence 24, Appl
128	6	2.6	388	4	US-09-191-608-22	Sequence 22, Appl	201	6	2.6	1477	4	US-09-368-431-24	Sequence 24, Appl
129	6	2.6	406	1	US-08-487-823B-5	Sequence 5, Appl1	202	6	2.6	1754	4	US-07-745-206A-13	Sequence 10, Appl
130	6	2.6	406	2	US-08-997-040-5	Sequence 5, Appl1	203	6	2.6	1754	4	US-08-311-363-13	Sequence 13, Appl
131	6	2.6	406	2	US-09-203-237-5	Sequence 5, Appl1	204	6	2.6	4302	3	US-08-658-136-5	Sequence 5, Appl1
132	6	2.6	407	1	US-08-487-823B-2	Sequence 2, Appl1	205	6	2.6	4302	3	US-08-460-751-2	Sequence 2, Appl1
133	6	2.6	407	1	US-08-997-040-2	Sequence 2, Appl1	206	6	2.6	4544	1	US-08-469-486-52	Sequence 52, Appl
134	6	2.6	407	2	US-09-203-237-2	Sequence 2, Appl1	207	6	2.6	4544	2	US-08-469-486-52	Sequence 52, Appl
135	6	2.6	410	3	US-08-948-997-2	Sequence 2, Appl1	208	6	2.6	5588	4	US-09-036-987A-6	Sequence 6, Appl1
136	6	2.6	410	3	US-08-348-817A-2	Sequence 2, Appl1	209	6	2.6	5588	4	US-08-370-700-6	Sequence 6, Appl1
137	6	2.6	420	1	US-08-487-823B-4	Sequence 4, Appl1	210	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
138	6	2.6	420	2	US-08-997-040-4	Sequence 4, Appl1	211	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
139	6	2.6	420	2	US-09-203-237-4	Sequence 4, Appl1	212	6	2.6	5588	4	US-08-437-013A-39	Sequence 39, Appl
140	6	2.6	428	1	US-07-973-324A-4	Sequence 4, Appl1	213	6	2.6	5588	4	US-08-980-357-29	Sequence 29, Appl
141	6	2.6	428	1	US-08-343-380-4	Sequence 4, Appl1	214	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
142	6	2.6	428	4	US-09-072-435-4	Sequence 4, Appl1	215	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
143	6	2.6	428	4	US-09-072-917A-4	Sequence 4, Appl1	216	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
144	6	2.6	428	4	US-07-923-692C-6	Sequence 6, Appl1	217	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
145	6	2.6	434	1	US-08-184-237-6	Sequence 6, Appl1	218	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
146	6	2.6	434	1	US-08-482-920-6	Sequence 6, Appl1	219	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
147	6	2.6	434	3	US-08-484-341-6	Sequence 6, Appl1	220	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
148	6	2.6	434	3	US-08-483-502-6	Sequence 6, Appl1	221	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
149	6	2.6	434	3	US-08-801-344-9	Sequence 9, Appl1	222	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
150	6	2.6	462	4	US-09-498-599-9	Sequence 9, Appl1	223	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
151	6	2.6	462	4	US-08-218-943-2	Sequence 2, Appl1	224	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
152	6	2.6	487	1	US-08-999-723-2	Sequence 2, Appl1	225	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
153	6	2.6	518	3	US-08-999-723-2	Sequence 2, Appl1	226	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
154	6	2.6	518	4	US-09-434-427-2	Sequence 2, Appl1	227	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
155	6	2.6	529	3	US-08-821-984-6	Sequence 6, Appl1	228	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
156	6	2.6	529	3	US-08-821-984-8	Sequence 6, Appl1	229	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
157	6	2.6	529	3	US-09-329-749-6	Sequence 6, Appl1	230	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
158	6	2.6	529	4	US-09-329-749-8	Sequence 8, Appl1	231	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
159	6	2.6	542	4	US-08-675-816-6	Sequence 6, Appl1	232	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
160	6	2.6	547	4	US-08-930-001-2	Sequence 2, Appl1	233	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
161	6	2.6	549	2	US-08-676-279-59	Sequence 59, Appl	234	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
162	6	2.6	569	2	US-08-750-723A-2	Sequence 2, Appl1	235	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
163	6	2.6	569	2	US-09-191-275-2	Sequence 2, Appl1	236	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
164	6	2.6	583	4	US-09-311-311C-24	Sequence 24, Appl	237	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
165	6	2.6	609	4	US-08-980-115-11	Sequence 11, Appl	238	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
166	6	2.6	609	4	US-09-232-200-69	Sequence 69, Appl	239	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
167	6	2.6	609	4	US-09-232-197-69	Sequence 69, Appl	240	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
168	6	2.6	609	4	US-09-232-201-69	Sequence 69, Appl	241	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
169	6	2.6	613	4	US-09-232-191-7	Sequence 7, Appl1	242	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
170	6	2.6	613	4	US-09-232-200-7	Sequence 7, Appl1	243	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
171	6	2.6	613	4	US-09-232-200-94	Sequence 94, Appl	244	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
172	6	2.6	613	4	US-09-232-197-7	Sequence 7, Appl1	245	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl
173	6	2.6	613	4	US-09-232-197-94	Sequence 94, Appl	246	6	2.6	5588	4	US-08-666-473-34	Sequence 34, Appl

247	5	2.1	17	1	US-08-518-474-10	Sequence 10, Appl	320	5	2.1	30	3	US-08-433-522A-19	Sequence 19, Appl
248	5	2.1	18	1	US-08-050-319B-5	Sequence 5, Appl	321	5	2.1	30	3	US-08-801-028-82	Sequence 82, Appl
249	5	2.1	18	2	US-08-465-982-5	Sequence 5, Appl	322	5	2.1	30	3	US-09-135-166-19	Sequence 19, Appl
250	5	2.1	19	2	US-08-836-791-4	Sequence 4, Appl	323	5	2.1	30	3	US-09-340-154-82	Sequence 82, Appl
251	5	2.1	19	3	US-08-792-832A-42	Sequence 42, Appl	324	5	2.1	30	4	US-08-477-046-7	Sequence 246, App
252	5	2.1	20	1	US-08-103-742-30	Sequence 30, Appl	325	5	2.1	30	4	US-08-942-046-19	Sequence 19, Appl
253	5	2.1	20	2	US-08-749-852-53	Sequence 53, Appl	326	5	2.1	30	4	US-08-473-089-246	Sequence 246, App
254	5	2.1	20	2	US-08-749-852-55	Sequence 55, Appl	327	5	2.1	30	5	PCT-US95-09338-82	Sequence 82, Appl
255	5	2.1	21	1	US-07-969-931-2	Sequence 2, Appl	328	5	2.1	30	5	PCT-US95-09339-82	Sequence 82, Appl
256	5	2.1	21	1	US-07-855-417A-2	Sequence 2, Appl	329	5	2.1	31	1	US-08-149-839B-7	Sequence 7, Appl
257	5	2.1	21	2	US-08-997-080-4	Sequence 4, Appl	330	5	2.1	31	1	US-08-451-568-7	Sequence 7, Appl
258	5	2.1	21	2	US-08-997-080-13	Sequence 13, Appl	331	5	2.1	31	1	US-08-451-566-7	Sequence 7, Appl
259	5	2.1	21	2	US-08-997-362-4	Sequence 4, Appl	332	5	2.1	31	2	US-08-244-951A-4	Sequence 4, Appl
260	5	2.1	21	2	US-08-997-362-13	Sequence 13, Appl	333	5	2.1	31	2	US-08-777-113-7	Sequence 7, Appl
261	5	2.1	21	3	US-08-873-970-4	Sequence 4, Appl	334	5	2.1	31	4	US-09-248-588-27	Sequence 27, Appl
262	5	2.1	21	3	US-08-873-970-13	Sequence 13, Appl	335	5	2.1	32	6	5208144-16	Patent No. 5208144
263	5	2.1	21	3	US-08-478-208-14	Sequence 14, Appl	336	5	2.1	33	2	US-08-244-951A-2	Sequence 2, Appl
264	5	2.1	21	4	US-09-095-855-4	Sequence 4, Appl	337	5	2.1	33	2	US-08-389-011-2	Sequence 2, Appl
265	5	2.1	21	4	US-09-095-855-13	Sequence 13, Appl	338	5	2.1	33	3	US-08-403-917A-2	Sequence 2, Appl
266	5	2.1	21	4	US-08-705-347A-4	Sequence 4, Appl	339	5	2.1	33	4	US-09-348-952A-2	Sequence 2, Appl
267	5	2.1	21	4	US-08-705-347A-13	Sequence 13, Appl	340	5	2.1	34	2	US-08-602-264A-10	Sequence 10, Appl
268	5	2.1	21	4	US-09-324-542-4	Sequence 4, Appl	341	5	2.1	34	2	US-08-372-887-11	Sequence 11, Appl
269	5	2.1	21	4	US-09-324-542-13	Sequence 13, Appl	342	5	2.1	34	3	US-08-461-018A-10	Sequence 10, Appl
270	5	2.1	23	1	US-07-656-566-1	Sequence 1, Appl	343	5	2.1	34	5	US-09-216-958-10	Sequence 5, Appl
271	5	2.1	23	2	US-08-244-951A-3	Sequence 3, Appl	344	5	2.1	35	1	US-07-621-670-3	Sequence 3, Appl
272	5	2.1	23	4	US-09-227-357-467	Sequence 467, App	345	5	2.1	35	1	US-08-418-893D-15	Sequence 15, Appl
273	5	2.1	24	2	US-08-765-179B-22	Sequence 22, Appl	346	5	2.1	35	2	US-08-244-951A-6	Sequence 6, Appl
274	5	2.1	24	2	US-08-749-852-49	Sequence 49, Appl	347	5	2.1	35	4	US-09-227-357-228	Sequence 228, App
275	5	2.1	24	2	US-08-455-968E-23	Sequence 23, Appl	348	5	2.1	36	4	US-08-789-933F-22	Sequence 22, Appl
276	5	2.1	26	1	US-08-484-635-94	Sequence 94, Appl	349	5	2.1	36	4	US-09-169-015-32	Sequence 32, Appl
277	5	2.1	26	2	US-08-484-631-94	Sequence 94, Appl	350	5	2.1	36	4	US-09-133-944-21	Sequence 21, Appl
278	5	2.1	26	2	US-08-139-609-12	Sequence 12, Appl	351	5	2.1	38	1	US-08-176-500-66	Sequence 66, Appl
279	5	2.1	26	2	US-08-837-570-94	Sequence 94, Appl	352	5	2.1	38	1	US-08-471-052A-66	Sequence 66, Appl
280	5	2.1	26	6	5510466-5	Patent No. 5510466	353	5	2.1	38	1	US-08-189-331-65	Sequence 65, Appl
281	5	2.1	27	2	US-08-244-951A-5	Sequence 5, Appl	354	5	2.1	38	2	US-08-471-839-66	Sequence 66, Appl
282	5	2.1	28	4	US-09-058-459-3	Sequence 3, Appl	355	5	2.1	38	2	US-08-471-800-66	Sequence 66, Appl
283	5	2.1	28	4	US-09-058-459-5	Sequence 5, Appl	356	5	2.1	38	2	US-08-471-068-66	Sequence 66, Appl
284	5	2.1	28	4	US-09-058-459-6	Sequence 6, Appl	357	5	2.1	40	3	US-09-037-524-4	Sequence 4, Appl
285	5	2.1	28	4	US-09-058-459-7	Sequence 7, Appl	358	5	2.1	40	6	5177197-36	Patent No. 5177197
286	5	2.1	28	4	US-09-058-459-10	Sequence 10, Appl	359	5	2.1	42	1	US-08-239-256-17	Sequence 17, Appl
287	5	2.1	28	4	US-09-058-459-11	Sequence 11, Appl	360	5	2.1	42	1	US-08-050-319B-42	Sequence 42, Appl
288	5	2.1	28	4	US-09-058-459-12	Sequence 12, Appl	361	5	2.1	42	2	US-08-465-982-42	Sequence 42, Appl
289	5	2.1	28	4	US-09-058-459-16	Sequence 16, Appl	362	5	2.1	43	1	US-08-050-319B-31	Sequence 31, Appl
290	5	2.1	28	4	US-09-058-459-17	Sequence 17, Appl	363	5	2.1	43	1	US-08-616-368A-33	Sequence 33, Appl
291	5	2.1	28	4	US-09-058-459-21	Sequence 21, Appl	364	5	2.1	43	2	US-08-465-982-11	Sequence 11, Appl
292	5	2.1	28	4	US-09-058-459-21	Sequence 21, Appl	365	5	2.1	43	4	US-09-054-298-33	Sequence 33, Appl
293	5	2.1	28	4	US-09-127-926-3	Sequence 3, Appl	366	5	2.1	43	4	US-08-818-655-33	Sequence 33, Appl
294	5	2.1	28	4	US-09-127-926-4	Sequence 4, Appl	367	5	2.1	44	2	US-08-559-492-13	Sequence 13, Appl
295	5	2.1	28	4	US-09-127-926-5	Sequence 5, Appl	368	5	2.1	45	4	US-08-881-450A-16	Sequence 16, Appl
296	5	2.1	28	4	US-09-127-926-6	Sequence 6, Appl	369	5	2.1	46	2	US-08-613-235-1	Sequence 1, Appl
297	5	2.1	28	4	US-09-127-926-10	Sequence 10, Appl	370	5	2.1	48	1	US-08-485-455D-65	Sequence 65, Appl
298	5	2.1	28	4	US-09-127-926-11	Sequence 11, Appl	371	5	2.1	48	2	US-08-637-750B-297	Sequence 297, App
299	5	2.1	28	4	US-09-127-926-12	Sequence 12, Appl	372	5	2.1	48	2	US-08-482-139C-65	Sequence 65, Appl
300	5	2.1	28	4	US-09-127-926-16	Sequence 16, Appl	373	5	2.1	48	2	US-08-484-211C-65	Sequence 65, Appl
301	5	2.1	28	4	US-09-127-926-17	Sequence 17, Appl	374	5	2.1	48	3	US-08-871-355A-297	Sequence 297, App
302	5	2.1	28	4	US-09-127-926-21	Sequence 21, Appl	375	5	2.1	48	3	US-08-906-769-65	Sequence 65, Appl
303	5	2.1	29	1	US-08-149-839B-5	Sequence 5, Appl	376	5	2.1	48	3	US-08-906-616-65	Sequence 65, Appl
304	5	2.1	29	1	US-08-451-568-5	Sequence 5, Appl	377	5	2.1	48	4	US-08-817-795-65	Sequence 65, Appl
305	5	2.1	29	1	US-08-451-566-5	Sequence 5, Appl	378	5	2.1	48	4	US-08-485-443B-65	Sequence 65, Appl
306	5	2.1	29	2	US-08-686-594-22	Sequence 22, Appl	379	5	2.1	48	4	US-08-639-075A-65	Sequence 65, Appl
307	5	2.1	29	2	US-08-505-486-81	Sequence 81, Appl	380	5	2.1	48	4	US-09-012-431-65	Sequence 65, Appl
308	5	2.1	29	3	US-08-777-113-5	Sequence 5, Appl	381	5	2.1	48	4	US-09-012-692-55	Sequence 65, Appl
309	5	2.1	29	3	US-08-801-028-81	Sequence 81, Appl	382	5	2.1	48	4	US-08-906-613-65	Sequence 65, Appl
310	5	2.1	29	3	US-09-340-154-81	Sequence 81, Appl	383	5	2.1	48	4	US-09-201-945-297	Sequence 297, App
311	5	2.1	29	5	PCT-US95-09338-81	Sequence 81, Appl	384	5	2.1	48	5	PCT-US95-14442A-65	Patent No. 517685-7
312	5	2.1	29	5	PCT-US95-09339-81	Sequence 81, Appl	385	5	2.1	48	6	517685-7	Patent No. 517685
313	5	2.1	30	1	US-08-149-839B-6	Sequence 6, Appl	386	5	2.1	51	6	US-08-870-518-23	Sequence 23, Appl
314	5	2.1	30	1	US-08-190-802A-246	Sequence 246, App	387	5	2.1	51	3	US-08-974-022-44	Sequence 44, Appl
315	5	2.1	30	1	US-08-451-568-6	Sequence 6, Appl	388	5	2.1	51	3	US-08-795-445A-44	Sequence 44, Appl
316	5	2.1	30	1	US-08-451-566-6	Sequence 6, Appl	389	5	2.1	51	4	US-08-795-447A-44	Sequence 44, Appl
317	5	2.1	30	2	US-08-372-887-12	Sequence 12, Appl	390	5	2.1	51	4	US-08-974-186-44	Sequence 44, Appl
318	5	2.1	30	2	US-08-505-486-82	Sequence 82, Appl	391	5	2.1	51	4	US-08-795-446B-44	Sequence 44, Appl
319	5	2.1	30	2	US-08-777-113-6	Sequence 6, Appl	392	5	2.1	51	4		

393	5	2.1	52	4	US-09-330-330-10	Sequence 10, Appl	466	5	2.1	100	1	US-08-681-812-6	Sequence 6, Appl1
394	5	2.1	52	4	US-09-227-357-575	Sequence 575, App	467	5	2.1	101	2	US-08-574-959A-5	Sequence 5, Appl1
395	5	2.1	57	1	US-08-241-853-3	Sequence 3, Appl1	468	5	2.1	101	4	US-09-357-014-5	Sequence 5, Appl1
396	5	2.1	57	2	US-08-850-917-3	Sequence 3, Appl1	469	5	2.1	102	2	US-08-820-754-7-4	Sequence 24, Appl
397	5	2.1	58	2	US-08-465-380-60	Sequence 60, Appl	470	5	2.1	102	3	US-08-956-652-24	Sequence 24, Appl
398	5	2.1	58	2	US-08-486-397-60	Sequence 60, Appl	471	5	2.1	102	3	US-08-956-869-24	Sequence 24, Appl
399	5	2.1	58	2	US-08-486-399-60	Sequence 60, Appl	472	5	2.1	102	3	US-08-948-547-24	Sequence 24, Appl
400	5	2.1	58	2	US-08-461-965-60	Sequence 60, Appl	473	5	2.1	103	2	US-08-853-659A-55	Sequence 55, Appl
401	5	2.1	58	2	US-08-634-641-60	Sequence 60, Appl	474	5	2.1	105	3	US-08-867-381A-4	Sequence 4, Appl1
402	5	2.1	58	3	US-09-249-471-60	Sequence 60, Appl	475	5	2.1	105	4	US-09-521-144-4	Sequence 4, Appl1
403	5	2.1	58	3	US-09-249-472-60	Sequence 60, Appl	476	5	2.1	106	2	US-08-440-354-2	Sequence 2, Appl1
404	5	2.1	58	3	US-09-249-451-60	Sequence 60, Appl	477	5	2.1	106	2	US-08-463-087-2	Sequence 2, Appl1
405	5	2.1	58	3	US-08-809-455-60	Sequence 60, Appl	478	5	2.1	106	3	US-08-776-404B-1	Sequence 1, Appl1
406	5	2.1	58	3	US-09-249-461-60	Sequence 60, Appl	479	5	2.1	108	4	US-09-199-637A-227	Sequence 227, App
407	5	2.1	58	3	US-09-249-448-60	Sequence 60, Appl	480	5	2.1	108	5	PCT-US94-01840-6	Sequence 6, Appl1
408	5	2.1	58	4	US-09-227-357-297	Sequence 297, App	481	5	2.1	109	2	US-08-672-345C-3	Sequence 3, Appl1
409	5	2.1	60	2	US-08-968-542C-13	Sequence 13, Appl	482	5	2.1	109	2	US-08-672-345C-93	Sequence 93, Appl
410	5	2.1	62	1	US-07-662-005A-14	Sequence 14, Appl	483	5	2.1	109	4	US-09-214-095D-3	Sequence 3, Appl1
411	5	2.1	62	3	US-08-904-446A-17	Sequence 17, Appl	484	5	2.1	109	4	US-09-214-095D-121	Sequence 121, App
412	5	2.1	67	1	US-08-435-040-3	Sequence 3, Appl1	485	5	2.1	110	4	US-08-122-546-14	Sequence 14, Appl
413	5	2.1	67	2	US-08-244-951A-1	Sequence 1, Appl1	486	5	2.1	110	2	US-08-764-938-14	Sequence 14, Appl
414	5	2.1	67	2	US-08-389-011-1	Sequence 1, Appl1	487	5	2.1	110	3	US-09-131-052-14	Sequence 14, Appl
415	5	2.1	67	3	US-08-403-917A-1	Sequence 1, Appl1	488	5	2.1	110	4	US-09-131-053A-14	Sequence 14, Appl
416	5	2.1	67	4	US-09-020-216-3	Sequence 3, Appl1	489	5	2.1	111	4	US-09-091-725-39	Sequence 39, Appl
417	5	2.1	67	4	US-09-348-952A-1	Sequence 1, Appl1	490	5	2.1	112	1	US-07-754-918A-12	Sequence 12, Appl
418	5	2.1	68	4	US-08-936-165A-434	Sequence 434, App	491	5	2.1	112	3	US-08-666-360-1	Sequence 1, Appl1
419	5	2.1	71	1	US-07-704-288C-15	Sequence 15, Appl	492	5	2.1	112	4	US-09-157-370-6	Sequence 6, Appl1
420	5	2.1	71	1	US-08-379-259-15	Sequence 15, Appl	493	5	2.1	113	4	US-09-056-556-230	Sequence 230, App
421	5	2.1	72	4	US-09-188-930-182	Sequence 182, App	494	5	2.1	114	4	US-09-055-113-3	Sequence 3, Appl1
422	5	2.1	74	4	US-08-866-545-1	Sequence 1, Appl1	495	5	2.1	115	2	US-08-580-988A-25	Sequence 25, Appl
423	5	2.1	75	3	US-09-042-012-8	Sequence 8, Appl1	496	5	2.1	115	4	US-09-374-135-3	Sequence 3, Appl1
424	5	2.1	75	4	US-09-305-086-2	Sequence 2, Appl1	497	5	2.1	115	6	US-09-374-135-3	Sequence 3, Appl1
425	5	2.1	75	4	US-09-457-324-8	Sequence 8, Appl1	498	5	2.1	116	3	US-08-542-363-23	Sequence 23, Appl
426	5	2.1	76	2	US-08-465-380-29	Sequence 29, Appl	499	5	2.1	116	3	US-08-621-018B-4	Sequence 22, Appl1
427	5	2.1	76	2	US-08-480-478-58	Sequence 58, Appl	500	5	2.1	116	4	US-09-100-089-23	Sequence 23, Appl
428	5	2.1	76	2	US-08-486-397-29	Sequence 29, Appl	501	5	2.1	118	4	US-08-300-386A-64	Sequence 64, Appl
429	5	2.1	76	2	US-08-486-399-29	Sequence 29, Appl	502	5	2.1	118	3	US-08-931-645-64	Sequence 64, Appl
430	5	2.1	76	2	US-08-461-965-29	Sequence 29, Appl	503	5	2.1	118	5	US-08-881-771A-1	Sequence 1, Appl1
431	5	2.1	76	2	US-08-326-110A-58	Sequence 58, Appl	504	5	2.1	118	3	PCT-US95-11235-64	Sequence 64, Appl
432	5	2.1	76	2	US-08-634-641-29	Sequence 29, Appl	505	5	2.1	119	1	US-08-497-025-6	Sequence 6, Appl1
433	5	2.1	76	3	US-09-249-471-29	Sequence 29, Appl	506	5	2.1	119	1	US-08-256-077-6	Sequence 4, Appl1
434	5	2.1	76	3	US-09-249-472-29	Sequence 29, Appl	507	5	2.1	119	1	US-08-466-127-4	Sequence 4, Appl1
435	5	2.1	76	3	US-09-249-451-29	Sequence 29, Appl	508	5	2.1	120	1	US-08-047-033-2	Sequence 2, Appl1
436	5	2.1	76	3	US-08-809-455-29	Sequence 29, Appl	509	5	2.1	120	2	US-08-869-733-3	Sequence 3, Appl1
437	5	2.1	76	3	US-09-249-461-29	Sequence 29, Appl	510	5	2.1	121	1	US-08-047-033-1	Sequence 1, Appl1
438	5	2.1	76	3	US-09-249-448-29	Sequence 29, Appl	511	5	2.1	124	1	US-08-050-319B-4	Sequence 4, Appl1
439	5	2.1	77	4	US-09-025-151-20	Sequence 20, Appl	512	5	2.1	124	2	US-08-465-982-4	Sequence 4, Appl1
440	5	2.1	80	3	US-09-040-285A-3	Sequence 3, Appl1	513	5	2.1	128	4	US-08-348-548-2	Sequence 2, Appl1
441	5	2.1	81	2	US-08-332-362A-86	Sequence 86, Appl	514	5	2.1	128	5	PCT-US95-15716-2	Sequence 2, Appl1
442	5	2.1	84	2	US-08-332-562A-89	Sequence 89, Appl	515	5	2.1	129	4	US-09-476-482-8	Sequence 8, Appl1
443	5	2.1	86	1	US-08-149-839B-14	Sequence 14, Appl	516	5	2.1	129	6	5428135-6	Patent No. 5428135
444	5	2.1	86	1	US-08-451-568-14	Sequence 14, Appl	517	5	2.1	134	1	US-08-246-242-5	Sequence 5, Appl1
445	5	2.1	86	1	US-08-451-566-14	Sequence 14, Appl	518	5	2.1	134	2	US-08-684-101-2	Sequence 2, Appl1
446	5	2.1	86	2	US-08-777-113-14	Sequence 14, Appl	519	5	2.1	138	2	US-08-771-602D-45	Sequence 45, Appl
447	5	2.1	89	1	US-08-241-853-32	Sequence 32, Appl	520	5	2.1	138	4	US-09-205-814-2	Sequence 2, Appl1
448	5	2.1	89	2	US-08-850-917-32	Sequence 32, Appl	521	5	2.1	146	4	US-07-998-003A-91	Sequence 91, Appl
449	5	2.1	89	1	US-08-633-682-5	Sequence 5, Appl1	522	5	2.1	146	1	US-08-453-274B-91	Sequence 91, Appl
450	5	2.1	91	3	US-08-936-772-5	Sequence 5, Appl1	523	5	2.1	146	1	US-08-453-695A-91	Sequence 91, Appl
451	5	2.1	91	4	US-09-395-918-5	Sequence 5, Appl1	524	5	2.1	146	1	US-08-268-161A-91	Sequence 91, Appl
452	5	2.1	91	6	5196194-19	Patent No. 5196194	525	5	2.1	146	2	US-08-453-702A-91	Sequence 91, Appl
453	5	2.1	92	1	US-08-725-531-3	Sequence 3, Appl1	526	5	2.1	146	4	US-09-099-639-91	Sequence 91, Appl
454	5	2.1	92	2	US-08-738-127-1	Sequence 1, Appl1	527	5	2.1	146	5	PCT-US93-12588-91	Sequence 91, Appl
455	5	2.1	92	2	US-08-738-127-3	Sequence 3, Appl1	528	5	2.1	146	5	PCT-US93-08071-91	Sequence 91, Appl
456	5	2.1	92	2	US-09-213-392-3	Sequence 3, Appl1	529	5	2.1	148	1	US-08-256-077-2	Sequence 2, Appl1
457	5	2.1	92	2	US-09-083-661-3	Sequence 3, Appl1	530	5	2.1	148	1	US-08-466-127-2	Sequence 2, Appl1
458	5	2.1	92	4	US-09-247-155-120	Sequence 120, App	531	5	2.1	148	3	US-08-329-799-35	Sequence 35, Appl
459	5	2.1	94	2	US-08-717-169-8	Sequence 8, Appl1	532	5	2.1	149	2	US-08-815-175-3	Sequence 3, Appl1
460	5	2.1	96	1	US-08-565-386-33	Sequence 23, Appl	533	5	2.1	152	1	US-08-602-100A-16	Sequence 16, Appl
461	5	2.1	97	4	US-09-227-357-465	Sequence 465, App	534	5	2.1	152	1	US-08-680-726A-16	Sequence 16, Appl
462	5	2.1	98	1	US-08-308-086-4	Sequence 4, Appl1	535	5	2.1	152	4	US-09-092-409-16	Sequence 16, Appl
463	5	2.1	98	4	US-08-479-078-5	Sequence 5, Appl1	536	5	2.1	153	2	US-08-219-337B-4	Sequence 4, Appl1
464	5	2.1	98	4	US-08-975-040-22	Sequence 22, Appl	537	5	2.1	153	3	US-08-477-347-12	Sequence 12, Appl
465	5	2.1	99	1	US-08-202-389-38	Sequence 38, Appl	538	5	2.1	153	4	US-08-476-862-3	Sequence 3, Appl1

539	5	2.1	153	4	US-08-468-560C-4	Sequence 4, Appl	612	5	2.1	190	3	US-09-332-934-12	Sequence 12, Appl
540	5	2.1	154	2	US-08-232-087A-10	Sequence 10, Appl	613	5	2.1	190	4	US-08-858-207A-505	Sequence 505, App
541	5	2.1	156	1	US-08-074-121-5	Sequence 5, Appl	614	5	2.1	191	4	US-09-011-961-1	Sequence 1, Appl
542	5	2.1	156	2	US-08-162-402B-20	Sequence 20, Appl	615	5	2.1	192	2	US-08-469-537A-37	Sequence 37, Appl
543	5	2.1	156	5	PCT-US94-06447-5	Sequence 5, Appl	616	5	2.1	192	2	US-08-469-537A-37	Sequence 37, Appl
544	5	2.1	157	1	US-08-050-319B-50	Sequence 50, Appl	617	5	2.1	193	1	US-08-616-368A-8	Sequence 8, Appl
545	5	2.1	157	2	US-08-465-982-50	Sequence 50, Appl	618	5	2.1	193	1	US-08-616-368A-8	Sequence 8, Appl
546	5	2.1	158	1	US-08-050-319B-54	Sequence 54, Appl	619	5	2.1	193	1	US-08-616-368A-13	Sequence 13, Appl
547	5	2.1	158	2	US-08-465-982-54	Sequence 54, Appl	620	5	2.1	193	2	US-08-739-485A-9	Sequence 9, Appl
548	5	2.1	159	2	US-08-232-087A-11	Sequence 11, Appl	621	5	2.1	193	2	US-08-661-549-4	Sequence 4, Appl
549	5	2.1	159	2	US-08-219-237B-6	Sequence 6, Appl	622	5	2.1	193	2	US-08-765-536-1	Sequence 1, Appl
550	5	2.1	159	4	US-08-477-347-15	Sequence 15, Appl	623	5	2.1	193	3	US-08-842-976-3	Sequence 3, Appl
551	5	2.1	159	4	US-08-476-862-6	Sequence 6, Appl	624	5	2.1	193	3	US-08-842-976-4	Sequence 4, Appl
552	5	2.1	159	4	US-08-468-560C-6	Sequence 6, Appl	625	5	2.1	193	3	US-08-842-976-4	Sequence 4, Appl
553	5	2.1	161	4	US-09-336-394-2	Sequence 2, Appl	626	5	2.1	193	3	US-09-213-397-3	Sequence 3, Appl
554	5	2.1	163	1	US-08-475-213-5	Sequence 5, Appl	627	5	2.1	193	3	US-09-416-489-3	Sequence 3, Appl
555	5	2.1	163	5	PCT-US93-11703-1	Sequence 1, Appl	628	5	2.1	193	3	US-09-416-489-4	Sequence 4, Appl
556	5	2.1	165	2	US-08-955-138-8	Sequence 8, Appl	629	5	2.1	193	4	US-09-054-298-1	Sequence 1, Appl
557	5	2.1	167	1	US-08-050-319B-2	Sequence 2, Appl	630	5	2.1	193	4	US-09-054-298-8	Sequence 8, Appl
558	5	2.1	167	1	US-08-050-319B-57	Sequence 57, Appl	631	5	2.1	193	4	US-09-054-298-13	Sequence 13, Appl
559	5	2.1	167	2	US-08-465-982-2	Sequence 2, Appl	632	5	2.1	193	4	US-08-818-655-1	Sequence 1, Appl
560	5	2.1	167	2	US-08-465-982-57	Sequence 57, Appl	633	5	2.1	193	4	US-08-818-655-8	Sequence 8, Appl
561	5	2.1	167	4	US-09-062-440-9	Sequence 9, Appl	634	5	2.1	193	4	US-08-818-655-13	Sequence 13, Appl
562	5	2.1	168	3	US-09-052-830B-2	Sequence 2, Appl	635	5	2.1	193	5	PCT-US95-08401-1	Sequence 1, Appl
563	5	2.1	171	5	PCT-US95-04910-12	Sequence 12, Appl	636	5	2.1	194	1	US-08-117-083-21	Sequence 21, Appl
564	5	2.1	172	2	US-08-812-645-1	Sequence 1, Appl	637	5	2.1	194	4	US-09-364-083-2	Sequence 2, Appl
565	5	2.1	172	2	US-08-756-387B-13	Sequence 13, Appl	638	5	2.1	195	4	US-09-011-961-2	Sequence 2, Appl
566	5	2.1	172	4	US-09-285-873-13	Sequence 13, Appl	639	5	2.1	196	2	US-08-484-126-7	Sequence 7, Appl
567	5	2.1	174	4	US-09-011-961-3	Sequence 3, Appl	640	5	2.1	197	2	US-07-914-284A-8	Sequence 8, Appl
568	5	2.1	174	4	US-09-011-961-5	Sequence 5, Appl	641	5	2.1	197	2	US-08-505-606-1	Sequence 1, Appl
569	5	2.1	174	4	US-08-858-207A-424	Sequence 424, App	642	5	2.1	197	2	US-08-756-387B-11	Sequence 11, Appl
570	5	2.1	175	1	US-07-783-705A-6	Sequence 6, Appl	643	5	2.1	197	3	US-08-756-387B-11	Sequence 2, Appl
571	5	2.1	175	1	US-08-078-683A-34	Sequence 34, Appl	644	5	2.1	197	4	US-08-788-954-2	Sequence 2, Appl
572	5	2.1	175	1	US-08-624-125-7	Sequence 7, Appl	645	5	2.1	198	4	US-09-285-873-11	Sequence 11, Appl
573	5	2.1	178	3	US-08-791-522-1	Sequence 1, Appl	646	5	2.1	198	4	US-08-842-906B-2	Sequence 2, Appl
574	5	2.1	178	3	US-09-314-777-1	Sequence 1, Appl	647	5	2.1	198	4	US-08-838-973B-2	Sequence 2, Appl
575	5	2.1	179	1	US-08-193-977-6	Sequence 6, Appl	648	5	2.1	199	1	US-08-838-973B-2	Sequence 2, Appl
576	5	2.1	179	2	US-08-469-537A-84	Sequence 84, Appl	649	5	2.1	199	2	US-08-050-319B-48	Sequence 48, Appl
577	5	2.1	179	2	US-08-993-328-33	Sequence 33, Appl	650	5	2.1	200	6	US-08-465-982-48	Sequence 48, Appl
578	5	2.1	179	3	US-08-867-381A-52	Sequence 52, Appl	651	5	2.1	200	6	5189147-10	Patent No. 5189147
579	5	2.1	179	4	US-09-521-144-52	Sequence 52, Appl	652	5	2.1	202	2	US-08-948-616-11	Sequence 11, Appl
580	5	2.1	180	2	US-08-624-650-1	Sequence 1, Appl	653	5	2.1	202	2	US-09-193-510-11	Sequence 11, Appl
581	5	2.1	181	1	US-08-185-432-6	Sequence 6, Appl	654	5	2.1	204	1	US-08-247-946A-4	Sequence 4, Appl
582	5	2.1	181	1	US-08-353-476-74	Sequence 74, Appl	655	5	2.1	204	2	US-08-516-801-3	Sequence 3, Appl
583	5	2.1	181	4	US-09-087-465-16	Sequence 16, Appl	656	5	2.1	204	3	US-09-078-917-14	Sequence 14, Appl
584	5	2.1	181	4	US-09-011-961-4	Sequence 4, Appl	657	5	2.1	204	4	US-08-248-355-3	Sequence 3, Appl
585	5	2.1	182	1	US-08-308-883-2	Sequence 2, Appl	658	5	2.1	204	5	PCT-US95-06420-4	Sequence 4, Appl
586	5	2.1	182	1	US-08-720-163-2	Sequence 2, Appl	659	5	2.1	204	5	PCT-US95-06683-3	Sequence 3, Appl
587	5	2.1	182	2	US-08-353-476-93	Sequence 93, Appl	660	5	2.1	205	2	US-08-861-549-1	Sequence 1, Appl
588	5	2.1	182	4	US-08-256-799-2	Sequence 2, Appl	661	5	2.1	205	2	US-08-861-549-3	Sequence 3, Appl
589	5	2.1	182	4	US-08-462-437-2	Sequence 2, Appl	662	5	2.1	205	4	US-07-396-357-2	Sequence 2, Appl
590	5	2.1	182	4	US-08-462-437-2	Sequence 2, Appl	663	5	2.1	207	1	US-07-656-566-2	Sequence 2, Appl
591	5	2.1	185	1	US-08-278-091-14	Sequence 14, Appl	664	5	2.1	207	3	US-08-957-302A-10	Sequence 10, Appl
592	5	2.1	185	1	US-08-483-859-14	Sequence 14, Appl	665	5	2.1	207	4	US-09-542-403-10	Sequence 10, Appl
593	5	2.1	185	1	US-08-472-173-14	Sequence 14, Appl	666	5	2.1	207	4	US-09-415-522-2	Sequence 2, Appl
594	5	2.1	185	1	US-08-487-167-14	Sequence 14, Appl	667	5	2.1	208	4	US-08-934-627B-2	Sequence 2, Appl
595	5	2.1	185	2	US-08-482-816-14	Sequence 14, Appl	668	5	2.1	209	3	US-09-040-285A-4	Sequence 4, Appl
596	5	2.1	185	2	US-08-296-149-14	Sequence 14, Appl	669	5	2.1	210	4	US-08-849-764C-4	Sequence 4, Appl
597	5	2.1	185	2	US-08-106-465A-14	Sequence 14, Appl	670	5	2.1	210	4	US-09-171-161-14	Sequence 14, Appl
598	5	2.1	185	2	US-08-801-499-14	Sequence 14, Appl	671	5	2.1	211	1	US-08-588-163-4	Sequence 4, Appl
599	5	2.1	185	2	US-08-615-271-14	Sequence 14, Appl	672	5	2.1	211	1	US-08-588-163-4	Sequence 4, Appl
600	5	2.1	185	3	US-09-074-660-14	Sequence 14, Appl	673	5	2.1	211	2	US-09-111-070-4	Sequence 4, Appl
601	5	2.1	185	3	US-09-074-659-14	Sequence 14, Appl	674	5	2.1	214	3	US-08-846-790A-1	Sequence 1, Appl
602	5	2.1	185	3	US-09-106-468-14	Sequence 14, Appl	675	5	2.1	215	4	US-08-935-333-1	Sequence 1, Appl
603	5	2.1	185	4	US-09-106-465A-14	Sequence 14, Appl	676	5	2.1	215	4	US-09-198-723A-46	Sequence 46, Appl
604	5	2.1	185	4	US-09-106-467-14	Sequence 14, Appl	677	5	2.1	215	4	US-09-198-723A-50	Sequence 50, Appl
605	5	2.1	188	6	5514590-10	Patent No. 5514590	678	5	2.1	215	4	US-09-198-723A-53	Sequence 53, Appl
606	5	2.1	188	2	US-08-160-524A-5	Sequence 5, Appl	679	5	2.1	216	4	US-09-198-723A-57	Sequence 57, Appl
607	5	2.1	188	3	US-08-722-126A-5	Sequence 5, Appl	680	5	2.1	216	4	US-09-198-723A-1	Sequence 1, Appl
608	5	2.1	188	3	US-09-332-934-2	Sequence 2, Appl	681	5	2.1	216	4	US-09-198-723A-2	Sequence 2, Appl
609	5	2.1	189	5	PCT-US95-04258-5	Sequence 5, Appl	682	5	2.1	216	4	US-09-198-723A-3	Sequence 3, Appl
610	5	2.1	189	6	5171685-2	Patent No. 5171685	683	5	2.1	216	4	US-09-198-723A-4	Sequence 4, Appl
611	5	2.1	189	6	5518916-2	Patent No. 5518916	684	5	2.1	216	4	US-09-198-723A-5	Sequence 5, Appl
												US-09-198-723A-6	Sequence 6, Appl
												US-09-198-723A-7	Sequence 7, Appl

685	5	2.1	216	4	US-09-198-723A-8	Sequence 8, Appl1	758	5	2.1	238	6	5405943-2	Patent No. 5405943
686	5	2.1	216	4	US-09-198-723A-9	Sequence 9, Appl1	759	5	2.1	240	1	US-08-261-822A-82	Sequence 82, Appl
687	5	2.1	216	4	US-09-198-723A-10	Sequence 10, Appl1	760	5	2.1	240	5	PCT-US95-0744A-82	Sequence 82, Appl
688	5	2.1	218	1	US-07-816-679A-3	Sequence 3, Appl1	761	5	2.1	245	2	US-08-874-138-2	Sequence 2, Appl1
689	5	2.1	218	1	US-08-247-946A-3	Sequence 3, Appl1	762	5	2.1	245	4	US-08-879-941-4	Sequence 4, Appl1
690	5	2.1	218	5	PCT-US92-11270-3	Sequence 3, Appl1	763	5	2.1	245	4	US-07-747-116-4	Sequence 4, Appl1
691	5	2.1	218	5	PCT-US95-06420-3	Sequence 3, Appl1	764	5	2.1	246	3	US-08-906-769-127	Sequence 127, App
692	5	2.1	219	2	US-08-625-317-2	Sequence 23, Appl1	765	5	2.1	246	3	US-08-906-616-127	Sequence 127, App
693	5	2.1	219	3	US-08-479-733A-23	Sequence 23, Appl1	766	5	2.1	246	4	US-08-639-075A-127	Sequence 127, App
694	5	2.1	219	3	US-08-487-427-23	Sequence 23, Appl1	767	5	2.1	246	4	US-09-012-431-127	Sequence 127, App
695	5	2.1	219	3	US-08-479-727A-23	Sequence 23, Appl1	768	5	2.1	246	4	US-09-012-692-127	Sequence 127, App
696	5	2.1	219	3	US-08-482-359A-23	Sequence 23, Appl1	769	5	2.1	246	4	US-08-908-613-127	Sequence 127, App
697	5	2.1	219	4	US-09-009-217-8	Sequence 8, Appl1	770	5	2.1	246	4	US-09-336-093-5	Sequence 5, Appl1
698	5	2.1	219	4	US-09-009-217-9	Sequence 9, Appl1	771	5	2.1	247	2	US-08-465-980-3	Sequence 3, Appl1
699	5	2.1	219	4	US-09-009-656-8	Sequence 9, Appl1	772	5	2.1	247	2	US-09-053-303-3	Sequence 3, Appl1
700	5	2.1	219	4	US-09-009-656-9	Sequence 9, Appl1	773	5	2.1	247	3	US-09-129-888-2	Sequence 2, Appl1
701	5	2.1	219	4	US-09-204-841-2	Sequence 23, Appl1	774	5	2.1	247	5	PCT-US95-07093-3	Sequence 3, Appl1
702	5	2.1	219	5	PCT-US95-07439-23	Sequence 23, Appl1	775	5	2.1	248	2	US-08-755-559-1	Sequence 1, Appl1
703	5	2.1	220	4	US-09-009-217-1	Sequence 1, Appl1	776	5	2.1	248	3	US-09-210-474-1	Sequence 1, Appl1
704	5	2.1	220	4	US-09-009-217-4	Sequence 4, Appl1	777	5	2.1	248	4	US-09-539-774-1	Sequence 1, Appl1
705	5	2.1	220	4	US-09-009-217-5	Sequence 5, Appl1	778	5	2.1	248	6	5169835-15	Patent No. 5169835
706	5	2.1	220	4	US-09-009-656-1	Sequence 1, Appl1	779	5	2.1	249	1	US-08-597-236-5	Sequence 5, Appl1
707	5	2.1	220	4	US-09-009-656-4	Sequence 4, Appl1	780	5	2.1	249	1	US-08-746-682A-5	Sequence 28, Appl
708	5	2.1	220	4	US-09-009-656-5	Sequence 5, Appl1	781	5	2.1	249	2	US-08-665-992-28	Sequence 28, Appl
709	5	2.1	220	4	US-09-052-089A-4	Sequence 4, Appl1	782	5	2.1	249	2	US-09-144-925-28	Sequence 6, Appl1
710	5	2.1	222	1	US-07-969-931-9	Sequence 9, Appl1	783	5	2.1	249	3	US-09-189-760-6	Sequence 6, Appl1
711	5	2.1	222	1	US-07-855-417A-9	Sequence 9, Appl1	784	5	2.1	249	3	US-09-188-811-6	Sequence 6, Appl1
712	5	2.1	222	2	US-08-491-204A-18	Sequence 18, Appl1	785	5	2.1	249	4	US-09-514-422-6	Sequence 6, Appl1
713	5	2.1	223	4	US-08-121-436A-2	Sequence 2, Appl1	786	5	2.1	251	1	US-07-882-202A-2	Sequence 2, Appl1
714	5	2.1	223	4	US-09-254-733-7	Sequence 7, Appl1	787	5	2.1	251	1	US-07-693-682B-4	Sequence 4, Appl1
715	5	2.1	224	1	US-08-707-793A-6	Sequence 6, Appl1	788	5	2.1	251	1	US-08-021-615A-2	Sequence 2, Appl1
716	5	2.1	224	1	US-08-707-792A-6	Sequence 6, Appl1	789	5	2.1	251	1	US-08-321-777-2	Sequence 2, Appl1
717	5	2.1	224	3	US-08-974-022-50	Sequence 50, Appl1	790	5	2.1	251	1	US-08-463-931-6	Sequence 6, Appl1
718	5	2.1	224	4	US-08-795-445A-50	Sequence 50, Appl1	791	5	2.1	251	1	US-08-464-237A-6	Sequence 4, Appl1
719	5	2.1	224	4	US-08-795-447A-50	Sequence 50, Appl1	792	5	2.1	251	5	PCT-US92-02898A-4	Sequence 4, Appl1
720	5	2.1	224	4	US-08-974-186-50	Sequence 50, Appl1	793	5	2.1	251	5	PCT-US93-04493-2	Sequence 2, Appl1
721	5	2.1	224	4	US-08-795-446B-50	Sequence 50, Appl1	794	5	2.1	253	4	US-08-963-035A-30	Sequence 30, Appl1
722	5	2.1	224	4	US-09-199-637A-305	Sequence 305, App	795	5	2.1	254	2	US-08-475-427-1	Sequence 1, Appl1
723	5	2.1	225	4	US-08-944-483-32	Sequence 32, Appl1	796	5	2.1	254	2	US-07-842-165-1	Sequence 1, Appl1
724	5	2.1	228	2	US-08-997-080-147	Sequence 147, App	797	5	2.1	254	4	US-08-448-398-3	Sequence 3, Appl1
725	5	2.1	228	2	US-08-997-362-147	Sequence 147, App	798	5	2.1	254	4	US-09-199-637A-325	Sequence 325, App
726	5	2.1	228	4	US-09-095-855-147	Sequence 147, App	799	5	2.1	256	1	US-07-959-369-1	Sequence 1, Appl1
727	5	2.1	228	3	US-09-324-542-147	Sequence 147, App	800	5	2.1	256	4	US-08-804-166-2	Sequence 2, Appl1
728	5	2.1	229	3	US-09-040-285A-7	Sequence 7, Appl1	801	5	2.1	256	4	US-08-910-991-2	Sequence 2, Appl1
729	5	2.1	230	2	US-08-471-371-2	Sequence 2, Appl1	802	5	2.1	257	2	US-07-869-933-11	Sequence 11, Appl
730	5	2.1	231	1	US-07-656-566-3	Sequence 3, Appl1	803	5	2.1	257	2	US-08-756-387B-2	Sequence 2, Appl1
731	5	2.1	231	2	US-08-902-655A-6	Sequence 6, Appl1	804	5	2.1	257	4	US-09-103-663-11	Sequence 11, Appl
732	5	2.1	231	2	US-08-997-080-152	Sequence 152, App	805	5	2.1	257	4	US-09-285-873-2	Sequence 2, Appl1
733	5	2.1	231	3	US-08-997-362-152	Sequence 152, App	806	5	2.1	258	1	US-07-959-369-10	Sequence 10, Appl
734	5	2.1	231	3	US-08-771-098-2	Sequence 2, Appl1	807	5	2.1	258	4	US-08-961-083-90	Sequence 90, Appl
735	5	2.1	231	3	US-09-022-875-4	Sequence 4, Appl1	808	5	2.1	259	3	US-08-476-509B-29	Sequence 29, Appl
736	5	2.1	231	4	US-09-095-855-152	Sequence 152, App	809	5	2.1	260	3	US-08-857-213-3	Sequence 3, Appl1
737	5	2.1	231	4	US-09-354-040-2	Sequence 2, Appl1	810	5	2.1	261	2	US-08-879-561-1	Sequence 1, Appl1
738	5	2.1	231	1	US-07-869-933-13	Sequence 13, Appl	811	5	2.1	261	4	US-08-163-019A-2	Sequence 2, Appl1
739	5	2.1	232	2	US-08-456-670B-39	Sequence 39, Appl	812	5	2.1	261	4	US-09-414-436-3	Sequence 3, Appl1
740	5	2.1	232	2	US-08-456-670B-39	Sequence 39, Appl	813	5	2.1	261	5	PCT-US94-14073-2	Sequence 2, Appl1
741	5	2.1	232	2	US-08-756-387B-6	Sequence 6, Appl1	814	5	2.1	262	1	US-08-106-981-6	Sequence 6, Appl1
742	5	2.1	232	4	US-09-103-663-13	Sequence 13, Appl	815	5	2.1	262	4	US-08-948-265-2	Sequence 2, Appl1
743	5	2.1	232	4	US-09-285-873-6	Sequence 6, Appl1	816	5	2.1	262	4	US-08-948-265-4	Sequence 4, Appl1
744	5	2.1	233	4	US-08-607-269-23	Sequence 23, Appl	817	5	2.1	263	1	US-07-662-005A-12	Sequence 12, Appl
745	5	2.1	233	5	PCT-US95-04600-23	Sequence 23, Appl	818	5	2.1	263	1	US-08-416-872-2	Sequence 2, Appl1
746	5	2.1	234	4	US-09-009-217-2	Sequence 2, Appl1	819	5	2.1	263	4	US-09-035-241-12	Sequence 12, Appl
747	5	2.1	234	4	US-09-009-217-3	Sequence 3, Appl1	820	5	2.1	263	4	US-09-009-217-12	Sequence 12, Appl
748	5	2.1	234	4	US-09-009-656-2	Sequence 2, Appl1	821	5	2.1	263	4	US-09-009-656-12	Sequence 12, Appl
749	5	2.1	234	4	US-09-009-656-3	Sequence 3, Appl1	822	5	2.1	263	5	PCT-US94-06197-2	Sequence 2, Appl1
750	5	2.1	235	4	US-09-009-217-6	Sequence 6, Appl1	823	5	2.1	264	2	US-08-460-309-10	Sequence 10, Appl
751	5	2.1	235	4	US-09-009-656-6	Sequence 6, Appl1	824	5	2.1	264	2	US-08-125-077-10	Sequence 10, Appl
752	5	2.1	236	1	US-08-167-035-39	Sequence 39, Appl	825	5	2.1	266	1	US-07-959-369-2	Sequence 2, Appl1
753	5	2.1	236	1	US-08-208-887A-39	Sequence 39, Appl	826	5	2.1	266	1	US-08-443-568B-16	Sequence 16, Appl
754	5	2.1	236	2	US-08-539-005-39	Sequence 39, Appl	827	5	2.1	266	5	PCT-US94-06997-16	Sequence 16, Appl
755	5	2.1	236	4	US-09-009-217-7	Sequence 7, Appl1	828	5	2.1	267	3	US-07-706-872-3	Sequence 3, Appl1
756	5	2.1	236	4	US-09-009-656-7	Sequence 7, Appl1	829	5	2.1	267	3	US-08-301-162-16	Sequence 16, Appl
757	5	2.1	238	2	US-08-483-101-2	Sequence 2, Appl1	830	5	2.1	267	3	US-08-867-381A-6	Sequence 6, Appl1



831	5	2.1	267	4	US-09-521-144-6	Sequence 6, Appli	904	5	2.1	297	2	US-08-780-749A-3	Sequence 3, Appli
832	5	2.1	267	5	US-09-461-240-16	Sequence 16, Appl	905	5	2.1	297	3	US-09-105-298-4	Sequence 4, Appli
833	5	2.1	268	6	5320958-6	Patent No. 5320958	906	5	2.1	297	3	US-08-706-281A-8	Sequence 8, Appli
834	5	2.1	269	2	US-08-428-257A-72	Sequence 72, Appl	907	5	2.1	297	3	US-08-629-335B-4	Sequence 4, Appli
835	5	2.1	269	2	US-08-481-988-3	Sequence 3, Appli	908	5	2.1	297	4	US-09-262-635A-6	Sequence 6, Appli
836	5	2.1	270	2	US-09-031-485-7	Sequence 7, Appli	909	5	2.1	297	4	US-09-201-746-7	Sequence 7, Appli
837	5	2.1	270	2	US-08-847-429A-7	Sequence 7, Appli	910	5	2.1	297	4	US-09-097-231-8	Sequence 8, Appli
838	5	2.1	270	3	US-09-065-474-7	Sequence 7, Appli	911	5	2.1	297	4	US-08-870-511-3	Sequence 3, Appli
839	5	2.1	270	4	US-09-013-881-6	Sequence 6, Appli	912	5	2.1	299	4	US-08-961-083-24	Sequence 24, Appl
840	5	2.1	270	4	US-08-983-035A-32	Sequence 32, Appli	913	5	2.1	299	6	5514590-4	Patent No. 5514590
841	5	2.1	274	1	US-07-959-369-12	Sequence 12, Appl	914	5	2.1	300	3	US-09-064-703-10	Sequence 10, Appl
842	5	2.1	274	2	US-08-836-854-3	Sequence 3, Appli	915	5	2.1	300	4	US-09-277-078-2	Sequence 2, Appli
843	5	2.1	277	1	US-07-959-369-3	Sequence 3, Appli	916	5	2.1	301	3	US-08-303-861-21	Sequence 21, Appl
844	5	2.1	279	2	US-07-959-369-11	Sequence 11, Appl	917	5	2.1	301	4	US-09-011-073A-1	Sequence 1, Appli
845	5	2.1	279	2	US-08-836-854-8	Sequence 8, Appli	918	5	2.1	301	4	US-09-230-421-2	Sequence 2, Appli
846	5	2.1	280	3	US-08-974-022-46	Sequence 46, Appl	919	5	2.1	301	4	US-09-231-227-4	Sequence 4, Appli
847	5	2.1	280	4	US-09-383-586-18	Sequence 18, Appl	920	5	2.1	302	2	US-08-836-854-5	Sequence 5, Appli
848	5	2.1	280	4	US-08-795-445A-46	Sequence 46, Appl	921	5	2.1	302	2	US-08-475-427-6	Sequence 6, Appli
849	5	2.1	280	4	US-08-795-447A-46	Sequence 46, Appl	922	5	2.1	302	2	US-07-842-165-6	Sequence 6, Appli
850	5	2.1	280	4	US-08-974-186-46	Sequence 46, Appl	923	5	2.1	303	2	US-08-599-171A-32	Sequence 32, Appli
851	5	2.1	280	4	US-08-795-446B-46	Sequence 46, Appl	924	5	2.1	303	2	US-08-646-590B-32	Sequence 32, Appli
852	5	2.1	281	1	US-07-959-369-4	Sequence 4, Appli	925	5	2.1	303	3	US-09-066-226-32	Sequence 32, Appl
853	5	2.1	281	2	US-08-469-537A-52	Sequence 52, Appli	926	5	2.1	303	3	US-08-867-381A-5	Sequence 5, Appli
854	5	2.1	281	4	US-08-652-877-7	Sequence 7, Appli	927	5	2.1	303	4	US-09-412-184-32	Sequence 32, Appl
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856	5	2.1	282	4	US-08-482-918-56	Sequence 56, Appl	929	5	2.1	304	4	US-09-105-390-40	Sequence 40, Appl
857	5	2.1	282	4	US-09-224-681-56	Sequence 56, Appl	930	5	2.1	305	1	US-08-680-726A-80	Sequence 80, Appl
858	5	2.1	282	4	US-08-336-728A-56	Sequence 56, Appl	931	5	2.1	305	3	US-09-064-703-11	Sequence 11, Appl
859	5	2.1	283	1	US-07-959-369-13	Sequence 13, Appli	932	5	2.1	305	4	US-09-092-409-80	Sequence 80, Appl
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863	5	2.1	285	4	US-08-804-166-6	Sequence 6, Appli	936	5	2.1	306	1	US-08-424-682A-1	Sequence 1, Appli
864	5	2.1	285	4	US-08-910-991-6	Sequence 6, Appli	937	5	2.1	306	1	US-08-454-196-11	Sequence 11, Appli
865	5	2.1	286	1	US-08-467-155A-9	Sequence 9, Appli	938	5	2.1	306	2	US-08-286-819A-33	Sequence 33, Appl
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870	5	2.1	287	4	US-09-065-474-145	Sequence 145, App	943	5	2.1	308	1	US-08-499-568-2	Sequence 2, Appli
871	5	2.1	287	4	US-09-031-962D-2	Sequence 2, Appli	944	5	2.1	308	2	US-08-793-958-2	Sequence 2, Appli
872	5	2.1	288	1	US-08-368-852-15	Sequence 15, Appl	945	5	2.1	309	2	US-08-403-115A-7	Sequence 7, Appli
873	5	2.1	288	1	US-08-690-457-3	Sequence 3, Appli	946	5	2.1	309	2	US-08-405-175A-8	Sequence 8, Appli
874	5	2.1	288	2	US-08-628-187-3	Sequence 3, Appli	947	5	2.1	310	2	US-08-469-537A-74	Sequence 74, Appli
875	5	2.1	288	2	US-08-525-940-15	Sequence 15, Appl	948	5	2.1	312	4	US-09-216-295-21	Sequence 21, Appli
876	5	2.1	288	2	US-08-976-838-15	Sequence 15, Appl	949	5	2.1	312	4	US-08-446-806-1	Sequence 1, Appli
877	5	2.1	288	3	US-08-493-071-1	Sequence 1, Appli	950	5	2.1	313	2	US-08-990-379-7	Sequence 7, Appli
878	5	2.1	292	2	US-08-333-476-111	Sequence 111, App	951	5	2.1	313	2	US-08-988-876-7	Sequence 7, Appli
879	5	2.1	292	2	US-08-973-461A-4	Sequence 4, Appli	952	5	2.1	314	3	US-09-385-028-6	Sequence 6, Appli
880	5	2.1	292	3	US-08-648-010-4	Sequence 4, Appli	953	5	2.1	314	4	US-09-164-193-22	Sequence 22, Appl
881	5	2.1	294	2	US-08-701-191A-20	Sequence 20, Appli	954	5	2.1	315	3	US-09-363-318-2	Sequence 3, Appli
882	5	2.1	294	2	US-08-468-576B-18	Sequence 18, Appl	955	5	2.1	315	3	US-08-957-351-27	Sequence 27, Appl
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885	5	2.1	295	1	US-08-463-931-2	Sequence 2, Appli	958	5	2.1	316	5	PCT-US93-08528-44	Sequence 44, Appli
886	5	2.1	295	2	US-08-372-887-20	Sequence 20, Appli	959	5	2.1	318	3	US-08-816-977-6	Sequence 6, Appli
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890	5	2.1	296	1	US-09-006-535-5	Sequence 5, Appli	963	5	2.1	321	4	US-09-417-286-4	Sequence 4, Appli
891	5	2.1	296	3	US-09-116-622-6	Sequence 6, Appli	964	5	2.1	323	2	US-08-044-812A-4	Sequence 4, Appli
892	5	2.1	296	4	US-09-219-277-6	Sequence 6, Appli	965	5	2.1	323	2	US-08-475-637-4	Sequence 4, Appli
893	5	2.1	296	4	US-09-599-661-6	Sequence 6, Appli	966	5	2.1	323	4	US-09-191-359-4	Sequence 4, Appli
894	5	2.1	297	1	US-07-866-560-4	Sequence 4, Appli	967	5	2.1	325	2	US-08-467-948A-29	Sequence 29, Appl
895	5	2.1	297	1	US-08-180-761B-2	Sequence 2, Appli	968	5	2.1	325	3	US-08-867-381A-50	Sequence 50, Appl
896	5	2.1	297	1	US-08-077-673-4	Sequence 4, Appli	969	5	2.1	325	3	US-08-467-947A-29	Sequence 29, Appl
897	5	2.1	297	1	US-08-671-525B-4	Sequence 4, Appli	970	5	2.1	326	4	US-09-521-144-50	Sequence 50, Appl
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899	5	2.1	297	1	US-08-478-992-4	Sequence 4, Appli	972	5	2.1	327	4	US-09-290-640-66	Sequence 66, Appl
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901	5	2.1	297	2	US-08-466-906B-7	Sequence 7, Appli	974	5	2.1	328	1	US-08-186-529-2	Sequence 2, Appli
902	5	2.1	297	2	US-08-842-238-4	Sequence 4, Appli	975	5	2.1	328	1	US-08-621-493-2	Sequence 2, Appli
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993 5 2.1 332 2 US-08-405-175A-5  
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## ALIGNMENTS

Sequence 7, Appl1  
Sequence 2, Appl1  
Sequence 4, Appl1  
Sequence 5, Appl1  
Sequence 2, Appl1  
Sequence 7, Appl1  
Sequence 13, Appl1  
Sequence 39, Appl1  
Sequence 8, Appl1  
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Sequence 56, Appl1  
Sequence 13, Appl1  
Sequence 75, Appl1  
Sequence 64, Appl1  
Sequence 5, Appl1  
Sequence 4, Appl1  
Sequence 4, Appl1  
Sequence 44, Appl1  
Sequence 50, Appl1  
Sequence 8, Appl1

RESULT 1  
US-09-006-353A-2  
Sequence 2, Application US/09006353A  
Patent No. 6261801

GENERAL INFORMATION:  
APPLICANT: WEI, YING-FEI  
APPLICANT: YU, GUO-LIANG  
APPLICANT: GENTZ, REINER  
APPLICANT: RUBEN, STEVEN  
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/006,353A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ANDERS A  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PR341  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 259 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-006-353A-2

Query Match 100.0%; Score 233; DB 4; Length 259;

Best Local Similarity 100.0%; Pred. No. 9,5e-235;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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87 PCTVCKSDQKHKSCTMTMDYVCOCKEGTFRRENSPEMCKRCSRPSGSEVOVSNCTSMDD 146  
QY 121 IQCVEFGANATVETPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPA 180  
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QY 181 PAAETMTSPGTPAPAAEETMTSPGTPASSHYLSCTIVGIIVLIVFV 233  
Db 207 PAAETMTSPGTPAPAAEETMTSPGTPASSHYLSCTIVGIIVLIVFV 259

## RESULT 2

US-09-153-927-3  
Sequence 3, Application US/09153927A  
Patent No. 6297022

GENERAL INFORMATION:  
APPLICANT: McDonnell, Peter C.  
APPLICANT: Young, Peter R.  
APPLICANT: Zou, Jun  
TITLE OF INVENTION: A Method of Identifying Agonists and  
TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3  
TITLE OF INVENTION: and TR5  
FILE REFERENCE: GH50031  
CURRENT APPLICATION NUMBER: US/09/153,927A  
CURRENT FILING DATE: 1998-09-16  
EARLIER APPLICATION NUMBER: 60/061,334  
EARLIER FILING DATE: 1997-10-08  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 299  
TYPE: PRT  
ORGANISM: Human  
US-09-153-927-3

Query Match 100.0%; Score 233; DB 4; Length 299;  
Best Local Similarity 100.0%; Pred. No. 1,1e-234;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 127 PCTVCKSDQKHKSCTMTMDYVCOCKEGTFRRENSPEMCKRCSRPSGSEVOVSNCTSMDD 186  
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Db 247 PAAETMTSPGTPAPAAEETMTSPGTPASSHYLSCTIVGIIVLIVFV 299

## RESULT 3

US-09-086-483A-2  
Sequence 2, Application US/09086483A  
Patent No. 6214580

GENERAL INFORMATION:  
APPLICANT: NI, et al.  
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10

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; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,483A
; FILING DATE: May-29-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,936
; FILING DATE: May-30-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/069,112
; FILING DATE: Dec-9-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF399
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 386 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-086-483A-2

Query Match      6.08; Score 14; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 TGACNPCTEGVDYT 50
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Db 93 TGACNPCTEGVDYT 106

RESULT 4
; Sequence 4, Application US/09333593A
; Patent No. 6313269
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; APPLICANT: YOUNG, PETER R.
; APPLICANT: MARSHALL, LISA A.
; APPLICANT: ROSHAK, AMY K.
; APPLICANT: TAN, KONG B.
; APPLICANT: TRUNH, ALEMSSEGD
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
; FILE REFERENCE: TR6
; CURRENT APPLICATION NUMBER: US/09/333,593A
; PRIOR APPLICATION NUMBER: 08/916,625
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/853,684
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/041,230
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 8
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 303
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-333-593A-4

Query Match      3.48; Score 8; DB 4; Length 303;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 SPEMCRKC 102
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Db 41 SPEMCRKC 48

RESULT 5
; Sequence 2, Application US/09329633A
; Patent No. 6252050
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapal, Anan
; APPLICANT: Kim, K. Jin
; TITLE OF INVENTION: METHOD FOR MAKING MONOCLONAL ANTIBODIES AND
; FILE REFERENCE: P14681 (REVISED)
; CURRENT APPLICATION NUMBER: US/09/329,633A
; PRIOR FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: US 60/089,253
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: xaa
; LOCATION: 410
; OTHER INFORMATION: xaa = leu or met
; US-09-329-633A-2

Query Match      3.48; Score 8; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 SPEMCRKC 102
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Db 149 SPEMCRKC 156

RESULT 6
; Sequence 1, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntharapal, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-1
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Query Match          3.4%: Score 8; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 149 SPEMCRKC 156
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RESULT 7
US-09-333-593A-2
Sequence 2, Application US/09333593A
Patent No. 6313269
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH C.
APPLICANT: YOUNG, PETER R.
APPLICANT: MARSHALL, LISA A.
APPLICANT: ROSHAK, AMY K.
APPLICANT: TAN, KONG B.
APPLICANT: TRUNEH, ALEMESEGED
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
TITLE OF INVENTION: TR6
FILE REFERENCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 08/853,684
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 412
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-333-593A-2
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Query Match          3.4%: Score 8; DB 4; Length 412;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 95 SPEMCRKC 102
    |||||||
Db 149 SPEMCRKC 156
```

```
RESULT 8
US-09-333-593A-8
```

```
Sequence 8, Application US/09333593A
Patent No. 6313269
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH C.
APPLICANT: YOUNG, PETER R.
APPLICANT: MARSHALL, LISA A.
APPLICANT: ROSHAK, AMY K.
APPLICANT: TAN, KONG B.
APPLICANT: TRUNEH, ALEMESEGED
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
TITLE OF INVENTION: TR6
FILE REFERENCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 08/853,684
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 424
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-333-593A-8
```

```
Query Match          3.4%: Score 8; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 95 SPEMCRKC 102
    |||||||
Db 149 SPEMCRKC 156
```

```
RESULT 9
US-08-883-036A-2
Sequence 2, Application US/08883036A
Patent No. 6072047
GENERAL INFORMATION:
APPLICANT: Rauch, Charles
APPLICANT: Walczak, Henning
TITLE OF INVENTION: Receptor That Binds TRAIL
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle,
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Macintosh 7.6
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,036A
FILING DATE: 26-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US --to be assigned--
FILING DATE: 04-JUN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/829,536
FILING DATE: 28-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/815,255
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: US 08/799,861  
FILING DATE: 13-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2625-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 440 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-883-036A-2

Query Match 3.4%; Score 8; DB 3; Length 440;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 SPEMCRKC 102  
|||  
Db 149 SPEMCRKC 156

RESULT 10  
US-08-465-380-61  
Sequence 61, Application US/08465380  
Patent No. 5863894  
GENERAL INFORMATION:  
APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
APPLICANT: Peter W. Bergum  
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,380  
FILING DATE: June 5, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 213/268  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Necator americanus  
US-08-465-380-61

Query Match 3.0%; Score 7; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 VCQCKEG 88  
|||  
Db 37 VCQCKEG 43

RESULT 11  
US-08-486-397-61  
Sequence 61, Application US/08486397  
Patent No. 5865542  
GENERAL INFORMATION:  
APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,  
APPLICANT: Peter W. Bergum  
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 357  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,397  
FILING DATE: June 5, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 213/269  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Necator americanus  
US-08-486-397-61

Query Match 3.0%; Score 7; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 VCCKEG 88  
|||||  
Db 37 VCCKEG 43

## RESULT 12

US-08-486-399-61  
; Sequence 61, Application US/08486399  
; Patent No. 5865543

## GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
APPLICANT: Yannick G.J. Ganssemans, Matthew Moyle,  
APPLICANT: Peter W. Bergum

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

COUNTRY: California

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,399

FILING DATE: June 5, 1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/326,110

FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 213/270

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Necator americanus

US-08-486-399-61

Query Match 3.0%; Score 7; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 VCCKEG 88  
|||||  
Db 37 VCCKEG 43

## RESULT 13

US-08-461-965-61

; Sequence 61, Application US/08461965  
; Patent No. 5872098

GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,  
APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
APPLICANT: Yannick G.J. Ganssemans, Matthew Moyle,  
APPLICANT: Peter W. Bergum

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

COUNTRY: California

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,965

FILING DATE: June 5, 1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/326,110

FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 210/243

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 61:

SEQUENCE CHARACTERISTICS:

LENGTH: 61 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Necator americanus

US-08-461-965-61

Query Match 3.0%; Score 7; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 VCCKEG 88  
|||||  
Db 37 VCCKEG 43

## RESULT 14

US-08-634-641-61

; Sequence 61, Application US/08634641  
; Patent No. 5955294

GENERAL INFORMATION:

APPLICANT: Vlasuk, George P. Vlasuk

APPLICANT: Stanssens, Patric Eric Hugo

APPLICANT: Mensens, Joris Hilda Lieven

APPLICANT: Lauwereys, Marc Josef

APPLICANT: Jespers, Laurent Stephane

APPLICANT: Ganssemans, Yannick Georges Jozef

APPLICANT: Moyle, Matthew

APPLICANT: Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/634,641  
FILING DATE: April 19, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 219/136  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Necator americanus  
US-08-634-641-61

Query Match 3.0%; Score 7; DB 2; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 VCCKEG 88  
|||||  
Db 37 VCCKEG 43

RESULT 15  
US-09-249-471-61  
Sequence 61, Application US/09249471  
Patent No. 6040441  
GENERAL INFORMATION:  
APPLICANT: Vlausk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Lieven  
APPLICANT: Lauwereys, Marc Josef  
APPLICANT: Laroche, Yves Rene  
APPLICANT: Jaspers, Laurent Stephane  
APPLICANT: Ganssemans, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
APPLICANT: Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/249,471  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,455  
FILING DATE: April 17, 1997  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Necator americanus  
US-09-249-471-61

Query Match 3.0%; Score 7; DB 3; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 VCCKEG 88  
|||||  
Db 37 VCCKEG 43

RESULT 16  
US-09-249-472-61  
Sequence 61, Application US/09249472  
Patent No. 6046318  
GENERAL INFORMATION:  
APPLICANT: Vlausk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Lieven  
APPLICANT: Lauwereys, Marc Josef

APPLICANT: Laroche, Yves Rene  
APPLICANT: Jespers, Laurent Stephane  
APPLICANT: Ganseman, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
APPLICANT: Bergum, Peter W.  
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/249,472  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,455  
FILING DATE: April 17, 1997  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Necator americanus  
US-09-249-472-61  
Query Match 3.0%; Score 7; DB 3; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 VCCKEG 88  
|||||  
Db 37 VCCKEG 43

RESULT 17  
US-09-249-451-61  
; Sequence 61, Application US/09249451  
; Patent No. 6087487

GENERAL INFORMATION:  
APPLICANT: Vlasuk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Llieven  
APPLICANT: Lauwereys, Marc Josef  
APPLICANT: Laroche, Yves Rene  
APPLICANT: Jespers, Laurent Stephane  
APPLICANT: Ganseman, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
APPLICANT: Bergum, Peter W.  
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/249,451  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,455  
FILING DATE: April 17, 1997  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Necator americanus  
US-09-249-451-61  
Query Match 3.0%; Score 7; DB 3; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 VCCKEG 88  
|||||  
Db 37 VCCKEG 43



RESULT 18  
US-08-809-455-61  
Sequence 61, Application US/08809455  
Patent No. 6090916  
GENERAL INFORMATION:  
APPLICANT: Vlasuk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Lieven  
APPLICANT: Lauwereys, Marc Josef  
APPLICANT: Laroche, Yves Rene  
APPLICANT: Jespers, Laurent Stephane  
APPLICANT: Ganssemans, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/809,455  
FILING DATE: April 17, 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Necator americanus  
US-08-809-455-61

Query Match 3.0%; Score 7; DB 3; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 VCCCKEG 88

Db 37 VCCCKEG 43

RESULT 19  
US-09-249-461-61  
Sequence 61, Application US/09249461  
Patent No. 6096877  
GENERAL INFORMATION:  
APPLICANT: Vlasuk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Lieven  
APPLICANT: Lauwereys, Marc Josef  
APPLICANT: Laroche, Yves Rene  
APPLICANT: Jespers, Laurent Stephane  
APPLICANT: Ganssemans, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/249,461  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,455  
FILING DATE: April 17, 1997  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 61 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Necator americanus  
US-09-249-461-61

Query Match 3.0%; Score 7; DB 3; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 VQCKEG 88  
DB 37 VQCKEG 43

RESULT 20  
US-09-249-448-61  
; Sequence 61, Application US/09249448  
; Patent No. 6121435  
; GENERAL INFORMATION:  
; APPLICANT: Vlasuk, George Phillip  
; APPLICANT: Stanssens, Patrick Eric Hugo  
; APPLICANT: Messens, Joris Hilda Llieven  
; APPLICANT: Lauwereys, Marc Josef  
; APPLICANT: Laroche, Yves Rene  
; APPLICANT: Jespers, Laurent Stephane  
; APPLICANT: Ganssems, Yannick Georges Jozef  
; APPLICANT: Moyle, Matthew  
; APPLICANT: Bergum, Peter W.  
; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
; NUMBER OF SEQUENCES: 356  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Suite 4700  
; STATE: Los Angeles  
; COUNTRY: California  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/249,448  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/809,455  
; FILING DATE: April 17, 1997  
; APPLICATION NUMBER: PCT/US95/13231  
; FILING DATE: October 17, 1995  
; APPLICATION NUMBER: 08/486,399  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/486,397  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/465,380  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/461,965  
; FILING DATE: June 5, 1995  
; APPLICATION NUMBER: 08/326,110  
; FILING DATE: October 18, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 216/270  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELETYPE: 67-3510  
; INFORMATION FOR SEQ ID NO: 61:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 61 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

; ORIGINAL SOURCE:  
; ORGANISM: Necator americanus  
; US-09-249-448-61

Query Match 3.0%; Score 7; DB 3; Length 61;  
Best Local Similarity 100.0%; Pred. No. 3.7;  
Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 82 VQCKEG 88  
DB 37 VQCKEG 43

RESULT 21  
US-08-118-270-335  
; Sequence 335, Application US/08118270  
; Patent No. 5508384  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Randall B.  
; APPLICANT: Schuster, David I.  
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
; NUMBER OF SEQUENCES: 348  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/118,270  
; FILING DATE: 09-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/943,236  
; FILING DATE: 10-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Townsend, Kevin G.  
; REGISTRATION NUMBER: 34,033  
; REFERENCE/DOCKET NUMBER: MURPHY-2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELETYPE: 248633  
; INFORMATION FOR SEQ ID NO: 335:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 93 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-118-270-335

Query Match 3.0%; Score 7; DB 1; Length 93;  
Best Local Similarity 100.0%; Pred. No. 5.6;  
Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVLLIV 231  
DB 9 LIVLLIV 15

RESULT 22  
PCT-US93-08528-335  
; Sequence 335, Application PC/TUS9308528  
; GENERAL INFORMATION:

APPLICANT: New York University  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
CLASSIFICATION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEWMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08528  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 335:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 93 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-08528-335

Query Match 3.0%; Score 7; DB 5; Length 93;  
Best Local Similarity 100.0%; Pred. No. 5.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 225 LIVLLIV 231  
|||||  
DB 9 LIVLLIV 15

RESULT 23  
US-08-928-213B-60  
Sequence 60, Application US/08928213B  
Patent No. 6238905  
GENERAL INFORMATION:  
APPLICANT: McHenry, Charles S.  
Seville, Mark  
Cull, Millard G.  
TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III  
NUMBER OF SEQUENCES: 195  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/928,213B  
FILING DATE: 12-Sep-1997  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: ENZYCO-02550  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-705-8410  
TELEFAX: 415-397-8338  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 219 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 60:  
US-08-928-213B-60

Query Match 3.0%; Score 7; DB 4; Length 219;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 105 CPSEGEVQ 111  
|||||  
DB 165 CPSEGEVQ 171

RESULT 24  
US-08-818-112-142  
Sequence 142, Application US/08818112  
Patent No. 6290969  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skelky, Yasir A.W.  
APPLICANT: Dillon, Davin C.  
APPLICANT: Campos-Neto, Antonio  
APPLICANT: Houghton, Raymond  
APPLICANT: Vedyick, Thomas S.  
APPLICANT: Twardzik, Daniel R.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/818,112  
FILING DATE: 13-MAR-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.41106  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 142:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 267 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-818-112-142

Query Match 3.0%; Score 7; DB 4; Length 267;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 QQTVAPO 16  
|||||  
Db 236 QQTVAPO 242

RESULT 25  
US-08-818-111-137  
; Sequence 137, Application US/08818111  
; Patent No. 6338852  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Dillon, David C.  
; APPLICANT: Campos-Neto, Antonia  
; APPLICANT: Houghton, Raymond  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Twardzik, Daniel R.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF  
; NUMBER OF SEQUENCES: 148  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/818, 111  
; FILING DATE: 13-MAR-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.417C6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 137:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-818-111-137

Query Match 3.0%; Score 7; DB 4; Length 267;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 QQTVAPO 16  
|||||  
Db 236 QQTVAPO 242

RESULT 26  
US-09-056-556-142  
; Sequence 142, Application US/090565556

Patent No. 6350456  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Dillon, David C.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND  
; NUMBER OF SEQUENCES: 241  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/056, 556  
; FILING DATE: 07-APR-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maki, David J.  
; REGISTRATION NUMBER: 31,392  
; REFERENCE/DOCKET NUMBER: 210121.457  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 142:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 267 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-056-556-142

Query Match 3.0%; Score 7; DB 4; Length 267;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 QQTVAPO 16  
|||||  
Db 236 QQTVAPO 242

RESULT 27  
US-08-467-559B-9  
; Sequence 9, Application US/08467559B  
; Patent No. 5928890  
; GENERAL INFORMATION:  
; APPLICANT: Li, Yi  
; TITLE OF INVENTION: HUMAN AMINE RECEPTOR  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN AND FOX, P.L.L.C.  
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467, 559B  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0840000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 365 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
US-08-467-559B-9

Query Match 3.0%; Score 7; DB 2; Length 365;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVLLIV 231  
|||||  
DB 38 LIVLLIV 44

RESULT 28  
US-08-118-270-14  
Sequence 14, Application US/08118270  
Patent No. 5508384  
GENERAL INFORMATION:  
APPLICANT: Murphy, Randall B.  
APPLICANT: Schuster, David I.  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
City: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/118,270  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY-2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 377 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-118-270-14

Query Match 3.0%; Score 7; DB 1; Length 377;

Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVLLIV 231  
|||||  
DB 9 LIVLLIV 15

RESULT 29  
PCT-US93-08528-14  
Sequence 14, Application PC/TUS9308528  
GENERAL INFORMATION:  
APPLICANT: New York University  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
City: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08528  
FILING DATE: 09-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 377 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-08528-14

Query Match 3.0%; Score 7; DB 5; Length 377;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVLLIV 231  
|||||  
DB 9 LIVLLIV 15

RESULT 30  
PCT-US96-09848-31  
Sequence 31, Application PC/TUS9609848  
GENERAL INFORMATION:  
APPLICANT: Tippi, Cynthia A.  
APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: NOVEL FILARID NEMATODE CYSTEINE  
TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, Suite 3500

CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/09848  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/486,036  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-33-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 401 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-09848-31

Query Match 3.0%; Score 7; DB 5; Length 401;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 226 IIVLIVF 232  
Db 5 IIVLIVF 11

RESULT 31  
PCT-US96-09848-15  
Sequence 15, Application PC/TUS9609848  
GENERAL INFORMATION:  
APPLICANT: Tripp, Cynthia A.  
APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: NOVEL FILARIID NEMATODE CYSTEINE  
TITLE OF INVENTION: PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, Suite 3500  
City: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/09848  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/486,036  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-33-PCT

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 407 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-09848-15

Query Match 3.0%; Score 7; DB 5; Length 407;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 226 IIVLIVF 232  
Db 11 IIVLIVF 17

RESULT 32  
US-09-086-483A-6  
Sequence 6, Application US/09086483A  
Patent No. 6214580  
GENERAL INFORMATION:  
APPLICANT: NI, et al.  
TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/086,483A  
FILING DATE: May-29-98  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/050,936  
FILING DATE: May-30-97  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/069,112  
FILING DATE: Dec-9-97  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ANDERS A.  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF379  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-086-483A-6

Query Match 3.0%; Score 7; DB 4; Length 467;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 49 YTNASN 55  
Db 154 YTNASN 160

## RESULT 33

US-08-390-000A-7  
Sequence 7, Application US/08390000A  
Patent No. 5985583  
GENERAL INFORMATION:  
APPLICANT: Sealion, Stuart C.  
TITLE OF INVENTION: Cloning and Expression of  
TITLE OF INVENTION: Gonadotropin-Releasing Hormone Receptor  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,000A  
FILING DATE: 17-FEB-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 6923-052  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 790-9090  
TELEFAX: 212 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 468 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-390-000A-7

Query Match 3.0%; Score 7; DB 2; Length 468;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 225 LIVLLIV 231  
Db 58 LIVLLIV 64

## RESULT 34

US-09-013-895A-2  
Sequence 2, Application US/09013895A  
Patent No. 6342363  
GENERAL INFORMATION:  
APPLICANT: Ni, Jian  
APPLICANT: Rosen, Craig A.  
APPLICANT: Pan, James G.  
APPLICANT: Gentz, Reiner L.  
TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4): Death  
TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor  
TITLE OF INVENTION: Superfamily and Binding to Trall (AP02-L)  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/013,895A  
FILING DATE: 27-JAN-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1300002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 468 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-013-895A-2

Query Match 3.0%; Score 7; DB 4; Length 468;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 49 YTNASN 55  
Db 154 YTNASN 160

## RESULT 35

US-08-194-338-6  
Sequence 6, Application US/08194338  
Patent No. 5474898  
GENERAL INFORMATION:  
APPLICANT: Venter, John C.  
APPLICANT: Fraser, Claire M.  
APPLICANT: McCombie, William R.  
TITLE OF INVENTION: OCTOPAMINE RECEPTOR  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson and Bear  
STREET: 620 Newport Center Drive, Sixteenth Floor  
CITY: Newport Beach  
STATE: CA  
COUNTRY: USA  
ZIP: 92660  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/194,338  
FILING DATE: 08-FEB-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/676,174  
FILING DATE: 28-MAR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Istreisen, Ned A.  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER: NIH101.001DV1  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 472 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
US-08-194-338-6

Query Match 3.0%; Score 7; DB 1; Length 472;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVLLIV 231  
|||||  
Db 67 LIVLLIV 73

RESULT 36  
US-08-087-772A-16  
Sequence 16, Application US/08087772A  
Patent No. 5691155  
GENERAL INFORMATION:  
APPLICANT: Nahmlas, Clara  
APPLICANT: Emorine, Jean L.  
APPLICANT: Strosberg, Donny A.  
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine  
TITLE OF INVENTION: Beta3-Adrenergic Receptor and their Applications  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bell, Seltzer, Park & Gibson  
STREET: Post Office Drawer 34009  
CITY: Charlotte  
STATE: No. 5691155th Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/087,772A  
FILING DATE:  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Linker, Raymond O.  
REGISTRATION NUMBER: 26,419  
REFERENCE/DOCKET NUMBER: 3339-195  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-881-3140  
TELEFAX: 919-881-3175  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 477 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-087-772A-16

Query Match 3.0%; Score 7; DB 1; Length 477;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 225 LIVLLIV 231

Db 67 LIVLLIV 73  
|||||

RESULT 37  
US-09-404-650-5  
Sequence 5, Application US/09404650  
Patent No. 6309858  
GENERAL INFORMATION:  
APPLICANT: Dietrich, Paul S.  
APPLICANT: McGivern, Joseph G.  
TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;  
TITLE OF INVENTION: AND USES  
FILE REFERENCE: R0043B-REG sequence listing  
CURRENT APPLICATION NUMBER: US/09/404,650  
CURRENT FILING DATE: 1999-09-23  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 1835  
TYPE: PRT  
ORGANISM: Rattus sp.  
US-09-404-650-5

Query Match 3.0%; Score 7; DB 4; Length 1835;  
Best Local Similarity 100.0%; Pred. No. 98;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 PGTAPA 152  
|||||  
Db 467 PGTAPA 473

RESULT 38  
US-09-320-878-2  
Sequence 2, Application US/09320878A  
Patent No. 6117659  
GENERAL INFORMATION:  
APPLICANT: ASHLEY, Gary  
APPLICANT: BETLACH, Melanie C.  
APPLICANT: MCDANIEL, Robert  
APPLICANT: TANG, Li  
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYPEPTIDE SYNTHASE  
FILE REFERENCE: 300622002120  
CURRENT APPLICATION NUMBER: US/09/320,878A  
CURRENT FILING DATE: 1999-05-27  
EARLIER APPLICATION NUMBER: CIP OF 09/141,908  
EARLIER FILING DATE: 1998-08-28  
EARLIER APPLICATION NUMBER: CIP OF 09/073,538  
EARLIER FILING DATE: 1998-05-06  
EARLIER APPLICATION NUMBER: CIP OF 08/846,247  
EARLIER FILING DATE: 1997-04-30  
EARLIER APPLICATION NUMBER: 60/119,139  
EARLIER FILING DATE: 1999-02-08  
EARLIER APPLICATION NUMBER: 60/100,880  
EARLIER FILING DATE: 1998-09-22  
EARLIER APPLICATION NUMBER: 60/087,080  
EARLIER FILING DATE: 1998-05-28  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 3739  
TYPE: PRT  
ORGANISM: Streptomyces venezuelae  
US-09-320-878-2

Query Match 3.0%; Score 7; DB 3; Length 3739;  
Best Local Similarity 100.0%; Pred. No. 1,9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 150 APAEET 156  
|111111|  
Db 464 APAEET 470

RESULT 39  
US-09-105-537-33  
; Sequence 33, Application US/09105537A  
; Patent No. 6265202  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, D.H.  
; APPLICANT: Liu, H.  
; APPLICANT: Xue, Y.  
; APPLICANT: Zhao, L.  
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin  
; FILE REFERENCE: 600 438US1  
; CURRENT APPLICATION NUMBER: US/09/105,537A  
; CURRENT FILING DATE: 1998-06-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 33  
; LENGTH: 3739  
; TYPE: PRT  
; ORGANISM: Streptomyces venezuelae  
US-09-105-537-33

Query Match 3.0%; Score 7; DB 4; Length 3739;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 APAEET 156  
|111111|  
Db 464 APAEET 470

RESULT 40  
US-09-105-537-6  
; Sequence 6, Application US/09105537A  
; Patent No. 6265202  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, D.H.  
; APPLICANT: Liu, H.  
; APPLICANT: Xue, Y.  
; APPLICANT: Zhao, L.  
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin  
; FILE REFERENCE: 600 438US1  
; CURRENT APPLICATION NUMBER: US/09/105,537A  
; CURRENT FILING DATE: 1998-06-26  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 11877  
; TYPE: PRT  
; ORGANISM: Streptomyces venezuelae  
US-09-105-537-6

Query Match 3.0%; Score 7; DB 4; Length 11877;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 APAEET 156  
|111111|  
Db 5413 APAEET 5419

RESULT 41  
US-08-630-916A-89  
; Sequence 89, Application US/08630916A  
; Patent No. 6011137  
; GENERAL INFORMATION:  
; APPLICANT: Pirozki, Gregorio

APPLICANT: Kay, Brian K.  
APPLICANT: Fowlkes, Dana M.  
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL  
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 124  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
City: New York  
STATE: New York  
COUNTRY: United States  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,916A  
FILING DATE: 03-APR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MISROCK, S. LESLIE  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-203  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 896-8864/9741  
INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-630-916A-89

Query Match 2.6%; Score 6; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 PGTPAP 151  
|111111|  
Db 1 PGTPAP 6

RESULT 42  
US-08-630-915A-145  
; Sequence 145, Application US/08630915A  
; Patent No. 6309820  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: HOFFMAN, No. 6309820h  
; APPLICANT: KAY, Brian K.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: MCCONNELL, Stephen J.  
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
City: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,915A  
FILING DATE: 03-APR-1996  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-174  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 145:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-630-915A-145

Query Match 2.6%; Score 6; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 PGRPAP 151  
|||||  
Db 1 PGRPAP 6

RESULT 43  
US-08-792-832A-39  
Sequence 39, Application US/08/92832A  
Patent No. 6017734  
GENERAL INFORMATION:  
APPLICANT: Summers Dr., Max D.  
APPLICANT: Braunagel Dr., Sharon C.  
APPLICANT: Hong Dr., Tao  
TITLE OF INVENTION: UNIQUE NUCLEOTIDE AND AMINO ACID  
TITLE OF INVENTION: SEQUENCE AND USES THEREOF  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/792,832A  
FILING DATE: 30-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,955  
FILING DATE: 07-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/678,435  
FILING DATE: 03-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hibler, David W.  
REGISTRATION NUMBER: 41,071  
REFERENCE/DOCKET NUMBER: TAMK:190  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/474-7577  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-792-832A-39

Query Match 2.6%; Score 6; DB 3; Length 18;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 IYLLIV 231  
|||||  
Db 4 IYLLIV 9

RESULT 44  
US-08-792-832A-33  
Sequence 33, Application US/08/92832A  
Patent No. 6017734  
GENERAL INFORMATION:  
APPLICANT: Summers Dr., Max D.  
APPLICANT: Braunagel Dr., Sharon C.  
APPLICANT: Hong Dr., Tao  
TITLE OF INVENTION: UNIQUE NUCLEOTIDE AND AMINO ACID  
TITLE OF INVENTION: SEQUENCE AND USES THEREOF  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/792,832A  
FILING DATE: 30-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,955  
FILING DATE: 07-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/678,435  
FILING DATE: 03-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hibler, David W.  
REGISTRATION NUMBER: 41,071  
REFERENCE/DOCKET NUMBER: TAMK:190  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/474-7577  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-792-832A-33

Query Match 2.6%; Score 6; DB 3; Length 24;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 IYLLIV 231  
|||||  
Db 4 IYLLIV 9

RESULT 45  
US-09-023-339-5  
Sequence 5, Application US/09023339  
Patent No. 6127145  
GENERAL INFORMATION:  
APPLICANT: Sutliff, Thomas D.  
TITLE OF INVENTION: Production of '1-Antitrypsin  
TITLE OF INVENTION: In Plants  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: P.O. Box 60850  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,339  
FILING DATE: 13-FEB-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/037,991  
FILING DATE: 13-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Petithory, Joanne R  
REGISTRATION NUMBER: P42,995  
REFERENCE/DOCKET NUMBER: 0665-0003.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
IMMEDIATE SOURCE:  
CLONE: Ramyla signal peptide  
US-09-023-339-5

Query Match 2.6%; Score 6; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 VLVVL 229  
Db 11 VLVVL 16

RESULT 46  
US-08-477-877B-56  
Sequence 56, Application US/08477877B  
Patent No. 5730979  
GENERAL INFORMATION:  
APPLICANT: Bazin, Herv  
TITLE OF INVENTION: LO-CD2a Antibody and Uses thereof for Inhibiting T-cell Active  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,  
ADDRESSEE: Cecchi, Stewart & Olstein  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07068

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,877B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/407,009  
FILING DATE: 29-MAR-1995  
APPLICATION NUMBER: 08/119,032  
FILING DATE: 09-SEP-1993  
APPLICATION NUMBER: 08/027,008  
FILING DATE: 05-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Olstein, Elliot M.  
REGISTRATION NUMBER: 24,025  
REFERENCE/DOCKET NUMBER: 61750-146  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: polypeptide  
US-08-477-877B-56

Query Match 2.6%; Score 6; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 76 TMTTDT 81  
Db 3 TMTTDT 8

RESULT 47  
US-08-472-281A-56  
Sequence 56, Application US/08472281A  
Patent No. 5817311  
GENERAL INFORMATION:  
APPLICANT: Bazin, Herv  
TITLE OF INVENTION: LO-CD2a Antibody and Uses thereof for Inhibiting T-cell Act  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,  
ADDRESSEE: Cecchi, Stewart & Olstein  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,281A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/407,009  
FILING DATE: 29-MAR-1995  
APPLICATION NUMBER: 08/119,032  
FILING DATE: 09-SEP-1993

APPLICATION NUMBER: 08/027,008  
FILING DATE: 05-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Olstein, Elliot M.  
REGISTRATION NUMBER: 24,025  
REFERENCE/DOCKET NUMBER: 61750-142  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: polypeptide  
US-08-472-281A-56

Query Match 2.6%; Score 6; DB 2; Length 32;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 TMTDPT 81  
Db 3 TMTDPT 8

RESULT 48  
US-08-477-989B-56  
Sequence 56, Application US/08477989B  
Patent No. 5951983  
GENERAL INFORMATION:  
APPLICANT: Bazin, Herv  
APPLICANT: Latune, Dominique  
APPLICANT: Kaplan, Ruth  
APPLICANT: Kleber-Emmons, Thomas  
APPLICANT: Postema, Christina E.  
APPLICANT: White-Scharf, Mary  
TITLE OF INVENTION: LO-CD2a Antibody and Uses  
TITLE OF INVENTION: Thereof for Inhibiting  
TITLE OF INVENTION: T-Cell Activation and  
TITLE OF INVENTION: Proliferation  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carrella, Byrne, Bain, Gillfillan,  
ADDRESSEE: Cecchi, Stewart & Olstein  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,989B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/407,009  
FILING DATE: 29-MAR-1995  
APPLICATION NUMBER: 08/119,032  
FILING DATE: 09-SEP-1993  
APPLICATION NUMBER: 08/027,008  
FILING DATE: 05-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Olstein, Elliot M.  
REGISTRATION NUMBER: 24,025  
REFERENCE/DOCKET NUMBER: 61750-147  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 32 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: polypeptide  
US-08-477-989B-56

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Best Local Similarity 100.0%; Pred. No. 22;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 TMTDPT 81  
Db 3 TMTDPT 8

RESULT 49  
US-08-792-832A-56  
Sequence 56, Application US/08792832A  
Patent No. 6017734  
GENERAL INFORMATION:  
APPLICANT: Summers Dr., Max D.  
APPLICANT: Braungel Dr., Sharon C.  
APPLICANT: Hong Dr., Tao  
TITLE OF INVENTION: UNIQUE NUCLEOTIDE AND AMINO ACID  
TITLE OF INVENTION: SEQUENCE AND USES THEREOF  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/792,832A  
FILING DATE: 30-JAN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,955  
FILING DATE: 07-JUL-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/678,435  
FILING DATE: 03-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Hibler, David W.  
REGISTRATION NUMBER: 41,071  
REFERENCE/DOCKET NUMBER: TAMK-190  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 34 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-792-832A-56

Query Match 2.6%; Score 6; DB 3; Length 34;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 226 IVLLIV 231  
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Db 4 IVLLIV 9

RESULT 50  
US-08-050-319B-30  
; Sequence 30, Application US/08050319B  
; Patent No. 5633145  
; GENERAL INFORMATION:  
; APPLICANT: M.Feldmann, P.W. Gray,  
; APPLICANT: M.J.C. Turner, F.M. Brennan  
; TITLE OF INVENTION: Modified human TNFalpha (Tumor  
; TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Reed & Robbins  
; STREET: 635 Bryant Street  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/050,319B  
; FILING DATE: 10-May-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robbins, Roberta L.  
; REGISTRATION NUMBER: 33,208  
; REFERENCE/DOCKET NUMBER: 5150-0030  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 617-8999  
; TELEFAX: (415) 327-3231  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-050-319B-30

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Db 30 TRDTVC 35

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Job time: 192 sec



16:24:31 2002

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

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August 13, 2002, 08:57:31 ; Search time 1842.34 seconds  
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8825.688 Million cell updates/sec

US-09-826-212-1\_COPY\_183\_959  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Scoring table: 1797656 seqs, 10463268293 residues  
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Total number of hits satisfying chosen parameters:  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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REFERENCE	AF012629	780 bp	linear	PRI 21-AUG-1997
AUTHORS	AF012629	780 bp	linear	PRI 21-AUG-1997
TITLE	AF012629	780 bp	linear	PRI 21-AUG-1997
JOURNAL	AF012629	780 bp	linear	PRI 21-AUG-1997
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AUTHORS	AF012629	780 bp	linear	PRI 21-AUG-1997
TITLE	AF012629	780 bp	linear	PRI 21-AUG-1997
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DEFINITION	Homo sapiens cytotoxic TRAIL receptor-3 (TRAIL-R3) mRNA, complete
ACCESSION	AF020502
VERSION	AF020502.1
KEYWORDS	GI:2443819
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	MacFarlane, M., Ahmad, M., Sriniwasula, S.M., Fernandes-Alnemri, T., Cohen, G.M. and Alnemri, E.S.
TITLE	Identification and molecular cloning of two novel receptors for the cytotoxic ligand TRAIL
JOURNAL	J. Biol. Chem. 272 (41), 25417-25420 (1997)
MEDLINE	97467318
REFERENCE	2 (bases 1 to 900)
AUTHORS	MacFarlane, M., Ahmad, M., Sriniwasula, S.M., Fernandes-Alnemri, T., Cohen, G.M. and Alnemri, E.S.
TITLE	Direct Substitution
JOURNAL	Submitted (21-Aug-1997) Department of Microbiology and Immunology, Kimmel Cancer Institute, 233 S. 10th Street, Philadelphia, PA 19107, USA
FEATURES	Location/Qualifiers
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FEATURES	
source	USA
Location/Qualifiers	233 S. 10th Street, Philadelphia, PA 19100

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Db 361 AATGAACCTTCTGTCTCCATGTACAGTTGTAAATCAGATCAAAAACATAAAGTTCC 420  
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LOCUS AX077019  
DEFINITION Sequence 7 from Patent WO0105972.  
ACCESSION AX077019  
VERSION AX077019.1 GI:13121655  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1102)  
AUTHORS Ashkenazi, A.J., Baker, K.P., Fong, S., Goddard, A., Godowski, P.J.,  
Gurney, A.L., Hillan, K.J., Mark, M.R., Marsters, S.A., Pitti, R.M.,  
Tuma, D., Watanabe, C.K. and Wood, W.I.  
COMPOSITIONS and methods for the treatment of immune related  
diseases  
TITLE JOURNAL Patent: WO 0105972-A 7 25-JAN-2001;  
Genentech, Inc. (US)  
FEATURES  
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location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 1.4e-210;  
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Db 373 GAACATATCGAGCCTGTAAACCGGTGCACAGAGGTGTGGATTACACCAAGCTTCCAAC 432  
QY 241 aatgaaccttctgtccctccatgtacagttgttgaagaattgtgtccaaatgccaatgtgaa 480  
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Db 433 AATGAACCTTCTGTCTCCATGTACAGTTGTAAATCAGATCAAAAACATAAAGTTCC 492  
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Db 493 TGCACATGACACAGACACAGTGTGTAAAGAGGACCTTCCGGAATGAANAAC 552  
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Db 553 TCCCCAGAGATGTGCCGAAGTGTAGCAGTGTCCCTAGTGGGAAGTCCAAAGTCAAT 612  
QY 421 ttagcgtccctggagatgatatccagttgttgaagaattgtgtccaaatgccaatgtgaa 480  
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Db 613 TGTACGTCTGTGGATGATTCAGTGTGTGAAGAAATTTGGTCCCAATGCCCACATGTGGAA 672  
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Db 673 ACCCAGCTGCTGAAGAGACATGACACACAGCCGGGACTCTGCCCCAGCTGTGAA 732  
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LOCUS AF012536  
DEFINITION Homo sapiens decoy receptor 1 (DcR1) mRNA, complete cds.  
ACCESSION AF012536  
VERSION AF012536.1 GI:2338421  
KEYWORDS human.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1180)  
AUTHORS Sheridan, J.P., Marsters, S.A., Pitti, R.M., Gurney, A., Skubatch, M.,  
Baldwin, D., Ramakrishnan, L., Gray, C.L., Baker, K., Wood, W.I.,  
Goddard, A.D., Godowski, P. and Ashkenazi, A.  
CONTROL OF TRAIL-INDUCED APOPTOSIS BY A FAMILY OF SIGNALING AND  
DECOY RECEPTORS  
TITLE JOURNAL Science 277 (5327), 818-821 (1997)  
MEDLINE 97390509  
REFERENCE 2 (bases 1 to 1180)





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DEFINITION	Tumor necrosis factor receptor-associated protein TR5.		
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VERSION	E63033.1	GI:18625351	
KEYWORDS	JP 2000078995-A/1.		
SOURCE	unidentified.		
ORGANISM	unidentified.		
REFERENCE	1 (bases 1 to 1410)		
AUTHORS	Young,P.R., Tan,K.B., Renox,A.R. and Lyn,S.D.P.		
TITLE	Tumor necrosis factor receptor-associated protein TR5		
JOURNAL	Patent: JP 2000078995-A 1 21-MAR-2000;		
COMMENT	SMITHKLINE BEECHAM CORP OS Unidentified PN JP 2000078995-A/1 PD 21-MAR-2000 PF 01-SEP-1999 JP 1999247636 PR 05-FEB-1997 US 08/795910, 28 -JUL-1997 US 08/901469 PI PEETER R YOUNG,KONG B TAN,ANA RISIA RENOX, PI SALLY DOREEN PATRICIA LYNN PC C12N15/09,A61K31/7052,A61K38/00,A61K45/00,A61K48/00,A61P31/04, PC A61P35/00,A61P37/02,C07K14/705,C07K16/28,C12N1/15,C12N1/19, PC C12N1/21, PC C12N5/10,C12P21/02//C12P21/08,C12N15/00,A61K37/02,C12N5/00 CC Strandedness: Single; CC Topology: Linear; FH Key Location/Qualifiers FT source 1..1410 Location/Qualifiers 1..1410 /organism='unidentified' /db_xref='taxon:32644'		
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OY	61	gtccactgaattctgcaccaacaactgcggcagagggaggaagttcccacagacagtgccc	120
Dd	249	gtccactgaattctgttcgccacacactgcggcagagggaggaagttcccacagacagtgccc	308
OY	121	ccaagcaacagaggcacagcttcaaagggggaggaagtgtccaagcagatatcatagatca	180
Dd	309	ccacagcaacagaggcacagcttcaaagggggaggaagtgtccaagcagatatcatagatca	368
OY	181	gaacatcttgagagcctgttaaaccctgtgcacagaggaagtgtggatttacccaagcgttccaac	240
Dd	369	gaacatcttgagagcctgttaaaccctgtgcacagaggaagtgtggatttacccaagcgttccaac	428
OY	241	aatgaaccttctgttcccatgtlccacgtlccagtttgttaaatcagatlcataaaaacataaaagtccc	300
Dd	429	aatgaaccttctgttcccatgtlccacgtlccagtttgttaaatcagatlcataaaaacataaaagtccc	488
OY	301	tgcaccatgacacagagacacagtggtgtcagtgttaagaagaagcaccttcoggaatgaaaaa	360
Dd	489	tgcaccatgacacagagacacagtggtgtcagtgttaagaagaagcaccttcoggaatgaaaaa	548

OY	361	ttcccaagagatgtgcggaaagtlttagcagggtgcccctagtgtgggaagtcaccaagttaac	420
OY	362	ttcccaagagatgtgcggaaagtlttagcagggtgcccctagtgtgggaagtcaccaagttaac	420
Db	549	tccccagagatgtgccgaagtgtagcagggtgcccctagtgtgggaagtcaccaagttaac	608
OY	421	tgtacgtccttggagaatacatcaagtgtatttgaagaatttgggtgccaatgtcacctgtgaa	480
Db	609	tgtacgtccttggagaatacatcaagtgtatttgaagaatttgggtgccaatgtcacctgtgaa	668
OY	481	accaccagctgtctgaagacaatatgaacacacagcccgaggactcctgtcccagctgtgaa	540
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OY	601	agcccgaggactcctgtcccagctgtctgaagagaataacacacagcccgaggactcct	660
Db	789	agcccgaggactcctgtcccagctgtctgaagagaataacacacagcccgaggactcct	848
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Db	849	gccccagctgtctgaagacaatatgaacacacagcccgaggactcctgtcccatttac	908
OY	721	cctcatcacatcatgttaggatataatgttatgttgtccttcgatttgttgc	777
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DEFINITION	Homo sapiens TRAIL receptor 3 mRNA, complete cds.		
ACCESSION	AF016267		
VERSION	AF016267.1	GI:2529564	
KEYWORDS	.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 1388)		
JOURNAL	Schneider,P., Bodmer,J.L., Thome,M., Hofmann,K., Holler,N. and		
MEDLINE	Tschopp,J.		
REFERENCE	Characterization of two receptors for TRAIL		
AUTHORS	FEBS Lett. 416 (3), 329-354 (1997)		
TITLE	2 (bases 1 to 1388)		
JOURNAL	Schneider,P., Bodmer,J.-L., Thome,M., Holler,N., Hofmann,K. and		
MEDLINE	Tschopp,J.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (28-JUL-1997) Institute of Biochemistry, University of		
TITLE	Lausanne, Chemin des Boveresses 155, Epalinges, VD 1066,		
JOURNAL	Switzerland		
MEDLINE			
REFERENCE			
AUTHORS			
TITLE	Location/Qualifiers		
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AUTHORS	/tissue_type="liver and spleen"		
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AUTHORS	/codon_start=1		
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LOCUS	AX088365		947 bp	DNA	linear	PAT 17-MAR-2003
DEFINITION	Sequence 4 from Patent WO0114542.					
ACCESSION	AX088365					
VERSION	AX088365.1		GI:13397238			
KEYWORDS						
SOURCE	.					
ORGANISM	synthetic construct. artificial sequence.					
REFERENCE	1 (bases 1 to 947)					
AUTHORS	Denome,S.A., Swain,P.M. and Trellas,N.					
TITLE	A transmembrane trap for isolating membrane bound proteins					
JOURNAL	Patent: WO 0114542-A 4 01-MAR-2001; Genome Therapeutics Corporation (US)					
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OY	94 gaagaaattccccacagacagltggccccaagacaagagcacagcttcaaagg99ag	153				
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DEFINITION	Homo sapiens TNF receptor-related receptor for TRAIL mRNA, complete cds.		
ACCESSION	AF023849		
VERSION	AF023849.1	GI:2653844	
KEYWORDS	human.		
SOURCE	Homo sapiens		
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REFERENCE	1 (bases 1 to 1161)		
AUTHORS	Pan,G., Ni,J., Yu,G., Wei,Y.F. and Dixit,V.M.		
TITLE	TRUND, a new member of the TRAIL receptor family that antagonizes TRAIL signalling		
JOURNAL	FEBS Lett. 424 (1-2), 41-45 (1998)		
MEDLINE	98196860		
REFERENCE	2 (bases 1 to 1161)		
AUTHORS	Pan,G., Ni,J. and Dixit,V.M.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-SEP-1997) Pathology, University of Michigan, 1301 Catherine Road, MSRI, RM520, Ann Arbor, MI 48109, USA		
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ACCESSION AF021232  
VERSION AF021232.1 GI:3452182  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1588)  
AUTHORS Degli-Esposti,M.A., Dougal,W.C., Smolak,P.J., Waugh,J.Y.,  
Smith,C.A. and Goodwin,R.G.  
TITLE The novel receptor TRAIL-R4 induces NF-kappaB and protects against  
TRAIL-mediated apoptosis, yet retains an incomplete death domain  
JOURNAL Immunity 7 (6), 813-820 (1997)  
MEDLINE 98090091  
REFERENCE 2 (bases 1 to 1588)  
AUTHORS Degli-Esposti,M.A.  
TITLE Direct Submission  
JOURNAL Submitted (28-AUG-1997) Biochemistry, Immunex, 51 University  
Street, Seattle, WA 98101, USA  
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RESULT 13  
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LOCUS Homo sapiens decoy receptor 2 mRNA, complete cds.  
DEFINITION AF029761  
ACCESSION AF029761  
VERSION AF029761.1 GI:4106963  
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SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1726)  
AUTHORS Masters,S.A., Sheridan,J.P., Pitti,R.M., Huang,A., Skubatch,M.,  
Baldwin,D., Yuan,J., Gurney,A., Goddard,A.D., Godowski,P. and  
Ashkenazi,A.  
TITLE A novel receptor for Apo2L/TRAIL contains a truncated death domain  
JOURNAL Curr. Biol. 7 (12), 1003-1006 (1997)  
MEDLINE 98044290  
REFERENCE 2 (bases 1 to 1726)  
AUTHORS Masters,S.A., Sheridan,J.P., Pitti,R.M., Huang,A., Skubatch,M.,  
Baldwin,D., Yuan,J., Gurney,A., Goddard,A.D., Godowski,P. and  
Ashkenazi,A.  
TITLE Direct Submission  
JOURNAL Submitted (14-OCT-1997) Molecular Oncology, Genentech, 1 DNA Way,  
South San Francisco, CA 94080, USA  
REFERENCE 3 (bases 1 to 1726)  
AUTHORS Masters,S.A., Sheridan,J.P., Pitti,R.M., Huang,A., Skubatch,M.,



Baldwin, D., Yuan, J., Gurney, A., Goddard, A.D., Godowski, P. and Ashkenazi, A.  
Direct Submission  
Submitted (06-JAN-1999) Molecular Oncology, Genentech, 1 DNA Way,  
South San Francisco, CA 94080, USA

REMARK  
COMMENT  
FEATURES  
Sequence update by submitter  
On Jan 6, 1999 this sequence version replaced gi:2688980.

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Matches 452; Conservative 0; Mismatches 96; Indels 3; Gaps 1;

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Qy 126 gcaacagagacacacgtctcaaggggagagagtgctcagcagagatctcacaagaaca 185
Db 298 GCAACAGAGGGGAGCCCTCAAGGAGAGAGAGTCTCAGACAGATCTCATAGATCA 357
Qy 186 tactggagcctgtacaaccgtgtcaacagaggtgtggaattacaccaaagcttccaacatga 245
Db 358 TACTGAGACCTGTAAACCCGTGCACAGAGGCTGTGATTACACCATTTGCTCCAA 417
Qy 246 acctcttgcctcccatgtacagttgttaattcagatacaaaaactaaagtctctgac 305
Db 418 GCCTTCTTGCTGCTATGTACAGTTTGAATCAAGTCAACAAATTAAGTTCCTGTAC 477
Qy 306 catgacagagacacacagctgtcagtgtaaaagagcaccctccggaattgaactccc 365
Db 478 CACGACCAAGAGACACCGGTGTCACTGTGAAGAAAGAGCTTCCAGATTAATAATCC 537
Qy 366 agagatgtgcgcgaagtgtacga--ggatgccttagtggggaagtcacaagtcagaattg 422
Db 538 TGAGATGTGCGCGAGCTGTAAACAGGGGTGTCCAGAGGAGTGTCAAGTCAAGTA 597
Qy 423 tagctccctggagatgatactcagtggtgtgaagaattgtgtccaatgctccatgtygaac 482
Db 598 TACGCCCCGGAGTGACATCAAGTCAAAAATGAATCACTGCAATTCACCTGCGGAA 657
Qy 483 cccaagctctgaagacatgaacacacagccgggagagctcctgccacagcttgcgaaga 542
Db 658 CCCAGCAGCGGAGGAGACAGTGTACACCATCTCTGGGGATGCTTGCCTCTCCATCACTA 717
Qy 543 gacaatgaca 553

```

Db 718 CCTATCATCA 728

## RESULT 14

AF021233

LOCUS Homo sapiens TRAIL-R4-B (TRAIL-R4) mRNA, complete cds. 1333 bp

DEFINITION AF021233

ACCESSION AF021233

VERSION AF021233.1

KEYWORDS

SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 1333)

Degli-Esposti, M.A., Dougall, W.C., Smolak, P.J., Waugh, J.Y.,

Smith, C.A. and Goodwin, R.G.

The novel receptor TRAIL-R4 induces NF-kappaB and protects against

TRAIL-mediated apoptosis, yet retains an incomplete death domain

Immunoty 7 (6), 813-820 (1997)

98090091

2 (bases 1 to 1333)

Degli-Esposti, M.A.

Direct Submission

Submitted (28-AUG-1997) Biochemistry, Immunex, 51 University

Street, Seattle, WA 98101, USA

location/Qualifiers

1. .1333

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/chromosome="8"

/map="8p22-p21"

1. .1333

/gene="TRAIL-R4"

/note="New TRAIL receptor"

/allele="B"

80. .1240

/protein\_id="AAC32766.1"

/db\_xref="GI:3452185"

/translation="MGLMGOSVPTASSRAGRYPGARTASGTRPMLDKILKFEVFI

VAVLLPVVDSATIPRODEVPOOTVAPOQORSIKKEPCPGASRSRSTGACNCFEG

VDYTIASNNPSCILCTYCKSGQTNKSCITTRPTVCCCEKGSQDNKSPKMTCTRT

GCPRGWVKSCTPRSDIKCNESAASSTGTPAEFTVTITLGLASPHYLIITIV

LVILAVVVGFSCKRKFISYLKIGISGGGGGPRVHVLFRRSRCSRYVGADNMR

NETLSNRYLQPTQVSEDIQOEIAGELTGVLEPPEPRLLEQAEAGCCORRLIVP

VNDASADISTILDASATLEGHAKETIQDLVGSSEKLFYEDEAGSATSL"

BASE COUNT 333 a 351 c 359 g 290 t

ORIGIN

Query Match 48.9%; Score 379.8; DB 9; Length 1333;

Best Local Similarity 81.9%; Pred. No. 2.7e-97;

Matches 451; Conservative 0; Mismatches 97; Indels 3; Gaps 1;

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Qy 6 ccgagatcccaagaccctaagttcgtcgtcgcacgcgcgcgtcgtcgaagtcct 65
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Qy 66 agcttacctctgcaccactctccggcgaaggaagttcccccagacagctgccccca 125
Db 235 GGTGACTCTGCGACCAATCCCGGAGAGAGAGTTCGCCAGCAGAGTGGCCCA 294
Qy 126 gcaacagagacacacgtctcaaggggagagagtgctcagcagagatctcacaagaaca 185
Db 295 GCAACAGAGGGGAGGAGCCCTCAAGGAGAGAGAGTCTCAGACAGATCTCATAGATCA 354
Qy 186 tactggagcctgtacaaccgtgtcaacagaggtgtggaattacaccaaagcttccaacatga 245

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Db 355 TACTGAGCCTGTACCCGTCGACAGAGGCTGTGATTCACCATTCCTCAACAATT 414  
Qy 246 accctctgtctccatgtacagtttgttaataatagatcaataaataaagttctgcac 305  
Db 415 GCTTCTGCTGCTGTATGTACACTTTGTAAATAGGTCAACAAATTAAGTTCTGTAC 474  
Qy 306 catgaccagagacacagtggtcagtgtaagaagacacctccggaatgaactccc 365  
Db 475 CACGACACAGAGACACCGTGTGTAGTGAAGAAAGAAAGTCCAGAGTAAGAACTCCCC 534  
Qy 366 agagatgtgcgcgaagtgtgca---ggtgcctagtgtgggaagtcacgaatgtg 422  
Db 535 TGAGATGTGCGGAGCGTGTGAACAGGGTCTCCAGAGGATGTCTAAGGTCAATTAATG 594  
Qy 423 tactgtcgtgagatgataccagtggtgtgaagaattgtgtccaatgccaatgtgaaac 482  
Db 595 TAGGCCCCGAGAGTACATCAAGTGCAGAAATGATATCAGTCCAGTTCCATGGGAAAC 654  
Qy 483 cccagctgtcgaagacacatgacacacccagcccgaggactcctgcccaagctgtgaa 542  
Db 655 CCCAGAGCGGAGAGACAGTACACACCATCTGTGGGATGCTTGCCTCCATATCACTA 714  
Qy 543 gacaaatgaca 553  
Db 715 CCTATCATCA 725

## RESULT 15

LOCUS BC012866 1723 bp mRNA 1linear PRI 22-AUG-2001  
DEFINITION Homo sapiens, similar to tumor necrosis factor receptor  
superfamily, member 10a, clone MGC:9365 IMAGE:3857315, mRNA,  
complete cds.  
ACCESSION BC012866  
VERSION BC012866.1 GI:15277526  
KEYWORDS MGC.  
SOURCE human.  
ORGANISM Homo sapiens  
Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
REFERENCE 1 (bases 1 to 1723)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (20-AUG-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,  
USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
COMMENT Contact: MGC help desk  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
Tissue Procurement: DCTD/DRP  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome  
Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [villalobcm.tmc.edu](mailto:villalobcm.tmc.edu)  
Villalon, D.K., Luna, R.A., Hale, S.M., Huliy, S., Lu, X., Garcia,  
A.M., Holloway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W.,  
Muzny, D.M., Gibbs, R.A.

## FEATURES

source  
1. 1723  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="MGC:9365 IMAGE:3857315"

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Series: IRAX Plate: 21 Row: b Column: 21  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Genomescan gene  
prediction, similarity but not identity to protein.  
Location/Qualifiers

CDS  
/issue\_type="Ovary, adenocarcinoma"  
/clone\_lib="NIH\_MGC\_66"  
/lab\_host="DH10B"  
/note="Vector: pCMV-Sport6"  
66..1472  
/codon\_start=1  
/product="Similar to tumor necrosis factor receptor  
superfamily, member 10a"  
/protein\_id="AAH12866.1"  
/db\_xref="GI:15277527"  
/translation="MAPPPRVHLGAFIAVTENPGSAAGTEAATAATPSKWSAGR  
IEPRGGKRALPTSMGQHGPSAARAGRAPAPAREASPRLRVHTKFEVVGVLQ  
VWPSAAITKLHDOSIGTQWHSPLGELCPGSHRSEHPGACNCTEGVGTNSNN  
LEACLPCTACKSDSEERSPCTTTRNACCKPOTFNDNSAEMCRKSCSGPGAWK  
KOOTPWSIDECYHKESSNGHNILWVILVTLVPLILVAVLVCCCTIGSGCGPKMD  
RYCFMRLLGRGAGADNHNELNSADLSPTFSQOMESQEPALPTVYQSGEA  
OCILGFAEBSQRRLLVPANGADTEFLMLFDFFAIVPDSMDLKRQDLTKN  
EIDVVRAGTAGPDALYAMLKMWNVNTHRNASITHLLDALERMEERHAKETIDLLVD  
SGFYLEGDTGSAYSLF"  
BASE COUNT 426 a 413 c 502 g 382 t  
ORIGIN

Query Match 29.8%; Score 231.4; DB 9; Length 1723;  
Best Local Similarity 73.4%; Pred. No. 6e-55;  
Matches 343; Conservative 0; Mismatches 106; Indels 18; Gaps 3;

Qy 6 ccgagatccccaagaacctaaagtgtcgtcgtatcgtgtgcggtcctgtgcagctc 65  
Db 323 CCGGCTCCACAAAGACCTTCAAGTTGTG-----TGTGCGGGTCTGTGCGAGGTCT 376  
Qy 66 agcttactctgcacacactgcgcgcgagaggaagttcccaagaacagtgccccaca 125  
Db 377 ACCTAGCTCAGCTGCAACATC-----AAACTTCATGATCAATCAATTTGGCACA 427  
Qy 126 gcaacagagacacagcttcaaggaggagtggttcacagagatcattatgacagaca 185  
Db 428 GCAATGGGAACATPAGCCCTTTGGAGAGTGTGTCCACACAGGATCTATGATGAGACA 487  
Qy 186 tactggaacctgtacacccgtgcacagagaggtgtgtatcaacacagctcccaatga 245  
Db 488 TCCTGGAGCCTGTACCGGTCGACAGAGGTTGTGTTACCAATCTTCCACAAATTT 547  
Qy 246 accctctgtctccatgtacagtttgttaataatagatcaataaataaagttctgcac 305  
Db 548 GTTTGCTTGGCTCCCATGTACAGTGTAAATGATGAGAAAGAGAGAGTCCCTGCAC 607  
Qy 306 catgaccagagacacagtggtcagtgtaagaagacacctccggaatgaactccc 365  
Db 608 CACGACACAGAGACACACATGTCTAGTCACCAACGAGAACTTCCGATATGACAAATTC 667  
Qy 366 agagatgtgcgcgaagtgtgca---ggtgcctagtgtgggaagtcacgaatgtg 422  
Db 668 TGAGATGTGCGGAGAGTGAAGTGAAGAGGAGGAGGAGTGTGTCAGAGTCAAGATTG 727  
Qy 423 tactgtcgtgagatgataccagtggtgtgaagaattgtgtccaatgtgcaatg 469  
Db 728 TAGCCCTTGAGATGACATCAAGTGTGTCCACAAAGATTCAGGCAATG 774

Search completed: August 13, 2002, 11:21:04  
Job time: 8613 sec

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PT Newly isolated polynucleotide encoding a mammalian TRAIL receptor  
 PT protein - useful in for screening for (ant)agonists that modulate  
 the apoptotic activity mediated by DR5 or TRAIL-R3 proteins  
 XX  
 PS Claim 7, Page 62-63; 71pp: English.  
 XX  
 CC This sequence encodes the human TRAIL receptor TRAIL-R3 of the invention.  
 CC An antibody against the TRAIL receptors is useful for detecting mammalian  
 CC DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in  
 CC bioassays for screening for (ant)agonists of DR5 or TRAIL-R3 proteins.  
 CC (Ant)agonists identified by the assay are useful for modulating the  
 CC apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis  
 CC related conditions which are treated in this way, include cancer  
 CC (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus  
 CC erythematosus and immune-mediated glomerulonephritis), viral infections  
 CC (e.g. herpes virus, poxvirus and adenovirus), degenerative disorders  
 CC (e.g. Alzheimer's disease and Parkinson's disease), amphotrophic lateral  
 CC sclerosis, retinitis pigmentosa, cerebellar degeneration, myelodysplastic  
 CC syndromes (e.g. aplastic anaemia) and ischemic injury (e.g. myocardial  
 CC infarction and stroke). The polynucleotides can also be used to treat  
 CC these diseases. Antisense oligonucleotides to the DNA sequences can be  
 CC used to form a composition that is useful for inhibiting expression of a  
 CC human DR5 or TRAIL-R3 protein.  
 CC  
 SQ Sequence 900 BP; 228 A; 262 C; 240 G; 170 T; 0 other;

Query Match 100.0%; Score 777; DB 20; Length 900;  
 Best Local Similarity 100.0%; Pred. No. 3.9e-224;  
 Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 atggccggatccccaagcctaagtctgctgcatcgtcgctgctgctgca 60  
 DB 121 atggccggatccccaagcctaagtctgctgcatcgtcgctgctgca 180  
 OY 61 gtctagctactctgcccacacgtccggcagaggaattcccgacagctggcc 120  
 DB 181 gtctagctactctgcccacacgtccggcagaggaattcccgacagctggcc 240  
 OY 121 ccacagcaacagagcagcttcaagggagagagctccagcagatcctatagta 180  
 DB 241 ccacagcaacagagcagcttcaagggagagagctccagcagatcctatagta 300  
 OY 181 gaacatactgagcgtctaacccgtgcacagaggtgtgattacacaaogcttcaac 240  
 DB 301 gaacatactgagcgtctaacccgtgcacagaggtgtgattacacaaogcttcaac 360  
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 DB 361 aatgaacctctgctcccatgtacagttgttaatacacaataaaacataaagttcc 420  
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 DB 541 tgtagctccggagatataccagtggtgtgaagaatttggtgcgaatgcacgttgaa 600  
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 DB 601 accccagctgtgaagagaatgaacaaccccgaggactctgcccagctgtgaa 660  
 OY 541 gagacaatgaacaacccagcaggaactctgcccagctgtgaaagacaatgacacc 600  
 DB 661 gagacaatgaacaacccagcaggaactctgcccagctgtgaaagacaatgacacc 720  
 OY 601 agcccgaggactctgcccagctgtgaaagacaatgacaccagccggagactct 660  
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DB 721 agcccgaggactctgcccagctgtgaaagacaatgacaccagccggagactct 780  
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 DB 781 gcccacgtctgtgaagagaatgaacaaccccgaggactctgcccagctgtgaa 840  
 OY 721 ctctcagcaccacatgagatagatattctaatctgtctcgtatgtttgt 777  
 DB 841 ctctcagcaccacatgagatagatattctaatctgtctcgtatgtttgt 897

## RESULT 2

AAS21393  
 ID AAS21393 standard; cDNA; 1102 BP.  
 XX

AC AAS21393;  
 XX

DT 24-OCT-2001 (first entry)  
 XX

DE Human cDNA sequence encoding for PRO366 polypeptide.  
 XX

KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
 XX breast; prostate; cervical; tumor necrosis factor-alpha; TNF-alpha;

KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
 XX adipocyte; A-peptide; factor VIIA; gene therapy; ss.

OS Homo sapiens.  
 XX

PN WO200140466-A2.  
 XX

PD 07-JUN-2001.  
 XX

XX 01-DEC-2000; 2000WO-US32678.  
 XX

PR 01-DEC-1999; 99WO-US28301.  
 XX

PR 01-DEC-1999; 99WO-US28634.  
 XX

PR 02-DEC-1999; 99WO-US28551.  
 XX

PR 02-DEC-1999; 99WO-US28564.  
 XX

PR 09-DEC-1999; 99WO-US28565.  
 XX

PR 09-DEC-1999; 99US-0170262.  
 XX

PR 16-DEC-1999; 99WO-US30095.  
 XX

PR 20-DEC-1999; 99WO-US30911.  
 XX

PR 20-DEC-1999; 99WO-US30999.  
 XX

PR 30-DEC-1999; 99WO-US31243.  
 XX

PR 06-JAN-2000; 2000WO-US00277.  
 XX

PR 06-JAN-2000; 2000WO-US00376.  
 XX

PR 11-FEB-2000; 2000WO-US03565.  
 XX

PR 18-FEB-2000; 2000WO-US04341.  
 XX

PR 18-FEB-2000; 2000WO-US04342.  
 XX

PR 22-FEB-2000; 2000WO-US04414.  
 XX

PR 24-FEB-2000; 2000WO-US04914.  
 XX

PR 24-FEB-2000; 2000WO-US05004.  
 XX

PR 01-MAR-2000; 2000WO-US05601.  
 XX

PR 20-MAR-2000; 2000WO-US07377.  
 XX

PR 21-MAR-2000; 2000WO-US07532.  
 XX

PR 30-MAR-2000; 2000WO-US08439.  
 XX

PR 17-MAY-2000; 2000WO-US13705.  
 XX

PR 22-MAY-2000; 2000WO-US14042.  
 XX

PR 30-MAY-2000; 2000WO-US14941.  
 XX

PR 02-JUN-2000; 2000WO-US15264.  
 XX

PR 10-NOV-2000; 2000WO-US30873.  
 XX

(GETH ) GENENTECH INC.

PI Baker KP, Beresini M, DeForge L, Deanoyers L, Fillaro E, Gao W;

PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

DR WPI; 2001-408281/43.

DR P-PDSB; AAU12321.

PT Isolated, secretory and transmembrane PRO polypeptide used to detect

other PRO polypeptides, link bioactive molecules to cells expressing





XX The invention relates to novel human angiogenesis-associated proteins  
 CC designated PRO proteins (AA53064-B53097), and to nucleic acids encoding  
 CC PRO proteins. The invention also relates to vectors and host cells  
 CC comprising a PRO nucleic acid, the recombinant production of a PRO  
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
 CC compounds which inhibit the expression of a PRO gene. The invention  
 CC additionally encompasses methods of identifying modulators of PRO  
 CC expression or activity; diagnosing a cardiovascular, endothelial or  
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
 CC mutations in a PRO gene, or the expression level of a PRO gene within a  
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
 CC administration of a PRO protein, or an agonist or antagonist thereof.  
 CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
 CC agonists and PRO antagonists may be used as therapeutic agents to treat  
 CC cardiovascular, endothelial or angiogenic disorders, such as  
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
 CC disease, or stroke. PRO nucleic acids are additionally useful in the  
 CC recombinant production of PRO proteins, as hybridisation probes to  
 CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
 CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
 CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
 CC animals useful for the development and screening of potential  
 CC therapeutic agents. The present sequence represents a cDNA encoding a PRO  
 CC protein of the invention.

SO Sequence 1102 BP: 269 A; 319 C; 297 G; 217 T; 0 other:

Query Match 100.0%; Score 777; DB 22; Length 1102;  
 Best Local Similarity 100.0%; Pred. No. 4,3e-224;  
 Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 373 gaacatacttgagctgttaaccgtgacagagagtgtgattcaccaagcttccaa 432  
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 Db 913 ctctcagacacactcgaagatcatagttctaatgtgtcttctgtgtgtgtgt 969

# RESULT 5

AAV84347  
 ID AAV84347 standard; cDNA; 1180 BP.

XX AAV84347;

XX 26-APR-1999 (first entry)

DE Human Apo-2DcR cDNA clone DNA33085.

XX Apo-2DcR; human; apoptosis; tumour necrosis factor receptor;  
 KW neurodegeneration; autoimmune disease; inflammation; cancer;  
 KW therapy; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

PH CDS 193..972

FT /\*tag= a

FT sig-peptide 193..279

FT mat-peptide 280..969

FT CDS 93..972

FT /\*tag= c

FT /\*note= d

FT /\*note= "alternative translational initiation

FT site at 93..95, encodes amino acid

FT residues -40 to 259 of Apo-2DcR"

XX WO9858062-A1.

XX 23-DEC-1998.

XX 12-JUN-1998; 98WO-US12456.

XX 18-JUN-1997; 97US-0878168.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Chuntharapai A, Gurney A;

XX Kim KU, Wood WI;

XX WPI; 1999-095340/08.

XX P-PSDB; AAV84347.

XX New Apo-2DcR polypeptide - used for modulation and diagnosis of  
 PT apoptosis, e.g. in neurodegeneration

XX Claim 36; Page 51-53; 88pp; English.

CC cDNA clone DNA33085 codes for human Apo-2DcR (see AAV88408), a novel  
 CC member of the tumour necrosis factor receptor family that binds to  
 CC Apo-2 ligand. It was isolated by: transformation of yeast with a





```

QY 61 gtccctactactctgccaaccatctcccgccgaggaagttccccaagacagtggcc 120
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Db 204 gtcttaactactctgtccaccactctcccgccgaggaagttccccaagacagtggcc 263
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Db 264 ccacagaacaagagagacagcttcaaggaggagagtgctccagaagatctcatagatca 323
QY 181 gaacatctgagagctgttaaccctgtcacagagagtggtgtgtttacccaagcttccaac 240
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Db 324 gaacatctgagagctgttaaccctgtcacagagagtggtgtgtttacccaagcttccaac 383
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    |||||||
Db 384 aatgaacctctctgtcccaatgagctgttaacatcagaatcaaaaataaagtctcc 443
QY 301 tgcacatgacacagagacacagtggtgtcagtgtaaaagagcaccttccggatgtaaac 360
    |||||||
Db 444 tgcacatgacacagagacacagtggtgtcagtgtaaaagagcaccttccggatgtaaac 503
QY 361 tccccaagaagtgtgcccgaagtgtgacaggtgtccctagtggggagagtcacagtcaat 420
    |||||||
Db 504 tccccaagaagtgtgcccgaagtgtgacaggtgtccctagtggggagagtcacagtcaat 563
QY 421 tgtacgtccctggagtgatcccaatgtgttgaagaattgtgtgcacatgccaactgtgaa 480
    |||||||
Db 564 tgtacgtccctggagtgatcccaatgtgttgaagaattgtgtgcacatgccaactgtgaa 623
QY 481 accccaagctctgagaagaacaatgaaacacagcccgaggactctctgcccagctgtgaa 540
    |||||||
Db 624 accccaagctctgagaagaacaatgaaacacagcccgaggactctctgcccagctgtgaa 683
QY 541 gagacaatgaaacacacacacagagactcctgtccccaagctgtgtgaagaacaatgaaac 600
    |||||||
Db 684 gagacaatgaaacacacacacagagactcctgtccccaagctgtgtgaagaacaatgaaac 743
QY 601 agcccgaggactcctgtccccaagctgtgtgaagaacaatgaaacacacagcccgaggactcct 660
    |||||||
Db 744 agcccgaggactcctgtccccaagctgtgtgaagaacaatgaaacacacagcccgaggactcct 803
QY 661 gcccagagctctgagaagaacaatgaaacacagcccgaggactcctgtccttccatgaa 720
    |||||||
Db 804 gcccagagctctgagaagaacaatgaaacacagcccgaggactcctgtccttccatgaa 863
QY 721 ctccacagacacacagctgagagatcatagttcctaattgtgtctgtgattgtgtgt 777
    |||||||
Db 864 ctccacagacacacagctgagagatcatagttcctaattgtgtctgtgattgtgtgt 920

```

RESULT 7  
AAV51348  
ID AAV51348 standard; DNA: 1392 BP.

AC AAV51348;

DT 23-OCT-1998 (first entry)

DE Human TR1D genomic DNA.

KW TRAIL receptor without intracellular domain; TR1D; TNFR-5; human;

KM tumour necrosis factor receptor-5; TNF-related apoptosis-inducing ligand;

KX haematopoietic tissue; immune system; ligand; apoptosis; treatment; ss.

OS Homo sapiens.

XX Homo sapiens.

XX Key

FT CDS

FT sig\_peptide

FT mat\_peptide

FT

```

FT /product= "TR1D"
FT /note= "TRAIL receptor without intracellular domain"
FT
XX
PN W09830693-A2.
XX
PD 16-JUL-1998.
XX
PE 13-JAN-1998; 98WO-US00152.
XX
PR 07-AUG-1997; 97US-0054885.
PR 14-JAN-1997; 97US-0035496.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PI EDner R, Feng P, Gentz RL, Ni J, Ruben SM, Wei Y;
PI Yu G;
DR WPI: 1998-399141/34.
DR P-PSDB: AAW64668.
XX
PT Human TRAIL receptor without an intracellular domain polypeptide -
PT used in the diagnosis of immune system-related disorder(s)
XX
PS Claim 2; Fig 1; 90pp; English.
XX

```

This sequence encodes a human TR1D (TRAIL, (TNF-related apoptosis-inducing ligand) receptor without an intracellular domain). TR1D is a member of the tumour necrosis factor receptor (TNFR) family also known as TNFR-5. CC TR1D is expressed in haematopoietic tissues and other normal human CC tissues. For a number of immune system-related disorders, substantially CC altered (whether increased or decreased) levels of TR1D gene expression CC can be detected, therefore the TR1D polypeptides, nucleic acids and CC antibodies are useful in the diagnosis of such immune system related CC disorders. Mutations of the TR1D gene can also be detected. TR1D can also CC be used to identify ligands which may be useful in the treatment of CC apoptosis related disorders. TR1D is administered to humans at a CC parenteral dose of 0.01 to 1 mg/kg/day.

Sequence 1392 BP; 329 A; 418 C; 368 G; 277 T; 0 other;

Query Match 100.0%; Score 777; DB 19; Length 1392;  
Best Local Similarity 100.0%; Pred. No. 4, 8e-224;  
Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 atggccggatcccccaagacctaaagtgtgtgtcgtacatgctcggtctgtgca 60
    |||||||
Db 183 atggccggatcccccaagacctaaagtgtgtgtcgtacatgctcggtctgtgca 242
QY 61 gtccctactactctgccaaccatctcccgccgaggaagttccccaagacagtggcc 120
    |||||||
Db 243 gtccctactactctgccaaccatctcccgccgaggaagttccccaagacagtggcc 302
QY 121 ccacagaacaagagagacagcttcaaggaggagagtgctccagaagatctcatagatca 180
    |||||||
Db 303 ccacagaacaagagagacagcttcaaggaggagagtgctccagaagatctcatagatca 362
QY 181 gaacatctgagagctgttaaccctgtcacagagagtggtgtgtttacccaagcttccaac 240
    |||||||
Db 363 gaacatctgagagctgttaaccctgtcacagagagtggtgtgtttacccaagcttccaac 422
QY 241 aatgaacctctctgtcccaatgagctgttaacatcagaatcaaaaataaagtctcc 300
    |||||||
Db 423 aatgaacctctctgtcccaatgagctgttaacatcagaatcaaaaataaagtctcc 482
QY 301 tgcacatgacacagagacacagtggtgtcagtgtaaaagagcaccttccggatgtaaac 360
    |||||||
Db 483 tgcacatgacacagagacacagtggtgtcagtgtaaaagagcaccttccggatgtaaac 542
QY 361 tccccaagaagtgtgcccgaagtgtgacaggtgtccctagtggggagagtcacagtcaat 420
    |||||||
Db 543 tccccaagaagtgtgcccgaagtgtgacaggtgtccctagtggggagagtcacagtcaat 602

```

QY	421	tgctctctctcggagtagatgcatccagctgtgttgaaagaatttggtgccaatgccactctgtgaa	480
Db	603	tgtatcgctcccgaggagctgatatccagctgtgtctgaaagaattctgtgtccaaatgcacctgtgtgaa	662
QY	481	accccaagctgtctgaaagagacaatgaaacaacacagcccgggagctctctgccccagctctgaa	540
Db	663	accccaagctgtctgaaagagacaatgaaacaacacagcccgggagctctctgccccagctctgaa	722
QY	541	gagagcaatgaaacaacagccccagagactcctctgccccagctgtctgaaagaagaacaatgacacac	600
Db	723	gagagcaatgaaacaacagccccagagactcctctgccccagctgtctgaaagaagaacaatgacacac	782
QY	601	agcccgggagactcctctgccccagctgtctgaaagagacaatgaaacaacacagcccgggagactct	660
Db	783	agcccgggagactcctctgccccagctgtctgaaagagacaatgaaacaacacagcccgggagactct	842
QY	661	gcccacagctgcttgaagagaaacaatgaaacaacacagcccgggagactctctctcttcaataac	720
Db	843	gcccacagctgcttgaagagaaacaatgaaacaacacagcccgggagactctctctcttcaataac	902
QY	721	ctctcatgcaaccatcgttaagagatcataatgtctctaatgtgtcttgaattgtgtgt 777	
Db	903	ctctcatgcaaccatcgttaagagatcataatgtctctaatgtgtcttgaattgtgtgt 959	

Result	8	
AAC90774		
ID	AAC90774	standard; cDNA; 1392 BP.
XX		
AC	AAC90774;	
XX		
DT	15-MAR-2001	(first entry)
XX		
DE	Human tumour necrosis factor receptor 5 (TRID) encoding cDNA seq	ID NO:1
XX		
KW	Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; neotrophic;	
KW	TRAIL receptor without intracellular domain; diagnosis; cytostatic;	
KW	tumour necrosis factor related apoptosis inducing ligand; vasotropic;	
KW	immunosuppressive; neuroprotective; antiviral; antiinflammatory;	
KW	anticonvulsant; antiparasitic; cardiact; anti-HIV; antiparkinsonian;	
KW	gene therapy; restenosis; graft versus host disease; tumour; cancer;	
KW	apoptotic cell death related disease; autoimmune disorder;	
KW	cardiovascular disorder; viral infection; ss.	
XX		
OS	Homo sapiens.	
XX		
EH	Key	Location/Qualifiers
FT	CDS	183..962
FT		/*tag= a
FT		/product= "TRID"
XX		
PN	W0200071150-A1.	
XX		
PD	30-NOV-2000.	
XX		
PF	18-MAY-2000; 2000MO-US13515.	
XX		
PR	20-MAY-1999; 99US-0135164.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Wei Y, Ruben SM, Gentz RL, Ni J;	
DR	WPI; 2001-041051/05.	
DR	P-PSDB; AAB36596.	
XX		
PT	Nucleic acid encoding a TRID polypeptide, also referred to as tumor	
PT	necrosis factor receptor 5, useful in the diagnosis, treatment or	
PT	prevention of cancer, autoimmune disorders and viral infection -	
XX		
XX	Example 8; Fig 1; 285pp; English.	
XX		

CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without  
CC intracellular domain, also referred to as tumour necrosis factor  
CC receptor 5 (TNFR-5 or TR3). TRID has cytostatic, immunosuppressive,  
CC neurotropic, neuroprotective, antiviral, antiinflammatory, anticoagulant,  
CC antiparasitic, cardiact, anti-HIV, antiparkinsonian and vasotropic  
CC activities, and can be used in gene therapy. The TRID polynucleotides  
CC are useful for detecting complementary polynucleotides. TRID proteins and  
CC polynucleotides are useful in the treatment of tumours, resistance to  
CC parasite, bacteria and viruses, reatensis and graft versus host disease.  
CC They are also useful for inducing proliferation of T-cells, endothelial  
CC cells and certain haematopoietic cells, to regulate antiviral responses  
CC and to prevent certain autoimmune diseases after stimulation of TRID by  
CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID  
CC polypeptides are useful for treating and/or preventing diseases  
CC associated with increased or decreased apoptotic cell death. The TRID  
CC polynucleotides, proteins, antibodies, agonists and antagonists are  
CC useful in the diagnosis, treatment or prevention of: (a) cancer;  
CC (b) autoimmune disorders; (c) diseases associated with increased  
CC apoptosis; (d) cardiovascular disorders; and (e) viral infection.

[illegible]

Db 843 gccccaagctgtgaagagacaatgaccacagccgggagactcgtctcttcattac 902  
 Oy 721 ctccacgacccatcgtgagagatcatatgtcttctgcttgattgtttgt 777  
 Db 903 ctccacgacacacatcgtgagagatcatatgtcttctctgcttgattgtttgt 939

RESULT 9  
 ID AAV56990 standard; cDNA: 1410 BP.  
 AAV56990:  
 11-JAN-1999 (first entry)

Human tumour necrosis related receptor TR5 cDNA.  
 Tumour necrosis related receptor; TR5; human; inflammation;  
 arthritis; septicemia; transplant rejection; autoimmune disease;  
 inflammatory bowel disease; graft versus host disease; infection;  
 stroke; ischemia; acute respiratory disease syndrome; psoriasis;  
 atherosclerosis; brain injury; AIDS; bone disease; cancer;  
 atherosclerosis; Alzheimer's disease; therapy; diagnosis; ss.  
 Homo sapiens.  
 Location/Qualifiers  
 Key 69..968  
 CDS /\*tag= a  
 sig\_peptide 69..263  
 /\*tag= b  
 mat\_peptide 264..965  
 /\*tag= b

EP867509-A2.  
 30-SEP-1998.  
 04-FEB-1998; 98EP-0300827.  
 28-JUL-1997; 97US-0901469.  
 05-FEB-1997; 97US-0795910.  
 (SMIK ) SMITHKLINE BEECHAM CORP.  
 Lyn SDP, Tan KB, Truneh A, Young PR;  
 WPI, 1998-497862/43.  
 P-PSDB; AAW76331.

New polynucleotide encoding TR5 polypeptide - used to diagnose,  
 prevent and treat e.g. inflammation, arthritis, septicemia,  
 autoimmune diseases, infections, stroke, ischemia, ARDS, psoriasis,  
 restenosis, brain injury, AIDS and bone diseases

Claim 4; Fig 1; 22pp; English.

This nucleotide sequence codes for human tumour necrosis related  
 receptor, TR5 (see AAW76331). An expressed sequence tag (EST 213397)  
 derived from a cDNA library made from human prostates was found to  
 have sequence similarity to the human tumour necrosis factor (TNF)  
 receptor. A search through several overlapping ESTs indicated that  
 this represented the 5' most EST of the assemble and so it was  
 completely sequenced. Analysis of the 1410 cDNA sequence indicated  
 that it encoded a complete open reading frame for a novel member of  
 the TNF receptor superfamily. A polynucleotide encoding TR5 can  
 be obtained from a cDNA library derived from mRNA in cells of  
 prostate, endothelial cells, interleukin-1 beta-treated smooth  
 muscle cells, foetal liver spleen cells, and pregnant uterus using  
 expressed sequence tag analysis. Treatment of a subject in need of  
 enhanced TR5 polypeptide activity comprises administering an agonist  
 to the polypeptide and/or providing TR5 polynucleotide in a form so  
 as to effect production of the polypeptide activity in vivo.

CC Treatment of a subject with the need to inhibit TR5 polypeptide  
 CC activity comprises administering an antagonist to the polypeptide,  
 CC administering a nucleic acid that inhibits the expression of the  
 CC nucleotide sequence encoding the polypeptide and/or administering a  
 CC polypeptide that competes with the polypeptide for its ligand.  
 CC substrate or receptor. Diagnosing a disease or a susceptibility  
 CC to a disease related to expression or activity of TR5 polypeptide,  
 CC comprises determining the presence or absence of mutation in the  
 CC nucleotide sequence encoding the TR5 polypeptide in the genome of  
 CC the subject and/or analysing for the presence or amount of TR5  
 CC polypeptide expression in a sample. Identification of compounds  
 CC which bind to TR5 comprises contacting host cells with a candidate  
 CC compound and assessing the ability of it to bind to the cells. The  
 CC active agents can be used for the treatment of chronic and acute  
 CC inflammation, arthritis, septicemia, autoimmune diseases (e.g.  
 CC inflammatory bowel disease, psoriasis), transplant rejection,  
 CC graft vs host disease, infection, stroke, ischemia, acute  
 CC respiratory disease syndrome, restenosis, brain injury, AIDS, bone  
 CC diseases, cancer (e.g. lymphoproliferative disorders),  
 CC atherosclerosis and Alzheimer's disease.

XX Sequence 1410 BP; 342 A; 420 C; 371 G; 277 T; 0 other;  
 SQ

Query Match 100.0%; Score 777; DB 19; Length 1410;  
 Best Local Similarity 100.0%; Pred. No. 4,9e-224;  
 Matches 777; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 atggccggatccccaagaccctaagttcgtcgtcatcgtcgcggtctctgcca 60  
 Db 189 atggccggatccccaagaccctaagttcgtcgtcatcgtcgcggtctctgcca 248  
 Oy 61 gtcttaactactctgcacacacgtcccgagagagaaftccccaagacgttggc 120  
 Db 249 gtcttaactactctgcacacacgtcccgagagagaaftccccaagacgttggc 308  
 Oy 121 ccacagcaacagagagacagcttcaaggggagagagtgctccagagatctcatagta 180  
 Db 309 ccacagcaacagagagacagcttcaaggggagagagtgctccagagatctcatagta 368  
 Oy 181 gaacatctggaagcctgtaaccgctgcacagagaggtgtgattacacaagcttccaac 240  
 Db 369 gaacatctggaagcctgtaaccgctgcacagagaggtgtgattacacaagcttccaac 428  
 Oy 241 aatgaacctcttctcccatgacagttgtgtaatacagatacaaaaataaagtctc 300  
 Db 429 aatgaacctcttctcccatgacagttgtgtaatacagatacaaaaataaagtctc 488  
 Oy 301 tgcacatgacagagacacagtgctcagtgtaagaagacacctccggaatgaaac 360  
 Db 489 tgcacatgacagagacacagtgctcagtgtaagaagacacctccggaatgaaac 548  
 Oy 361 tccccaagatgtgcggaaagttagcaggtgccttagtggggaagtccaagtcaat 420  
 Db 549 tccccaagatgtgcggaaagttagcaggtgccttagtggggaagtccaagtcaat 608  
 Oy 421 tgtacgtccctggagatgatatccagtggtgtaagaattgtgtccaatgacactgtgaa 480  
 Db 609 tgtacgtccctggagatgatatccagtggtgtaagaattgtgtccaatgacactgtgaa 668  
 Oy 481 accccaagctgtgaagagacaataaacacagccgggagactctgcccagctggaa 540  
 Db 669 accccaagctgtgaagagacaataaacacagccgggagactctgcccagctggaa 728  
 Oy 541 gagacaatgaaacacacagccagagactctgcccagctgtgtaagaagacaatgaaac 600  
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 Oy 601 agcccgagatctctgcccagctgtcgtgaagaagacaatgaaacacagccgggactct 660  
 Db 789 agcccgagatctctgcccagctgtcgtgaagaagacaatgaaacacagccgggactct 848  
 Oy 661 gccccaagctgtgaagagacaatgaccacagccgggagactctgctcttcattac 720

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Oy 721 ctctcatgaccatgtaggagatcatattcatgtctctgtagttgtt 777  
Db 909 ctctcatgaccatgtaggagatcatattcatgtctctgtagttgtt 965  
RESULT 10  
AAZ21096  
ID AAZ21096 standard; cDNA: 1121 BP.  
XX  
AC AAZ21096;  
DT 17-NOV-1999 (first entry)  
XX  
DE Human secreted protein clone ljl442\_1 encoding cDNA.  
XX  
KW Human; secreted protein; biological activity; nutritional; cytokine;  
KW cell proliferation; differentiation; immune stimulating; vaccine;  
KW haematopoiesis regulation; tissue growth; haemostatic; thrombolytic;  
KW anti-inflammatory; tumour inhibition; ss.  
XX  
OS Homo sapiens.  
XX  
PN MO9946287-A1.  
XX  
PD 16-SEP-1999.  
XX  
PE 11-MAR-1999; 99MO-US05243.  
XX  
PR 11-MAR-1998; 98US-0077521.  
PR 14-MAY-1998; 98US-0079124.  
PR 10-MAR-1999; 99US-0266105.  
XX  
PA (GENM ) GENETICS INST INC.  
XX  
PI Jacobs K, McCoy JM, Lavalie ER, Collins-Racie LA, Evans C;  
PI Merberg D, Treacy M, Agostino MJ, Steininger RJ;  
XX  
DR WPI: 1999-551362/46.  
DR P-PSDB: AAY29864.  
XX  
PT Polynucleotides encoding secreted human proteins, derived from human  
PT fetal brain, human adult blood, human adult bladder, or human adult  
PT neural tissue cDNA libraries.  
XX  
PS Claim 16; Page 103; 118bp; English.  
XX  
CC AAZ21093 to AAZ21102 encode new human secreted proteins and AAY29861 to  
CC AAY29873 represent the secreted proteins encoded by the polynucleotide  
CC sequences. AAZ21103 to AAZ21112 represent probes for the secreted  
CC proteins. The polynucleotides and proteins are predicted to have  
CC biological activities which would make them suitable for treating,  
CC preventing or ameliorating medical conditions in humans and animals,  
CC although no supporting data is given. Suggested activities include  
CC nutritional activity, cytokine and cell proliferation/differentiation  
CC activity, immune stimulating (e.g. as vaccines) or suppressing activity,  
CC haematopoiesis regulating activity, tissue growth activity,  
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory  
CC activity, cadherin/tumour invasion suppressor activity, and tumour  
CC inhibition activity. The polynucleotides and proteins can also be used  
CC as nutritional sources or supplements. Such uses include use as a protein  
CC or amino acid supplement, use as a carbon source, use as a nitrogen  
CC source and use as a source of carbohydrate. They may also have utility  
CC in compositions used for bone, cartilage, tendon, ligament, and/or nerve  
CC tissue growth or regeneration, as well as for wound healing and tissue  
CC repair and replacement, and in the treatment of burns, incisions and  
CC ulcers. The proteins which induce cartilage and/or bone growth in  
CC circumstances where bone is not normally formed, have application in  
CC the healing of bone fractures and cartilage damage or defects in humans  
CC and other animals.

XX  
SQ Sequence 1121 BP; 289 A; 325 C; 290 G; 216 T; 1 other;  
Query Match 99.8%; Score 775.4; DB 20; Length 1121;  
Best Local Similarity 99.9%; Pred. No. 1.3e-223;  
Matches 776; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Oy 1 atggcccgagatccccaagaccctaaagtctgctgcatcgtcgcggtccctgcga 60  
Db 183 atggcccgagatccccaagaccctaaagtctgctgcatcgtcgcggtccctgcga 242  
Oy 61 gtccatgactactctgtccaccactgtcccgagaggaagtccccaagacagtggcc 120  
Db 243 gtccatgactactctgtccaccactgtcccgagaggaagtccccaagacagtggcc 302  
Oy 121 ccacagcaacagagacagcttcaaggaggagagtgctccagagatctcattagatca 180  
Db 303 ccacagcaacagagagcagcttcaaggaggagagtgctccagagatctcattagatca 362  
Oy 181 gaacatactgagcctgttaaccctgtcacagagggtgtgattacacacagcttccaac 240  
Db 363 gaacatactgagcctgttaaccctgtcacagagggtgtgattacacacagcttccaac 422  
Oy 241 aatgaacctctgtctcccatgtacagttgttaattcaatacaaaaataaagtctcc 300  
Db 423 aatgaacctctgtctcccatgtacagttgttaattcaatacaaaaataaagtctcc 482  
Oy 301 tgcaccatgacacagacagctgtgtcagtgtaagaaggacacttccggaaatgaanaac 360  
Db 483 tgcaccatgacacagacagctgtgtcagtgtaagaaggacacttccggaaatgaanaac 542  
Oy 361 tccccaagatgtgtccggaagtgtcagcaggtgacctagtgaggagagtcacagtcaaat 420  
Db 543 tccccaagatgtgtccggaagtgtcagcaggtgacctagtgaggagagtcacagtcaaat 602  
Oy 421 tgtacgtctcgtgagatgatcatcagtggtgtgaagaatttggtccaaatgccaatgtgaa 480  
Db 603 tgtacgtctcgtgagatgatcatcagtggtgtgaagaatttggtccaaatgccaatgtgaa 662  
Oy 481 accccaagctgtgaaagagacattgaacacagcccgaggactctgtcccaagctcgaa 540  
Db 663 accccaagctgtgaaagagacattgaacacagcccgaggactctgtcccaagctcgaa 722  
Oy 541 gagaacaatgaacacagcccgaggactctgtcccaagctgtgaaagacatgaaccac 600  
Db 723 gagaacaatgaacacagcccgaggactctgtcccaagctgtgaaagacatgaaccac 782  
Oy 601 agcccgaggactctgtcccaagctgtgaaagacatgaaccacagcccgaggactct 660  
Db 783 agcccgaggactctgtcccaagctgtgaaagacatgaaccacagcccgaggactct 842  
Oy 661 gccccagctgtgaaagagacattgaacacagcccgaggactctgtcccttcattac 720  
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Oy 721 ctctcatgaccatgtaggagatcatattcatgtctctgtagttgtt 777  
Db 903 ctctcatgaccatgtaggagatcatattcatgtctctgtagttgtt 959  
RESULT 11  
AAZ23412  
ID AAZ23412 standard; DNA: 1365 BP.  
XX  
AC AAZ23412;  
XX  
DT 18-JUN-1999 (first entry)  
XX  
DE Human hAP09 DNA.  
XX  
KW Tumour necrosis factor receptor; signal transducer molecule; TNF; AP04;  
KW developmental abnormality; gestational abnormality; prostate cancer;

KM APO6; APO6; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;  
KM cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;  
KM apoptosis; human; ss.  
XX Homo sapiens.  
OS  
FH Key Location/Qualifiers  
FT CDS 123..955  
FT /tag= a  
FT /product= "APO9"  
XX  
XX WO9911791-A2.  
XX  
XX 11-MAR-1999.  
XX  
XX PD  
XX PF 04-SEP-1998; 98WO-US18393.  
XX  
XX PR 05-SEP-1997; 97US-0924634.  
XX  
XX PA (UNIM ) UNIV WASHINGTON.  
XX  
XX PI Chaudhary PM;  
XX  
XX WPI: 1999-205191/17.  
XX P-PSDB: AAM93578.  
XX  
XX DR  
XX  
XX PT New Tumor Necrosis Factor family receptor polypeptides and ligands -  
XX PT useful for diagnosis and treatment of prostate cancer and  
XX PT developmental or gestational abnormalities  
XX  
XX Example III: Fig 6; 156pp; English.  
XX  
XX PS  
XX  
XX CC This invention describes isolated Tumor Necrosis Factor (TNF) family  
XX CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active  
XX CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or  
XX CC their active fragments. APO4 is useful for diagnosing prostate cancer  
XX CC by determining levels of APO4 in an individual. Prostate cancer can also  
XX CC be treated using APO4 selective binding agents linked to a therapeutic  
XX CC moiety. APO4 polypeptides are also useful for identifying selective  
XX CC binding agents, useful in diagnosis/treatment of disease by binding of  
XX CC agents to the polypeptide/active fragment which is extracellular, or  
XX CC expressed on the cell surface. The binding is preferably performed in  
XX CC vivo. APO4 polypeptides/ active fragments are also useful for screening  
XX CC for agonists and antagonists by binding and observing the change in APO4  
XX CC activity. Effective pharmacological agents useful in diagnosis or  
XX CC treatment of disease are also identified using APO4 polypeptides/active  
XX CC fragments and APO4 signal transducer molecules that specifically interact  
XX CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4  
XX CC activity. The method is performed in vivo or in vitro. Apo polypeptides  
XX CC are all useful as immunogens for preparing antibodies. APO4 is also  
XX CC useful for diagnosis/treatment of developmental or gestational  
XX CC abnormalities. APO8 was transfected to human breast carcinoma cell line  
XX CC MCF-7, and induced apoptosis.  
XX  
XX SQ Sequence 1365 BP; 321 A; 411 C; 362 G; 271 T; 0 other;

Query Match 99.8%; Score 775.4; DB 20; Length 1365;  
Best Local Similarity 99.9%; Pred. No. 1.5e-223;  
Matches 776; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 atgcccggatccccaagcctaagtctgctgcgtcatcgtcgcggtcctctgcca 60  
DB 176 atgcccggatccccaagcctaagtctgctgcgtcatcgtcgcggtcctctgcca 235  
QY 61 gtccctagcttactctgcccacactgcccgcgaggaagattccccaagagaatggcc 120  
DB 236 gtccctagcttactctgcccacactgcccgcgaggaagattccccaagagaatggcc 295  
QY 121 ccacagcaacagagcagcagcttcaaggaggagagtgccacagcagatcatatataca 180  
DB 296 ccacagcaacagagcagcagcttcaaggaggagagtgccacagcagatcatatataca 355

QY 181 gaacatactggaagcctgtaacccgctgcacagaggtgtgtgattacaacacgtctccaac 240  
DB 356 gaacatactggaagcctgtaacccgctgcacagaggtgtgtgattacaacacgtctccaac 415  
QY 241 aatgaaccttctgtcttcccatgtaacgtttgttaatcagatccaaaataaagtcttc 300  
DB 416 aatgaaccttctgtcttcccatgtaacgtttgttaatcagatccaaaataaagtcttc 475  
QY 301 tgcacatgacagagacacagtgctcagtgtaaaagagacaccttcggaatgaaac 360  
DB 476 tgcacatgacagagacacagtgctcagtgtaaaagagacaccttcggaatgaaac 535  
QY 361 tccccaagatgtgcccgaagtgtacaggtgcccagtgagggaagtcaccaatcagtaac 420  
DB 536 tccccaagatgtgcccgaagtgtacaggtgcccagtgagggaagtcaccaatcagtaac 595  
QY 421 tgaagtcctggagatgatatccaagtgtgtgaagaatttggtgccaatgccaatgtgaa 480  
DB 596 tgaagtcctggagatgatatccaagtgtgtgaagaatttggtgccaatgccaatgtgaa 655  
QY 481 accccaagctgctggaagagacatgaaacacagcccgaggactcctgcccagctgtgaa 540  
DB 656 accccaagctgctggaagagacatgaaacacagcccgaggactcctgcccagctgtgaa 715  
QY 541 gagacaatgaaacacagcccgaggactcctgcccagctgctgaaagagaacatgaccac 600  
DB 716 gagacaatgaaacacagcccgaggactcctgcccagctgctgaaagagaacatgaccac 775  
QY 601 agcccgaggactcctgcccagctgctgaaagagaacatgaaacacagcccgaggactcct 660  
DB 776 agcccgaggactcctgcccagctgctgaaagagaacatgaaacacagcccgaggactcct 835  
QY 661 gccccaagctgctggaagagacatgaaacacagcccgaggactcctgcccagctgctaac 720  
DB 836 gccccaagctgctggaagagacatgaaacacagcccgaggactcctgcccagctgctaac 895  
QY 721 ctctcatgacacatcgtlaagagatcagatcgaatgtgctctcagatgtgtttgt 777  
DB 896 ctctcatgacacatcgtlaagagatcagatcgaatgtgctctcagatgtgtttgt 952

RESULT 12  
AAK25349  
ID AAK25349 standard; DNA; 1361 BP.  
XX  
XX AAK25349;  
AC  
XX 19-JUL-1999 (first entry)  
DT  
XX  
XX Tumour necrosis factor receptor TRAIL-R3 DNA.  
DE  
XX  
XX TRAIL-3; tumour necrosis factor receptor; apoptosis; cancer;  
KM therapy; ss.  
XX  
XX  
XX Mammalia.  
OS  
XX  
XX  
XX Key Location/Qualifiers  
FH 188..967  
FT CDS /tag= a  
FT /product= "TRAIL-R3"  
FT sig\_peptide 188..259  
FT /tag= b  
FT mat\_peptide 260..964  
FT /tag= c  
XX  
XX  
XX WO9912963-A2.  
XX  
XX PD 18-MAR-1999.  
XX  
XX PF 11-SEP-1998; 98WO-US19029.  
XX  
XX PR 06-MAY-1998; 98US-0084422.  
XX 12-SEP-1997; 97US-0058631.

(BL0J ) BIOGEN INC.  
 Tschoopp J;  
 WPI: 1999-276942/23.  
 DR P-PSDB; AAY05726.  
 Novel tumor necrosis factor receptor proteins TRAIL-R2 and TRAIL-R3  
 Disclosure; Page 27; 28pp: English.  
 This nucleotide sequence includes an open reading frame coding for  
 TRAIL-R3 (see AAY05726), a novel mammalian cysteine-rich receptor of  
 the tumour necrosis factor receptor family, i.e. TRAIL-3 and TRAIL-2 (see  
 related to novel receptors for TRAIL, i.e. TRAIL-3 and TRAIL-2 (see  
 AAY05725). TRAIL-3 is a putative glycosylphosphatidylinositol-anchored  
 protein, which is either cell-associated or processed and secreted.  
 Secreted TRAIL-R3 competes for the binding of TRAIL to TRAIL-R1  
 and/or TRAIL-R2, thereby acting as an inhibitor of apoptosis.  
 Expression of TRAIL-R3 is restricted to peripheral blood  
 lymphocytes and skeletal muscle. It is likely that TRAIL-3 acts  
 as an important regulator of TRAIL-R2 and -R3 induced cell death *in*  
*vivo*. A method for preventing or reducing the advancement, severity  
 or effects of an immunological disease involves administering a  
 TRAIL-R2 or TRAIL-R3 blocking agent such as a soluble TRAIL-R  
 (preferably comprising a human immunoglobulin Fc domain) and an  
 antibody. A method of treating cancer involves administration of  
 antibodies against TRAIL-R3 or TRAIL-R2. A method of inducing cell  
 death involves administration of an agent capable of inhibiting the  
 binding of TRAIL-R2 or -R3 to its ligand.

Query Match	99.6%;	Score 773.8;	DB 20;	Length 1361;
Best Local Similarity	99.7%;	Pred. No. 4.4e-223;		
Matches 775; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1	atggccggatccccaaagaccataaattctgtctgtcaatcgcgaggtccctgtgccca	60
Db	188	atggcccgagatccccaaagaccataaagtctgtctgtcaatcgcgaggtccctgtgccca	247
QY	61	gtccctagttactctgtgccacacactgtcccgagagaggaagtctcccagcagacgttgcc	120
Db	248	gtccctagttactctgtgccacacactgtcccgagagaggaagtctcccagcagacgttgcc	307
QY	121	ccacagcaacagagagcacagcttcaagggggagagtgctccagcaggatctcataagta	180
Db	308	ccacagcaacagagagcacagcttcaagggggagagtgctccagcaggatctcataagta	367
QY	181	gaacatactgaagctctgtaaacccgtgcaacagaggtgtgatatcaccaacgcttccaa	240
Db	368	gaacatactgtagcctgtlaaacccgtgcaacagaggtgtgatatcaccaacgcttccaa	427
QY	241	aatgaaccttcttgcttcccatgtgacagttgtgtataatcagatacaaaacataaagtctc	300
Db	428	aatgaaccttcttgcttcccatgtgacagttgtgtataatcagatacaaaacataaagtctc	487
QY	301	tgcaccatgacacagagacacagtggtgtcaagtgtaaagaagcaccttcggaatgaaac	360
Db	488	tgcaccatgacacagagacacagtggtgtcaagtgtaaagaagcaccttcggaatgaaac	547
QY	361	tccccaagagatgtcccggaatgtgaagagatggtccctgtggggaagtccaaagtcagta	420
Db	548	tccccaagagatgtcccggaatgtgaagagatggtccctgtggggaagtccaaagtcagta	607
QY	421	tgtatgtctccctggagatgatataccagtgtgttgaagaatttgggtgcatactgcacgttgaa	480
Db	608	tgtatgtctccctggagatgatataccagtgtgttgaagaatttgggtgcatactgcacgttgaa	667
QY	481	accccaagctgtctgaagagacaatgaacaccaagcccgaggatccctgtcccaagctgtgaa	540

Db	668	accocagctgtcgtgaaagagacaatgaacaacacagcccgvgagactctctgccacgctgtctgaa	727
OY	541	gagacaatvgaaacacacacagcccaaggagactctctcggcccaagctgcgtgaagagacaatvgaacac	600
Db	728	gagacaatvgaaacacacacagcccaaggagactctctcggcccaagctgtcgaagagacaatvgaacac	787
OY	601	agcccgvggagactctctcggcccaagctgcgtgaagagacaatvgaacacacaccccgvggagactct	660
Db	788	agcccgvggagactctctcggcccaagctgcgtgaagagacaatvgaacacacaccccgvggagactct	847
OY	661	gcccacagctcgtcgaagagacaatvgaacacacagcccgvggagactctcgtctcttcattac	720
Db	848	gcccacagctcgtcgaagagacaatvgaacacacagcccgvggagactctcgtctcttcattac	907
OY	721	ctctcaatgcaccatcgtatagagatcatatgtcttaattgtctctcgtatgtgttctgt	777
Db	908	ctctcaatgcaccatcgtatagagatcatatgtcttaattgtctctcgtatgtgttctgt	964

RESULT	13
AAH19325	
ID	AAH19325 standard; DNA; 1111 BP.

DT 23-JUL-2001 (first entry)

DE Coding sequence for FLAG-TRID clone with a transmembrane domain.

KM FLAG-epitope tag; transmembrane domain; death domain; apoptosis;  
cell suicide; tissue homeostasis; cell proliferation; KM

KW cell-cell signalling; Trail Receptor without Intracellular Domain; TRID;  
KW ds.

OS Synthetic.

FH	Key	Location/Qualifiers
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
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27	27	27
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31	31	31
32	32	32
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92	92	92
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94	94	94
95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

FT / \*tag= a

FT	sig_peptide	182..250
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FT mat\_peptide 251..985

XX

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DR P-PSDB; AAB82181.

PT Identifying a transmembrane domain of a membrane-spanning protein

PR comprises modifying the nucleic acid encoding a death domain-lacking

XX

XX

CC domain (TM) of a membrane-spanning protein. The method comprises

CC spanning protein (e.g. Trail Receptor without Intracellular Domain; TRID

CC membrane-spanning protein with a candidate nucleic acid sequence to

CC produce a nucleic acid encoding a modified DD-lacking membrane spanning  
 CC protein. The modified nucleic acid is then transfected into a host cell,  
 CC which expresses a DD-containing receptor. The absence of apoptosis of the  
 CC host cell is determined following exposure of the transfected cell to an  
 CC apoptosis-inducing ligand. Candidate nucleic acids encoding TM prevent  
 CC apoptosis of the host cell. The modified nucleic acid encoding the  
 CC modified death domain-lacking membrane-spanning protein can also include  
 CC a nucleic acid sequence encoding an epitope tag. The present sequence is  
 CC the coding sequence for a FLAG-TRID clone, which was used in the method  
 CC of the present invention. This sequence comprises the human TRID coding  
 CC sequence and a sequence encoding the FLAG-epitope tag. The FLAG-epitope  
 CC is a useful marker to purify proteins encoded by the modified DD-lacking  
 CC membrane-spanning protein. The identified TM and membrane-spanning  
 CC proteins may be used in defining processes involved in cell suicide and  
 CC tissue homeostasis, and to evaluate, interfere and treat events, such as  
 CC cell proliferation and cell-cell signalling pathways.

XX Sequence 1111 BP; 276 A; 315 C; 299 G; 221 T; 0 other;

Query Match 95.2%; Score 740; DB 22; Length 1111;

Best Local Similarity 96.6%; Pred. No. 6.3e-213; Mismatches 27; Gaps 1;

Matches 777; Conservative 0; Indels 27; Gaps 1;

QY 1 atggccggatccccaagaccctaagtctgctgcctacgtcgcgcgtctctgcca 60  
 Db 182 atggccggatccccaagaccctaagtctgctgcctacgtcgcgcgtctctgcca 241  
 QY 61 gtccatctactctgc-----accactgcccgcag 93  
 Db 242 gtccatctactctgcgattacaagacgatgacgataagcttaccacgtccgcgag 301  
 QY 94 gaggaagttccccaagacagatggccccaagacagagagagagagagagagag 153  
 Db 302 gaggaagttccccaagacagatggccccaagacagagagagagagagagagag 361  
 QY 154 gagtgtccagcagatctcatagatcagaacatactgagagctgttaaccgtgcacag 213  
 Db 362 gagtgtccagcagatctcatagatcagaacatactgagagctgttaaccgtgcacag 421  
 QY 214 ggtgtgattacaacacagcttccaacatgaaccttctgtccatgtacagttgt 273  
 Db 422 ggtgtgattacaacacagcttccaacatgaaccttctgtccatgtacagttgt 481  
 QY 274 aaatcagatcaaaaataaagtctctgcacatgacccaagacagatgtctcattgt 333  
 Db 482 aaatcagatcaaaaataaagtctctgcacatgacccaagacagatgtctcattgt 541  
 QY 334 aaagaagggacacttcggaaatgaactccccaagatgtgcccgaagtgtacaggtgc 393  
 Db 542 aaagaagggacacttcggaaatgaactccccaagatgtgcccgaagtgtacaggtgc 601  
 QY 394 cctagtggggaagtcgaatcgaatgtatgtctctgggagatgataccagtgtgttaa 453  
 Db 602 cctagtggggaagtcgaatcgaatgtatgtctctgggagatgataccagtgtgttaa 661  
 QY 454 gaattgtgccaatgtgcaatgtgaaaccccaagctgtgaaggagacaataaacccagc 513  
 Db 662 gaattgtgtccaatgtgcaatgtgaaaccccaagctgtgaaggagacaataaacccagc 721  
 QY 514 ccggggagctcctgcctcctcctgaagagacaatgaacacacagcccgagactctgcc 573  
 Db 722 ccggggagctcctgcctcctcctgaagagacaatgaacacacagcccgagactctgcc 781  
 QY 574 ccagctgtcgaagagacaatgaacacacagcccgagactctgcccagctgcgtgaagag 633  
 Db 782 ccagctgtcgaagagacaatgaacacacagcccgagactctgcccagctgcgtgaagag 841  
 QY 634 acaatggcacacagcccgagactctgcccagctgcgtgaagagacaatgaacacacagc 693  
 Db 842 acaatggcacacagcccgagactctgcccagctgcgtgaagagacaatgaacacacagc 901  
 QY 694 ccggggagctcctgcctcctcctcctcattacactcattcagcacacacatgtaggatagttcta 753

Db 902 ccggggagctcctgcctcctcctcctcattacactcattcagcacacacatgtaggatagttcta 961  
 QY 754 atgtgctctgattgtgtgt 777  
 Db 962 atgtgctctgattgtgtgt 985

#### RESULT 14

AAH19326 standard; DNA; 947 BP.

AAH19326;

23-JUL-2001 (first entry)

Coding sequence for FLAG-TRID clone without a transmembrane domain.

FLAG-epitope tag; transmembrane domain; death domain; apoptosis;

cell suicide; tissue homeostasis; cell proliferation;

cell-cell signalling; Trail Receptor without Intracellular Domain; TRID;

ds.

Synthetic.

Key

CDS

sig\_peptide

mat\_peptide

misc\_feature

W0200114542-A1.

01-MAR-2001.

23-AUG-2000; 2000MO-US23112.

25-AUG-1999; 99US-0150747.

(GENO-) GENOME THERAPEUTICS CORP.

Denome SA, Swain PM, Tzellas N;

WPI: 2001-374162/39.

P-PSDB: AAB62182.

Identifying a transmembrane domain of a membrane-spanning protein

useful in defining processes in cell suicide and tissue homeostasis,

comprises modifying the nucleic acid encoding a death domain-lacking

membrane spanning protein

Disclosure; Fig 2; 38pp; English.

The present invention relates to methods for identifying a transmembrane domain (TM) of a membrane-spanning protein. The method comprises modifying a nucleic acid encoding a death domain (DD)-lacking membrane spanning protein (e.g. Trail Receptor without Intracellular Domain; TRID) by replacing the nucleic acid encoding the TM of the DD-lacking membrane-spanning protein with a candidate nucleic acid sequence to produce a nucleic acid encoding a modified DD-lacking membrane spanning protein. The modified nucleic acid is then transfected into a host cell, which expresses a DD-containing receptor. The absence of apoptosis of the host cell is determined following exposure of the transfected cell to an apoptosis-inducing ligand. Candidate nucleic acids encoding TM prevent apoptosis of the host cell. The modified nucleic acid encoding the modified death domain-lacking membrane-spanning protein can also include



CC a nucleic acid sequence encoding an epitope tag. The present sequence is  
CC the coding sequence for a FLAG-TRID clone, which was used in the method  
CC of the present invention. This sequence comprises the human TRID coding  
CC sequence and a sequence encoding the FLAG-epitope tag. The FLAG-epitope  
CC is a useful marker to purify proteins encoded by the modified DD-lacking  
CC membrane-spanning protein. The identified TM and membrane-spanning  
CC proteins may be used in defining processes involved in cell suicide and  
CC tissue homeostasis, and to evaluate, interfere and treat events, such as  
CC cell proliferation and cell-cell signalling pathways.  
XX  
XX  
Sequence 947 BP; 246 A; 271 C; 256 G; 174 T; 0 other;

Query Match 87.9%; Score 683; DB 22; Length 947;  
Best Local Similarity 96.4%; Pred. No. 9.2e-196;  
Matches 720; Conservative 0; Mismatches 0; Indels 27; Gaps 1;

QY 1 atggccggaatcccaaacctaaagtgcgtcgtcatcgtgctgctgctgca 60  
DB 182 atggccggaatcccaaacctaaagtgcgtcgtcatcgtgctgctgca 241  
QY 61 gtccatgactctgccc-----accactgcccgagcag 93  
DB 242 gtccatgactctgcccgaatgacagagatgacgataagcttaccactgcccggcag 301  
QY 94 gaggaagttcccccagcagatggtgcccacagcagcagaggttccaaaggggag 153  
DB 302 gaggaagttcccccagcagatggtgcccacagcagcagaggttccaaaggggag 361  
QY 154 gaggttcagcagagatctcctatagatcagaacatactgagcgtgtaaccgtgacagag 213  
DB 362 gaggttcagcagagatctcctatagatcagaacatactgagcgtgtaaccgtgacagag 421  
QY 214 ggtgtggaattacacaaagcttccaaatgaaccttctgttccatgctacagttggt 273  
DB 422 ggtgtggaattacacaaagcttccaaatgaaccttctgttccatgctacagttggt 481  
QY 274 aaatcagatcaaaaacataaaagtctctgacacatgacacagacagatggtcaggtc 333  
DB 482 aaatcagatcaaaaacataaaagtctctgacacatgacacagacagatggtcaggtc 541  
QY 334 aaagaagacaccttcgcgaatgaaaacctccacagatggtccggaagtgtacagaggtgc 393  
DB 542 aaagaagacaccttcgcgaatgaaaacctccacagatggtccggaagtgtacagaggtgc 601  
QY 394 cctagtggaggaagtcacaagtcaatgtgtaagtcctggtggaatcagatcagtggtgaa 453  
DB 602 cctagtggaggaagtcacaagtcaatgtgtaagtcctggtggaatcagatcagtggtgaa 661  
QY 454 gaattggtgccaatgccaatgtggaacccacagctgctggaagagacaatggaaccagc 513  
DB 662 gaattggtgccaatgccaatgtggaacccacagctgctggaagagacaatggaaccagc 721  
QY 514 ccggggagactctgcccagctgctggaagagacaatggaaccacagcccggaactctgccc 573  
DB 722 ccggggagactctgcccagctgctggaagagacaatggaaccacagcccggaactctgccc 781  
QY 574 ccaactgctggaagagacaatggaaccacagcccggaactctgcccagctgctggaagag 633  
DB 782 ccaactgctggaagagacaatggaaccacagcccggaactctgcccagctgctggaagag 841  
QY 634 acaatgacacacagcccggaactctgcccagctgctggaagagacaatggaaccacagc 693  
DB 842 acaatgacacacagcccggaactctgcccagctgctggaagagacaatggaaccacagc 901  
QY 694 ccggggagactctgcccagctgctggaagagacaatggaaccacagc 720  
DB 902 ccggggagactctgcccagctgctggaagagacaatggaaccacagc 928

RESULT 15  
AAZ50893  
ID AAZ50893 standard; cDNA: 1431 BP.

XX  
AC AAZ50893;  
XX  
XX  
DT 31-MAY-2000 (first entry)  
XX  
XX  
DE Human receptor-associated protein cDNA from Incyte clone 3472455.  
KW Human receptor-associated protein; HRAP; Incyte clone 3472455;  
KW cytosolic; immunomodulatory; antiinflammatory; cardiant; antianaemic;  
KW antiarteriosclerotic; hepatotropic; antiarthritic antirheumatic;  
KW antiasthmatic; osteopathic; antiallergic; antidiabetic; dermatological;  
KW neuroprotective; diagnosis; treatment; prevention; reproductive disorder;  
KW cardiovascular; cell proliferative; autoimmune; inflammatory; allergy;  
KW gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS;  
KW arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis;  
KW multiple sclerosis; irritable bowel syndrome; ss.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 80..1240  
FT /tag= a  
FT /product= "HRAP"  
XX  
XX  
PN MO200008155-A2.  
XX  
PD 17-FEB-2000.  
XX  
XX  
PE 06-AUG-1999; 99WO-US17777.  
XX  
XX  
PR 07-AUG-1998; 98US-0160065.  
PR 01-SEP-1998; 98US-0098703.  
XX  
XX  
PA (INCY) INCYTE PHARM INC.  
XX  
XX  
PI Hillman JL, Yue H, Lal P, Tang YT, Gorgone GA, Guejler KJ;  
PI Corley NC, Baughn MR;  
XX  
DR WPI: 2000-205710/18.  
XX  
XX  
DR P-PSDB; AAY69991.  
XX  
XX  
PT New human receptor-associated proteins (HRAP) useful for the diagnosis,  
PT treatment and prevention of cell proliferative, autoimmune,  
PT inflammatory, reproductive, cardiovascular, and gastrointestinal  
PT disorders.  
XX  
XX  
PS Claim 9; Page 92; 99pp; English.  
XX  
XX  
CC The present sequence is a cDNA encoding human receptor-associated protein  
CC (HRAP) from Incyte clone 3472455 obtained from LUNGNOT27 cDNA library.  
CC This sequence is expressed in musculoskeletal, cardiovascular  
CC and urologic tissues. HRAP has cytosolic, immunomodulatory,  
CC antiinflammatory, cardiant, antiarteriosclerotic, hepatotropic,  
CC antiarthritic, antirheumatic, osteopathic, antiallergic, antianaemic,  
CC antiasthmatic, antidiabetic, dermatological and neuroprotective  
CC activities. The present sequence is useful in the diagnosis, treatment  
CC and prevention of disorders associated with HRAP expression, especially  
CC cell proliferative, autoimmune/inflammatory, reproductive,  
CC cardiovascular and gastrointestinal disorders (e.g. atherosclerosis,  
CC cirrhosis, leukaemia, cancer, AIDS, arthritis, allergies, anaemia, and  
CC asthma, dermatitis, diabetes, osteoporosis, multiple sclerosis and  
CC irritable bowel syndrome).  
XX  
XX  
SQ Sequence 1431 BP; 364 A; 377 C; 378 G; 312 T; 0 other;

Query Match 49.1%; Score 381.4; DB 21; Length 1431.  
Best Local Similarity 82.0%; Pred. No. 1.1e-104;  
Matches 452; Conservative 0; Mismatches 96; Indels 3; Gaps 1;  
QY 6 ccggaatcccaagaccctaaagtctgctgctatcgtgcggtgcgcgcagctctc 65  
DB 175 cctggaaccacaagatccttaagtctgcttctcctcgtcgtgctcgtcgcgtcgc 234







GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 13, 2002, 09:34:04 ; Search time 48.56 Seconds

(Without alignments)  
3930.338 Million cell updates/sec

Title: US-09-826-212-1-COPY\_183\_959

Perfect score: 777

Sequence: 1 atgcccgcgatacccaagac.....tgctctgattgtgtgtgt 777

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: Issued\_Patents\_NA:\*  
2: /cgn2\_6/prodata/1/lna/5A\_COMB.seq:\*  
3: /cgn2\_6/prodata/1/lna/5B\_COMB.seq:\*  
4: /cgn2\_6/prodata/1/lna/6A\_COMB.seq:\*  
5: /cgn2\_6/prodata/1/lna/6B\_COMB.seq:\*  
6: /cgn2\_6/prodata/1/lna/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	777	100.0	1392	US-09-006-353A-1	Sequence 1, Appl
2	381.4	49.1	356	US-09-086-483A-1	Sequence 1, Appl
3	262.8	33.8	398	US-09-086-483A-15	Sequence 15, Appl
4	229.8	29.6	1407	US-09-505-250-2	Sequence 2, Appl
5	229.8	29.6	2152	US-09-013-895A-1	Sequence 1, Appl
6	226.2	29.1	1323	US-08-883-036A-1	Sequence 1, Appl
7	195	25.1	1799	US-09-329-633A-1	Sequence 1, Appl
8	195	25.1	1799	US-09-079-029-2	Sequence 2, Appl
9	195	25.1	3881	US-09-333-593A-1	Sequence 1, Appl
10	165.2	21.3	506	US-09-006-353A-15	Sequence 15, Appl
11	109	14.0	1062	US-09-333-593A-3	Sequence 3, Appl
12	94.6	12.2	340	US-09-006-353A-17	Sequence 17, Appl
13	91.6	11.8	241	US-09-006-353A-18	Sequence 18, Appl
14	39.4	5.1	1392	US-09-006-353A-1	Sequence 1, Appl
15	39.2	5.0	336	US-07-814-220-3	Sequence 3, Appl
16	39.2	5.0	336	US-07-814-220-4	Sequence 4, Appl
17	38	4.9	336	US-07-814-220-4	Sequence 4, Appl
18	38	4.9	336	US-07-814-220-4	Sequence 4, Appl
19	38	4.9	1147	US-08-761-277A-44	Sequence 44, Appl
20	37.8	4.9	116	US-08-986-727-14	Sequence 14, Appl
21	37.6	4.9	568	US-08-986-727-5	Sequence 5, Appl
22	37.6	4.8	173	US-08-543-020-6	Sequence 6, Appl
23	37.6	4.8	173	US-08-735-692-8	Sequence 8, Appl
24	37.6	4.8	173	US-08-542-051-5	Sequence 5, Appl
25	36.4	4.7	3292	US-09-336-447A-14	Sequence 14, Appl
26	36.4	4.7	4403765	US-09-103-840A-2	Sequence 2, Appl
27	35.8	4.6	297	US-08-767-026-8	Sequence 8, Appl

28	35.8	4.6	6889	US-08-286-740-2	Sequence 2, Appl
29	35.8	4.6	6889	PCT-US95-09576-2	Sequence 2, Appl
30	35.4	4.6	426	US-09-013-895A-6	Sequence 6, Appl
31	35.4	4.6	3489	US-08-728-323A-1	Sequence 1, Appl
32	35.4	4.6	4614	US-08-325-267A-1	Sequence 1, Appl
33	35.4	4.6	5511	US-08-928-361B-2	Sequence 2, Appl
34	35.4	4.6	7334	US-08-928-361B-1	Sequence 1, Appl
35	35.4	4.6	32207	US-08-770-379-20	Sequence 20, Appl
36	35.4	4.6	32207	US-08-757-669A-20	Sequence 20, Appl
37	35.4	4.6	32207	US-09-230-371A-20	Sequence 20, Appl
38	34.6	4.5	1460	US-09-290-640-65	Sequence 65, Appl
39	34.6	4.5	2078	US-08-785-310A-1	Sequence 1, Appl
40	34.4	4.4	2464	US-07-863-169A-4	Sequence 4, Appl
41	34.4	4.4	2464	US-08-429-964-4	Sequence 4, Appl
42	34.4	4.4	2464	US-07-935-087-4	Sequence 4, Appl
43	34.4	4.4	2464	PCT-US93-08062-4	Sequence 4, Appl
44	34.2	4.4	2413	US-08-651-579-1	Sequence 1, Appl
45	34.2	4.4	3349	US-09-336-447A-2	Sequence 2, Appl

## ALIGNMENTS

RESULT 1  
US-09-006-353A-1  
; Sequence 1, Application US/09006353A  
; Patent No. 6261801  
; GENERAL INFORMATION:  
; APPLICANT: WEI, YING-FEI  
; APPLICANT: YU, GUO-LIANG  
; APPLICANT: GENTZ, REINER  
; APPLICANT: RUBEN, STEVEN  
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
; STREET: 9410 KEY WEST AVENUE  
; CITY: ROCKVILLE  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/006,353A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROOKES, ANDERS A  
; REGISTRATION NUMBER: 36,373  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1392 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 183..959  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 183..260  
; FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 261..959



QY 366 agaatgctgcgcgaagtgtaga---ggtccctagttgaggagttccaaagtcagtaattg 422  
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Db 564 TGAGATGTGCGGACGTGTAGAACAGGGTGTCCAGAGAGGATGGTCAAGTAAATG 623  
QY 423 taactcttgatgtatataccagttgtttgaaatttggtccaatgtcgaattgtgaaac 482  
|||||  
Db 624 TACGCCCCGGGTGACATCAAGTCAAAATGAATCAGCTGCGAGTTCCTGCGGAAAC 683  
QY 483 cccagctgtgaagaagaatgaaccagcccgaggactctcccaagctgtcgaaga 542  
|||||  
Db 684 CCCAGACGCGGAGAGACAGTACACCATCTCTGGGATGCTTCCCTTATCACTA 743  
QY 543 gacaaatgaaca 553  
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Db 744 CCTATCATCA 754

RESULT 3  
US-09-086-483A-15  
; Sequence 15, Application US/09086483A  
; Patent No. 6214580  
; GENERAL INFORMATION:  
; APPLICANT: NI, et al.  
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
; STREET: 9410 KEY WEST AVENUE  
; CITY: ROCKVILLE  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/086,483A  
; FILING DATE: May-29-98  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/050,936  
; FILING DATE: May-30-97  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/069,112  
; FILING DATE: Dec-9-97  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROOKES, ANDERS A.  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF379  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8439  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 398 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-09-086-483A-15

Query Match 33.8%; Score 262.8; DB 4; Length 398;  
Best Local Similarity 99.2%; Pred. No. 2.5e-71;  
Matches 264; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 atggccggatccccagaccctaagtgtgctgcatcgtcgaggtctgctgca 60  
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Db 133 ATGGCCGGATCCCCAGACCCTAAAGTGTCTGTCATCTGTCGCGGTCTGCTGCA 192

QY 61 gtccatagttactctgcccaccatgcccggcaggaggaaagttcccccagacagttggcc 120  
|||||  
Db 193 GTCTAGTTACTCTGCGCACCATCTBCCCGCAGAGGAAATTCCACACAGACTGGCC 252  
QY 121 ccacagcacacagagcacagcttcaaggaggagtgltccagcagatctcatagatca 180  
Db 253 CCACAGCAACAGAGGACACAGCTTCAAGGGGAGGAGTGTCCAGCAGATCTCATGATCA 312  
QY 181 gaacataatgagcctgtgaaccctgtgcacagagggtgtgatatcaaccaagcttcaac 240  
Db 313 GAACATACTGAGGCGCTGTACCCGTCACAGAGGOTGTGATATCACCAAGCTTCAC 372  
QY 241 aatgaaccttcttcttcccatgtac 266  
|||||  
Db 373 AATGAACCTTCTTCTTCCATGTAC 398

RESULT 4  
US-09-505-250-2  
; Sequence 2, Application US/09505250A  
; Patent No. 6329148  
; GENERAL INFORMATION:  
; APPLICANT: Rosen, Glenn  
; APPLICANT: Kao, Peter  
; TITLE OF INVENTION: Synergistic Anti-Cancer Therapy with  
; TITLE OF INVENTION: Triptolides and Death Domain Ligands  
; FILE REFERENCE: SUN-109PRV2  
; CURRENT APPLICATION NUMBER: US/09/505,250A  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 1407  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1407)  
; OTHER INFORMATION: Human TRAIL Receptor Coding Sequence  
; US-09-505-250-2

Query Match 29.6%; Score 229.8; DB 4; Length 1407;  
Best Local Similarity 73.2%; Pred. No. 6.2e-61;  
Matches 342; Conservative 0; Mismatches 107; Indels 18; Gaps 3;

QY 6 ccgagatcccaagaccctaagttcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 65  
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Db 258 ccgggtccacaagacccttcaagttgtcg-----tcgtcggtgtcgtcgagtgctg 311  
QY 66 agcttactctgccaccatgcccggcaggaggaaagttcccccagcagaagtggcccaca 125  
|||  
Db 312 accatgctcagctgtcaacatc-----aaacttatgatcatatcatgtgcacaca 362  
QY 126 gcaacagagagcagcttcaaggaggagggtgtccacagcagatctcatagatcagaaca 185  
|||||  
Db 363 gcaatgggaacataagccttgggagagttgtccacacagatctcatagatcagaacg 422  
QY 186 tactggaagcctgttaaccgtgcacagagggtgtgatatcaccaagcttccacaatga 245  
|||||  
Db 423 tcctggagcctgttaaccgtgtcacagagggtgtgttacaccaatgttccacaatlt 482  
QY 246 accttctgtctccatgtatcagtttgtaaatcagatcaaaaacataaaattcctgtac 305  
|||||  
Db 483 gttgtgtcctccatgtatcagcttgaatcagatgaagagagagatccctgtgac 542  
QY 306 catcaccaagacacagtggtcagtgtaagaagacaccttccggaaatgaactccc 365  
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Db 543 cagagaccagagacacagatgttcagtgcaaacccgaacttccggaaatgaactctgc 602  
QY 366 agaatgtgcgcgaagtgtaga---ggtccctagttgaggagttccaaagtcagtaattg 422  
|||||

Db 603 tgaagatgcccgaaggtgcagcacaggggtcccccagaggaatggtcgaagtcgaagatg 662  
Qy 423 tactccctggagatgatccagatgtgttcgaagaattgttgccaatg 469  
Db 663 taagccctggagatgacatcgaagtgtgtccacaagaatcacgaagcaatg 709

## RESULT 5

US-09-013-895A-1  
: Sequence 1, Application US/09013895A  
: Patent No. 6342363  
: GENERAL INFORMATION:  
: APPLICANT: NI, Jian  
: APPLICANT: Rosen, Craig A.  
: APPLICANT: Pan, James G.  
: APPLICANT: Gentz, Reiner L.  
: APPLICANT: Dixit, Vishva M.  
: TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death  
: TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor  
: TITLE OF INVENTION: Superfamily and Binding to Trail (Ap02-L)  
: NUMBER OF SEQUENCES: 12  
: CORRESPONDENCE ADDRESSES:  
: ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
: STREET: 9410 KEY WEST AVENUE  
: CITY: ROCKVILLE  
: STATE: MD  
: COUNTRY: US  
: ZIP: 20850  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patentin Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/09/013,895A  
: FILING DATE: 27-JAN-1998  
: CLASSIFICATION:  
: ATTORNEY/AGENT INFORMATION:  
: NAME: STEFFE, ERIC K.  
: REGISTRATION NUMBER: 36,688  
: REFERENCE/DOCKET NUMBER: 1488,1300002  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (202) 371-2540  
: TELEFAX: (202) 371-2540  
: INFORMATION FOR SEQ ID NO: 1:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 2152 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: DNA (genomic)  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: 19..1422  
: US-09-013-895A-1

Query Match 29.6%; Score 229, 8; DB 4; Length 2152;  
Best Local Similarity 73.2%; Pred. No. 7.6e-61;  
Matches 342; Conservative 0; Mismatches 107; Indels 18; Gaps 3;

Qy 6 ccgagatccccaagaacctaaagtctgtcgtcatcgtcgctcgctcgtcagctct 65  
Db 276 CCGGGTCCACAAAGACCTCAAGTTGTG-----TCGTCGGGGTCCGCTGCGACAGTGT 329  
Qy 66 agcttactctgccaccactgccgagaggaagtccccaagacagatggccca 125  
Db 330 ACCTAGCTCAGCTGCATC-----AACTTCATGATCAATCAATTCGACACA 380  
Qy 126 gcaacagaggacagctccaaggagagagatgtccagcagagatctatagatcaga 185  
Db 381 GCAATGGGAACATAGCCCTTTGGAGAGTGTGTCCACACAGATCTCATAGATGAGAAG 440

Qy 186 tactgaagccttgaaccctgtcacagaggtgtgtattaccaccaagcttccaacatga 245  
Db 441 TCCTGGAACCTGTATACCGGTGCACAGAGGTGTGGTTACACCATGCTTCCAAATTT 500  
Qy 246 accctctgtcttccatgtacagtttgaatcagatccaataaacaataaagttcctgac 305  
Db 501 GTTGTGCTTGCCTCCCATGTACAGCTTGAATCAGATGAAGAAAGAGATCCCTGCAC 560  
Qy 306 catgaccagaagacacagatgtcatgttaaagaagcagcttcggaatgaaactccc 365  
Db 561 CAGGACAGAGACACAGATGTCAAGTGCACAAACAGAACTTCCGGAATGACAAATTCG 620  
Qy 366 agagatgtccggaagtga--gggtccctagtgtgggaagtcacagtcagtaattg 422  
Db 621 TGAGATGTGCGGAGGTGCAGACAGGGTCCGCCAGAGGGAATGTCACAGGTCAAGATTG 680  
Qy 423 tactccctggagatgatccagatgtgttcgaagaattgttgccaatg 469  
Db 681 TAAGCCCTGGAGTGCATCAGATGTGTCCACAAAGAAATCAGGCATG 727

## RESULT 6

US-08-883-036A-1  
: Sequence 1, Application US/08883036A  
: Patent No. 6072047  
: GENERAL INFORMATION:  
: APPLICANT: Rauch, Charles  
: APPLICANT: Walczak, Henning  
: TITLE OF INVENTION: Receptor That Binds TRAIL  
: NUMBER OF SEQUENCES: 5  
: CORRESPONDENCE ADDRESSES:  
: ADDRESSEE: Kathryn A. Anderson, Immunex Corporation  
: STREET: 51 University Street  
: CITY: Seattle,  
: STATE: WA  
: COUNTRY: US  
: ZIP: 98101  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: Apple Power Macintosh  
: OPERATING SYSTEM: Macintosh 7.6  
: SOFTWARE: Microsoft Word, Version 6.0.1  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/883,036A  
: FILING DATE: 26-JUN-1997  
: CLASSIFICATION: 536  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US --to be assigned--  
: FILING DATE: 04-JUN-1997  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/829,536  
: FILING DATE: 28-MAR-1997  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/815,255  
: FILING DATE: 12-MAR-1997  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/799,861  
: FILING DATE: 13-FEB-1997  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Anderson, Kathryn A.  
: REGISTRATION NUMBER: 32,172  
: REFERENCE/DOCKET NUMBER: 2625-D  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (206) 587-0430  
: TELEFAX: (206) 233-0644  
: TELEX: 756822  
: INFORMATION FOR SEQ ID NO: 1:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1323 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: cDNA

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; ; HYPOTHETICAL: NO
; ; ANTI-SENSE: NO
; ; IMMEDIATE SOURCE:
; ; CLONE: huTra1-R
; ; FEATURE:
; ; NAME/KEY: CDS
; ; LOCATION: 1..1323
US-08-883-036A-1

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Query Match	29.1%;	Score 226.2;	DB 3;	Length 1323;
Best Local Similarity	65.6%;	Pred. No. 7.6e-60;		
Matches 381; Conservative	0;	Mismatches 188;	Indels 12;	Gaps 3

OY	3	gcccgcgtccccaagagccccaagttcgtcgtcgtatcgtcgtcgtccgtccgtccagt	62
Db	93	GCCCGGGTCCCCAAAGACC-----TTGTCGTCTGTGTGCGCGCGCTCTGCTTTGGT	146
OY	63	cctagcttactctctgcacaccatctcccgycgaggaagttccccaagaacatctgcgcc	122
Db	147	CTCAGCTGAGTCTCTCTGTGATCATCCCAAGACCTAGTCTCCGACGAGAGCGGGCCC	206
OY	123	acagcaacagagggcacagcttccaagggggagagtgctccagcaagatctatagataga	182
Db	207	ACAACAAAAGGCGCCAGCCCCCTAGAGGAGATTGTGTCCACTGGACACCATATCTCAGA	266
OY	183	acatactggagccgttaaccccgctcagaagggctgtgatatcaaccaagcttccacaac	242
Db	267	AGAGCGGTAGAGATTGTCATCTCTCTCAAAATATGGACAGGACTATATGCACTACTGGAATGA	326
OY	243	tgaacctctctgtcttccocatgttacaagtttlaaalcagatccaanaacataaaagttctg	302
Db	327	CCTCTTTTGTGCTTGGCGCTCCACAGGTGATTCAGTGGAATGAGTGAAGTCCGTC	386
OY	303	caccaatgaaccaagagacacaaagtgtgtcaagttlaaagaagcacttccggaatgaanaact	362
Db	387	CACACAGCCAGAAACACAGTGTCTCAGTCCGAAAGGACACTTCCGGGAAAGAAATTTC	446
OY	363	ccagagatatgtcccggaagtgtaaga---ggtgcctcagtggggaagttcaagttcaatga	419
Db	447	TTCTGTAGTGTGTGCGGAAGTCCCCCAAGGAGTGTCCAGAGGAGATGTCAAGTGGGTGA	506
OY	420	tttgcagtctcctggagatgatataccagtggtc---tgaagaatttggtgtccaaatgccactgt	476
Db	507	TTGTATCACCCCTGGAGTGTGATCATGATATGTGTCCACAAAGATTCAGGTTCAAAGCACAGTGG	566
OY	477	ggaacaccccaagctctgaagaagacaatgaacaaccaagcccggtgacttctgtcccaagctgc	536
Db	567	GGAAGCCCCACACTGTGGAGAGAGACGAGCTGACCTCCAGCCCAAGGAGCACTCTCTCCCTG	626
OY	537	tgaagagacaaatgaacacacagcccaaggaactctctgcgccag	577
Db	627	TTTCTCTTCAGGCATTCATCATAGGAGTCAACAGTTGTGACGCCG	667

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RESULT 7
US-09-329-633A-1
: Sequence 1, Application US/09329633A
: Patent No. 6252050
:
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Chuntarapai, Anan
: APPLICANT: Kim, K. Jin
: TITLE OF INVENTION: METHOD FOR MAKING MONOCLONAL ANTIBODIES AND
: TITLE OF INVENTION: CROSS-REACTIVE ANTIBODIES OBTAINABLE BY THE METHOD
: FILE REFERENCE: P14681 (REVISED)
: CURRENT APPLICATION NUMBER: US/09/329,633A
: PRIOR FILING DATE: 1999-06-10
: PRIOR APPLICATION NUMBER: US 60/089,253
: PRIOR FILING DATE: 1998-06-12
: NUMBER OF SEQ ID NOS: 2
: SEQ ID NO 1
: LENGTH: 1799

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; TYPE: DNA
; ORGANISM: human
US-09-329-633A-1

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Query Match	25.1%;	Score 195;	DB 4;	Length 1799;
Best Local Similarity	63.3%;	Pred. No. 3.4e-50;		
Matches 316;	Conservative	0;	Mismatches 180;	Indels 3; Gaps 1

OY	1	atggccggagatccccagaagacctaagtctgtgtctgtaactgtcggggtccgtgtccca	60
Db	224	aggcctgtgctcccggtgtcccaagaacctgtgtctgtgtgtcgcgtggtccctgtgtg	263
OY	61	gtctagctcttactctgtccaccactgtcccgagaggaagtctccacagacagtgtgcc	120
Db	284	gtctaaagtgtgtctgtctctgtatcacccaagaacctagtctccccagcagagcgtgcc	343
OY	121	ccacagcacaagagagcaagatctcaaggaggagagtggtccacgacagatctaaatgata	180
Db	344	ccacacacaaagaaggtccagccctcagagaggtatgtgtccacctgtgaacccataccta	403
OY	181	gaacatactgtgagcctgttaaccgtgtcacagaggtgtgtattacacaaagttccaa	240
Db	404	gaagacggttagagattgtatctctctgtcaaatatgtacagacataagcactcagtgaat	463
OY	241	aatgacctcttctgtcccaatgtgtacaggttgttaaatcaatcaaaaacataaaattcc	300
Db	464	gaacctcttctgtctgtcgtgtcaccaacaggtgtgtatctaaagtgtgaagtgaagctaa	523
OY	301	tgcacatgtacccaagacagacagtgtgtcaagtgttaagaagaagcaccttcggaattga	360
Db	524	tgcacacagacccaagaacacagtggtgtcaagtgtgaagaagaagcaccttcggaagaagat	583
OY	361	tcccaagagatgtgcccggaaatgttagca--gtgtccctgtgtgggaagtccaaagtcagt	417
Db	584	tctcctgtgagatgtgtccggaagaatgtccgcacagaagtgctcccaagaagatgtgtcaag	643
OY	418	aattgtacgtccctggatagatataccaagtgtgttgaagaatttgggtccaatgtccactgtg	477
Db	644	gattgtacacctgtgagatcatcgaattgtgtccacaagaatcatcaggcatcatcatagga	703
OY	478	gaaaccccaagctgtcgtgaag	496
Db	704	gtcacagttgacgacctag	722

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1      RESULT 8
2      US-09-079-029-2
3      Sequence 2, Application US/09079029
4      Patent No. 6342369
5      GENERAL INFORMATION:
6      APPLICANT: Adams, Camilla W.
7      APPLICANT: Ashkenazi, Avi J.
8      APPLICANT: Chuntcharapai, Anan
9      APPLICANT: Kim, Kyung J.
10     TITLE OF INVENTION: Apo-2 Receptor
11     NUMBER OF SEQUENCES: 14
12     CORRESPONDENCE ADDRESS:
13     ADDRESSEE: Genentech, Inc.
14     STREET: 1 DNA Way
15     CITY: South San Francisco
16     STATE: California
17     COUNTRY: USA
18     ZIP: 94080
19     COMPUTER READABLE FORM:
20     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
21     COMPUTER: IBM PC compatible
22     OPERATING SYSTEM: PC-DOS/MS-DOS
23     SOFTWARE: Winpatin (Genentech)
24     CURRENT APPLICATION DATA:
25     APPLICATION NUMBER: US/09/079, 029
26     FILING DATE:
27     CLASSIFICATION:

```

ATTORNEY/AGENT INFORMATION:  
NAME: Martschang, Diane L.  
REGISTRATION NUMBER: 35,600  
REFERENCE/DOCKET NUMBER: P110122  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5416  
TELEFAX: 650/952-9881  
INFORMATION FOR SEO ID NO: 2  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1799 base pairs  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear

Query Match	25.1%	Score 195;	DB 4;	Length 1799;
Best Local Similarity	63.3%	Pred. No. 3.4e-50;		
Matches 316; Conservative	0;	Mismatches 180;	Indels 3;	Gaps 1.

QY	1	atggcccgatgccccaagaacctaaagtcgtgctgctcaatcgctgagctgctcctccca	60
Db	224	AGGCGTGGGGCTCCGGGTCGCCAAGACCCCTTGTGCTGTGTGCGCGGGGCTCTGTTG	283
QY	61	gtccagctctacctcbyccaccactgccgcgagaggaagtlccccagcagatgccc	120
Db	284	GTCCTACGCTGATGTGCTCTGATCACCCACAMAGACCTAGCTCCCGACAGAGCGGCC	343
QY	121	ccacagacacagagagacacagcttaaggggaggaagtgctcagagagatcctataga	180
Db	344	CCACACAAAAGAGTCCAGCCCTCAGAGGGGATTGTGTCCACTGTGACACCATATCTCA	403
QY	181	gaacatactgagagcctgtaaccgctgacagagaggtgtgtaattacacaaacgcttcc	240
Db	404	GAAGACGCTAAGATGGATCTCTCGCAATATGAGCAGGACGACATATGACATCACTG	463
QY	241	aatgaaccttctctctcccatgtaacagttgttaacacagatcaaaaactaaagtcc	300
Db	464	GACCTCTTCTCTCTCTGCGCTGACCAAGGTGTATTCTAGGTGAAGTGAGCTTAAGTCC	523
QY	301	tgcacacatgaccagaagacacagtgctgcagtgtaaaagaagcaacctccgaaatgaa	360
Db	524	TGCACACGACCAAAACACAGTGTGTACAGTGCAGAGCAAGGACACCTTCCGGGAAGAT	583
QY	361	ttccccaagatgtgcggaagtgtgaaga---ggtgcacctagtgtgggaagtccaaagt	417
Db	584	TCTCTGTGAGTGTCCCGAAGTGCAGACAGGGGTGTCCAGAGGGATGATCAAGGTGGT	643
QY	418	aattgcacgtccctggaatgatataatcaagtggtgtgaaagaatttggctgcaatgca	477
Db	644	GATTGTACACCTCTGGAGTGCATGATGTGTGTCCAAAGATCAGCATTCATCATGGA	703
QY	478	gaaacccagctgtctgaag 496	
Db	704	GTCACAGTTTGACGCGGTAG 722	

RESULT 9  
US-09-333-593A-1  
Sequence 1, Application US/09333593A  
Patent No. 6313269  
GENERAL INFORMATION:  
APPLICANT: DEEN, KEITH C.  
APPLICANT: YOUNG, PETER R.  
APPLICANT: MARSHALL, LISA A.  
APPLICANT: ROSHAK, AMY K.  
APPLICANT: TAN, KONG B.  
APPLICANT: TRUENH, ALEMSSEGD  
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR  
TITLE OF INVENTION: TR6  
FILE REFERENCE: GH-50008-2  
CURRENT APPLICATION NUMBER: US/09/333,593A  
CURRENT FILING DATE: 1999-06-15

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? PRIOR APPLICATION NUMBER: 08/916,625
? PRIOR FILING DATE: 1997-08-22
? PRIOR APPLICATION NUMBER: 08/853,684
? PRIOR FILING DATE: 1997-05-09
? PRIOR APPLICATION NUMBER: 60/041,230
? PRIOR FILING DATE: 1997-03-14
? NUMBER OF SEQ ID NOS: 8
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 1
? LENGTH: 3881
? TYPE: DNA
? ORGANISM: HOMO SAPIENS
? FEATURE:
? NAME/KEY: UNSURE
? LOCATION: (3558)(3598)(3601)(3607)(3608)(3619)(3652)(3659)(3686)(3690)
? US-09-353-593A-1

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Query Match	25.1%;	Score 195;	DB 4;	Length 3881;
Best Local Similarity	65.0%;	Pred. No. 4.9e-50;		
Matches 323;	Conservative 0;	Mismatches 165;	Indels 9;	Gaps 2

QY	3	gccccgtgtccccaagagccccaagaattctgtctgtcatcgtgcgggtccgtccgtccag	62
Db	186	gccccgtgtccccaagacc-----ttgtgtctgtgtgtgcgcggtctctgtctgtgt	239
QY	63	ctcgtactactctgcaccaactctgcgggcagagagaattccccaagacagtgtgcc	122
Db	240	ctcgtactgtactctgtctgtatcaaccaagaacctagtctcccaagacagagtcggccc	299
QY	123	acagcaaacagagagacagagcttcaaggaggagagtgtctccagcagagatctatagataga	182
Db	300	acacacaaaagaggtcccgccccctcaaggaggtgtgtgtccactgtgaaacatatctcaga	355
QY	183	acatactgtgagcctctgtacccgtgtcaacagaggtgtgtgatcaccaacgcttccaaca	242
Db	360	agacgtgtagagattgcatctctctcgtcaaatatagacagactatagactcaatgtagta	419
QY	243	tgaacctctgtgtctcccatgtatgaagtgttgaatctgagatcaaaaataataaagtctgt	302
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QY	303	caccatgtgacccaagagacacagctgtgtcagtgftaagaagaagcactctcggatagaataatc	362
Db	480	caccacagtcacgaagaacacagctgtgtcagtgagaagaagcactctcggagaagaattc	533
QY	363	cccaagagatgtgcgggaagtgttaaca---ggtgcctcctagtgtgggaagtccaagtcagtaa	419
Db	540	tccctgagatgtgcgggaagtgtccgaacaggtgttcccaagagagatgtgttcaaggtcgtgtga	599
QY	420	ttgttatctccctgtgatatatccagtggtgttgaagaataattgtgtgccaagtccactgtgtga	479
Db	600	ttgttatccctcgtgtgtgcatctgaaatgtgttccacaagaatcagcatcatcatatagagtc	659
QY	480	aaccccagctgtgtgaag	496
Db	660	cacagttgcagtcgtag	676

RESULT 10  
 US-09-006-353A-15  
 Sequence 15, Application US/09006535A  
 Patent No. 6261801  
 GENERAL INFORMATION:  
 APPLICANT: WEI, YING-FEI  
 APPLICANT: YU, GUO-LIANG  
 APPLICANT: GENTZ, REINER  
 APPLICANT: RUBEN, STEVEN  
 TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
 NUMBER OF SEQUENCES: 26  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HUMAN GENOME SCIENCES, INC.,  
 STREET: 9410 KEY WEST AVENUE



RESULT 12  
US-09-006-353A-17  
Sequence 17, Application US/09006353A  
Patent No. 6261801  
GENERAL INFORMATION:  
APPLICANT: WEI, YING-FEI  
APPLICANT: YU, GUO-LIANG  
APPLICANT: GENTZ, REINER  
APPLICANT: RUBEN, STEVEN  
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
STREET: 9410 KEY WEST AVENUE  
CITY: ROCKVILLE  
STATE: MD  
COUNTRY: US  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/006,353A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BROOKES, ANDERS A  
REGISTRATION NUMBER: 36, 373  
REFERENCE/DOCKET NUMBER: PF41  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 17:



Db 760 GCTGGGGCAGAGTCCCTGGGCTGGTTCATGTCCTTCAGCAGCTGGGGCAGAGATC 701  
QY 662 cccagctgctgaagacaatgaccacccgag 698  
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Db 700 CCCGGGCTGGTTCATGTCCTTCAGCAGCTGGGG 664

## RESULT 15

US-07-814-220-3  
; Sequence 3, Application US/07814220  
; Patent No. 5925540  
; GENERAL INFORMATION:  
; APPLICANT: Cacecl, Thomas  
; APPLICANT: Toch, Thomas E.  
; APPLICANT: Szumanski, Maria B.W.  
; TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND  
; TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WHITHAM, CURTIS & WHITHAM  
; STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,  
; STREET: Suite 900  
; CITY: Reston  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 20191  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/814,220  
; FILING DATE: 23-DEC-1991  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/588,437  
; FILING DATE: 25-SEP-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Whitham, Michael E.  
; REGISTRATION NUMBER: 32,635  
; REFERENCE/DOCKET NUMBER: CIT. 016  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-391-2510  
; TELEFAX: 703-391-9035  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 336 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 31..324  
; US-07-814-220-3

Query Match 5.08; Score 39.2; DB 2; Length 336;  
Best Local Similarity 50.58; Pred. No. 0.01;  
Matches 95; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 526 gcccagctctgaagagacaatgaacacccagcagcagctctgcccagctgctgaagacaatgaacacc 585  
||| |||| |  
Db 49 GCCCGGCGCAGCAGCTGCTGCTGCTGCGCGCGCAGCGAGCGGCTGCGCGCAGCTACTGCG 108  
QY 586 gagacaatgacacccagcagcagctctgcccagctgctgaagacaatgaacacc 645  
||| |||| |  
Db 109 GCGACCGCAGCAGCGGCTGCGCGCAGCTACTGCGCGCGCAGCGGCTGCGCGCAGCT 168  
QY 646 agccggggagctctgcccagctgctgaagagacaatgaacaccagccggggagctcct 705  
||| |||| |  
Db 169 ACCGCTCTACCGCAGCAGCTGCTGCGCGCAGCACTGCGCGCGCAGCGGCTGCG 228

QY 706 gcctcttc 713  
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Search completed: August 13, 2002, 11:26:06  
Job time: 6722 sec





FT		/Label= epitope
ET	Region	142..148
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PN	MO9830693-A2.	
PD	16-JUL-1998.	
PE	13-JAN-1998;	98WO-US00152.
PR	07-AUG-1997;	97US-0054885.
PR	14-JAN-1997;	97US-0035496.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Ehner R, Feng P, Gentz RL, Ni J, Ruben SM, Wei Y,	
PI	Yu G;	
DR	WPI; 1998-399141/34.	
DR	N-PSSB; AAV51348.	
PT	Human TRAIL receptor without an intracellular domain polypeptide -	
PT	used in the diagnosis of immune system-related disorder(s)	
XX		
PS	Claim 1b; Fig 1; 90pp; English.	
XX		
CC	This sequence represents a human TRID (TRAIL (TNF-related	
CC	apoptosis-inducing ligand) receptor without an intracellular domain).	
CC	TRID is a member of the tumour necrosis factor receptor (TNFR) family	
CC	also known as TNRR-5. TRID is expressed in haematopoietic tissues and	
CC	other normal human tissues. For a number of immune system-related	
CC	disorders, substantially altered (whether increased or decreased) levels	
CC	of TRID gene expression can be detected, therefore the TRID polypeptides,	
CC	nucleic acids and antibodies are useful in the diagnosis of such immune	
CC	system related disorders. Mutations of the TRID gene can also be	
CC	detected. TRID can also be used to identify ligands which may be useful	
CC	in the treatment of apoptosis related disorders. TRID is administered to	
CC	humans at a parenteral dose of 0.01 to 1 mg/kg/day.	
XX		
SQ	Sequence 259 AA:	
Query Match	100.0%;	Score 1382; DB 19; Length 259;
Best Local Similarity	100.0%;	Pred. No. 2.5e-86;
Matches 259;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0
OY	1 MARIRKTEKFVVVIAVLLPLVAYSATTAROBEVPQQTVAPRQQRHSFGDEECPAGSHRS 60	
DB	1 marirklkllfvvvlvaavllprlavsataargevpqpqqrhsfxgeecpagshrs 60	
OY	61 EHTGACNCRCTEBVDVTNAASNNPSCSPRCVCVCKSDQHNKSSCTMTRTTVOOCEKSGTRNMEN 120	
DB	61 ehtgacnrcptegvdvtlnaasnnpsctprcvcvsdqkhksstctmttldtvockegtltmen 120	
OY	121 SPEMKRKCSRCSGSEGVQVNSCTSMWDIOCEVEFGANAATGPAAAEETMTMNTSPGTPAAPAE 180	
DB	121 spemkrkcsrcsgsegvqvnscstsmwdioceveefganatvetpraeeetmtspgtpapae 180	
OY	181 ETMTMNTSPGTAPAAEETMTMNTSPGTPAAPAEETMTMNTSPGTPASSHY 240	
DB	181 etmtmntspgtpapaaetmtmntspgtpapaaetmtntspgtpapaaetmtntspgtpasshy 240	
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DB	241 lscitvgitvlivliliv 259	
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ID	AAW88408	
NC	standard; Protein; 259 AA.	
AC	AAW88408;	
XX		

DT	26-Apr-1999	(first entry)
XX	Human Apo-2DCR protein (amino acids 1-259).	
DE		
XX	Apo-2DCR, human; apoptosis; tumour necrosis factor receptor;	
KW	neurodegeneration; autoimmune disease; inflammation; cancer;	
XX	therapy.	
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	Peptide	1..29
FT		/note= "predicted signal peptide"
FT	Domain	1..161
FT		/note= "extracellular domain, this domain is specifically claimed in Claim 5"
FT	Domain	68..109
FT		/note= "cysteine-rich domain"
FT	Domain	110..149
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FT	Peptide	162..176
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FT	Peptide	207..221
FT		/note= "tandem repeat peptide"
FT	Peptide	222..236
FT		/note= "tandem repeat peptide"
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FT		/note= "N-glycosylation"
FT	Modified-site	140
FT		/note= "N-glycosylation"
FT	Modified-site	156
FT		/note= "N-glycosylation"
FT	Modified-site	169
FT		/note= "N-glycosylation"
FT	Modified-site	184
FT		/note= "N-glycosylation"
XX		
PN	W09858062-A1.	
XX		
PD	23-DEC-1998.	
XX		
PF	12-JUN-1998;	98WO-US12456.
XX		
PR	18-JUN-1997;	97US-0878168.
XX		
PA	(GENTH ) GENENTECH INC.	
XX		
PI	Ashkenazi AJ, Baker KP, Chuntharapai A, Gurney A;	
PI	Kim KJ, Wood WI;	
XX		
DR	WPI: 1999-095340/08.	
XX		
XX	N-PSDB; AAV84347.	
XX		
PT	New Apo-2DCR polypeptide - used for modulation and diagnosis of	
PT	apoptosis, e.g. in neurodegeneration	
PS	Claim 1; Page 50-51; 88pp; English.	
XX		
CC	This polypeptide comprises human Apo-2DCR, a novel member of the	
CC	tumour necrosis factor receptor family that binds to Apo-2 ligand.	
CC	Its amino acid sequence was deduced from the nucleotide sequence	
CC	of an isolated cDNA clone (see AAV84347); an alternative translation	
CC	initiation site in this clone will encode a polypeptide (see	
CC	AAV84347) comprising amino acid residues 40 to 269 of Apo-2DCR.	
CC	Apo-2DCR shows more sequence identity to DR4 (60%) and Apo-2 (50%)	
CC	than to other apoptosis-linked receptors. The polypeptide can be	
CC	obtained by expression in host cells using the vector deposited as	

CC ATCC 209087. The invention provides vectors and host cells for  
 CC recombinant production of Apo-2Dcr polypeptides, antibodies, and  
 CC transgenic and knockout animals (useful e.g. for screening and  
 CC developing drugs that protect against excessive apoptosis).  
 CC Apo-2Dcr, or chimeras comprising Apo-2Dcr or its (claimed)  
 CC extracellular domain fused to a heterologous polypeptide are used  
 CC to modulate apoptosis of mammalian cells (claimed) and/or NF-kappaB  
 CC activation by Apo-2 ligand, and may be expressed in vivo or ex vivo  
 CC for gene therapy. They can be used in methods for the modulation  
 CC and diagnosis of apoptosis e.g. in cases of neurodegeneration,  
 CC autoimmune diseases and inflammation. Most human tumour cells do  
 CC not express Apo-2Dcr transcripts, but normal tissues do, suggesting  
 CC that Apo-2Dcr may permit selective killing of cancer cells by Apo-2  
 CC ligand, possibly by protecting normal, but not cancerous, cells.  
 XX Sequence 259 AA;

Query Match 100.0%; Score 1382; DB 20; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-86;  
 Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPKTKFVVYIYAVLLPVLAISATTARQEEVPOQIVAPQOQRHSFGECPPAGSHRS 60  
 Db 1 maripkltkfvvviavallpvlaysattarqeevpqqtvpqqrhsfkgcecpagshrs 60  
 QY 61 EHTGACNPCTEGVDYTNASNNPSCFPCIVCKSDOKHKSCTMTRTDYCOCKEGFRNEN 120  
 Db 61 ehtgacnptcegvdytnasnnepscfcipcvcksdqkhksctmttdtvcqckegfrnen 120  
 QY 121 SPENCRKCSRPCEGVQVSNCTSMDDIOCEFEFGANATVETPAEEMNTSPGTPAPAE 180  
 Db 121 spencrkcsrpscegvqvsncstsmddiocefefganativetpaeemntspgtpapae 180  
 QY 181 ETMTNSPCTPAPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPASSHY 240  
 Db 181 etmtnsptpapaeeetmtspgtpapaaeeetmtspgtpapaaeeetmtspgtpasshy 240  
 QY 241 LSCRTVGIIIVLILVIFV 259  
 Db 241 lscrtvgliivlilvifv 259

RESULT 3  
 AAU12321  
 ID AAU12321 standard; Protein: 259 AA.  
 XX  
 AC AAU12321;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Human PRO366 polypeptide sequence.  
 XX  
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
 KW adipocyte; A-peptide; factor VIIA; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200140466-A2.  
 XX  
 PD 07-JUN-2001.  
 XX  
 PE 01-DEC-2000; 2000WO-US32678.  
 XX  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 09-DEC-1999; 99WO-US28565.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31243.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 10-NOV-2000; 2000WO-US30873.  
 XX  
 PA (GENENTECH INC.  
 XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerilsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S;  
 PI Smith V, Stewart RA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI: 2001-408281/43.  
 DR N-PSDB: AAS21393.  
 XX  
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect  
 PT other PRO polypeptides, link bioactive molecules to cells expressing  
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 PT lung, breast, prostate, cervical  
 PS Claim 12: Fig 300; 813pp: English.  
 XX  
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane  
 CC PRO polypeptides. The PRO polypeptides are useful to detect other  
 CC PRO polypeptides, to link bioactive molecules to cells expressing  
 CC PRO polypeptides, to modulate biological activities of cells expressing  
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample.  
 CC Some of the 275 sequences are also useful to stimulate the release of  
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
 CC proliferation or differentiation of chondrocytes, the proliferation or  
 CC gene expression in pericyte cells, the release of proteoglycans from  
 CC cartilage, the proliferation of inner ear utricular supporting cells or  
 CC of T-lymphocytes, or the release of a cytokine from peripheral blood  
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by  
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify  
 CC molecules involved in binding interactions. The polynucleotides encoding  
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy.  
 XX  
 XX Sequence 259 AA;

Query Match 100.0%; Score 1382; DB 22; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-86;  
 Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPKTKFVVYIYAVLLPVLAISATTARQEEVPOQIVAPQOQRHSFGECPPAGSHRS 60  
 Db 1 maripkltkfvvviavallpvlaysattarqeevpqqtvpqqrhsfkgcecpagshrs 60  
 QY 61 EHTGACNPCTEGVDYTNASNNPSCFPCIVCKSDOKHKSCTMTRTDYCOCKEGFRNEN 120  
 Db 61 ehtgacnptcegvdytnasnnepscfcipcvcksdqkhksctmttdtvcqckegfrnen 120







xx The invention relates to novel human angiogenesis-associated proteins  
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
 CC PRO proteins. The invention also relates to vectors and host cells  
 CC comprising a PRO nucleic acid, the recombinant production of a PRO  
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
 CC compounds which inhibit the expression of a PRO gene. The invention  
 CC additionally encompasses methods of identifying modulators of PRO  
 CC expression or activity: diagnosing a cardiovascular, endothelial or  
 CC angiogenic disorder or a susceptibility to such a disorder by detecting  
 CC mutations in a PRO gene, or the expression level of a PRO gene within a  
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
 CC administration of a PRO protein, or an agonist or antagonist thereof.  
 CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
 CC agonists and PRO antagonists may be used as therapeutic agents to treat  
 CC cardiovascular, endothelial or angiogenic disorders, such as  
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
 CC disease, or stroke. PRO nucleic acids are additionally useful in the  
 CC recombinant production of PRO proteins, as hybridisation probes to  
 CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
 CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
 CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
 CC animals useful for the development and screening of potential  
 CC therapeutic agents. The present sequence represents a PRO protein of the  
 CC invention.

xx Sequence 259 AA;

Query Match 100.0%; Score 1382; DB 22; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 2, 5e-86;  
 Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARIPTKLEFVAVIAYVLLPVLAYSATTAPOEVPFOOTVAPQOORHSPKGECPAGSHRS 60  
 Db 1 MARIPTKLEFVAVIAYVLLPVLAYSATTAPOEVPFOOTVAPQOORHSPKGECPAGSHRS 60  
 QY 61 EHTGACNCTEGVDYTNASNNPSCFCTVCKSDOKHRSCTMTRTDVCQCKEGTFRNEN 120  
 Db 61 EHTGACNCTEGVDYTNASNNPSCFCTVCKSDOKHRSCTMTRTDVCQCKEGTFRNEN 120  
 QY 121 SPEMCRKCRSPSGENVQNSCTSMDDIOCVREFGANAIVFPAAEETMTSPGTPAPAAE 180  
 Db 121 SPEMCRKCRSPSGENVQNSCTSMDDIOCVREFGANAIVFPAAEETMTSPGTPAPAAE 180  
 QY 181 ETMTNTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPAPAAE 240  
 Db 181 ETMTNTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPAPAAE 240  
 QY 241 LSGTIVGIVLIVLIVFV 259  
 Db 241 LSGTIVGIVLIVLIVFV 259

RESULT 7  
 AAW76331  
 ID AAW76331 standard; Protein: 299 AA.  
 AC AAW76331;  
 XX

DT 11-JAN-1999 (first entry)  
 XX Human tumour necrosis related receptor TR5.  
 DE Tumour necrosis related receptor; TR5; human; inflammation;  
 XX arthritis; septicemia; transplant rejection; autoimmune disease;  
 KM

KW Inflammatory bowel disease; graft versus host disease; infection;  
 KW stroke; ischemia; acute respiratory disease syndrome; psoriasis;  
 KW restenosis; brain injury; AIDS; bone disease; cancer;  
 KW atherosclerosis; Alzheimer's disease; therapy; diagnosis.  
 XX Homo sapiens.  
 OS  
 XX  
 FH Key location/Qualifiers  
 FT Peptide 1..165  
 FT /label= Sig\_peptide  
 FT Protein 66..299  
 FT /label= Mat\_protein  
 XX  
 PM EP867509-A2.  
 XX  
 ED 30-SEP-1998.  
 XX  
 PF 04-FEB-1998; 98EP-0300827.  
 XX  
 PR 28-JUL-1997; 97US-0901469.  
 PR 05-FEB-1997; 97US-0795910.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI Lyn SDP, Tan KB, Truneh A, Young PR;  
 XX  
 DR WPI: 1998-497862/43.  
 DR N-PSDB: AAV56990.  
 XX  
 PT New polynucleotide encoding TR5 polypeptide - used to diagnose,  
 PT prevent and treat e.g. inflammation, arthritis, septicemia,  
 PT autoimmune diseases, infections, stroke, ischemia, ARDS, psoriasis,  
 PT restenosis, brain injury, AIDS and bone diseases  
 XX  
 PS Claim 5; Fig 1; 22pp; English.

XX This is the amino acid sequence of human tumour necrosis related  
 CC receptor TR5, as deduced from the sequence of an isolated cDNA  
 CC clone (see AAV56990). The protein is characterised as a GPI-linked  
 CC protein that has a membrane proximal O-glycosylation region. The  
 CC invention provides methods for the recombinant production of TR5  
 CC and its use in diagnostic and therapeutic methods. Treatment of a  
 CC subject in need of enhanced TR5 activity comprises administering an  
 CC agonist to the polypeptide and/or providing TR5 polynucleotide in a  
 CC form so as to effect production of the polypeptide activity in vivo.  
 CC Treatment of a subject with the need to inhibit TR5 polypeptide  
 CC activity comprises administering an antagonist to the polypeptide,  
 CC administering a nucleic acid that inhibits the expression of the  
 CC nucleotide sequence encoding the polypeptide and/or administering a  
 CC polypeptide that competes with the polypeptide for its ligand,  
 CC substrate or receptor. Diagnosing a disease or a susceptibility  
 CC to a disease related to expression or activity of TR5 polypeptide,  
 CC comprises determining the presence or absence of mutation in the  
 CC nucleotide sequence encoding the TR5 polypeptide in the genome of  
 CC the subject and/or analysing for the presence or amount of TR5  
 CC polypeptide expression in a sample. Identification of compounds  
 CC which bind to TR5 comprises contacting host cells with a candidate  
 CC compound and assessing the ability of it to bind to the cells. The  
 CC active agents can be used for the treatment of chronic and acute  
 CC inflammation, arthritis, septicemia, autoimmune diseases (e.g.  
 CC inflammatory bowel disease, psoriasis), transplant rejection,  
 CC graft vs host disease, infection, stroke, ischemia, acute  
 CC respiratory disease syndrome, restenosis, brain injury, AIDS, bone  
 CC diseases, cancer (e.g. lymphoproliferative disorders),  
 CC atherosclerosis and Alzheimer's disease.

XX Sequence 299 AA;

Query Match 100.0%; Score 1382; DB 19; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 2, 9e-86;  
 Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARIPTLKFVYVIVAVLLPVLAYSATTAAROEENVOQTVAPOOQRHSFKGECPCAGSHRS 60  
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 CC activity, cachectin/tumour invasion suppressor activity, and tumour  
 Db 41 maripkltklfvviavvllpvlaystatargeevpqqtvpqqrhskgcecpagshrs 100  
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 CC inhibition activity. The polynucleotides and proteins can also be used  
 CC as nutritional sources or supplements. Such uses include use as a protein  
 CC or amino acid supplement, use as a carbon source, use as a nitrogen  
 CC source and use as a source of carbohydrate. They may also have utility  
 CC in compositions used for bone, cartilage, tendon, ligament, and/or nerve  
 CC tissue growth or regeneration, as well as for wound healing and tissue  
 CC repair and replacement, and in the treatment of burns, incisions and  
 CC ulcers. The proteins which induce cartilage and/or bone growth in  
 CC circumstances where bone is not normally formed, have application in  
 CC the healing of bone fractures and cartilage damage or defects in humans  
 CC and other animals.  
 QY 121 SPEMCRKSRCPGSEVOVSNCTSMDDIQVEEFGANATVETPAAEETMNTSPGTPAPAAE 180  
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 CC 161 spemcrksrpsgevsqsnctswddiqveefganatvecpaaeetmtspgtpapaae 220  
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 181 ETMNTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPASSHY 240  
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 221 etmtspgtpapaaeetmtspgtpapaaeetmtspgtpapaaeetmtspgtpasshy 280  
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 241 LSCITVGIIVLIVLIVFV 259  
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 281 lscitvgliivlilivfv 299  
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 RESULT 8  
 AAY29864  
 ID AAY29864 standard; Protein; 299 AA.  
 AC AAY29864;  
 XX  
 DT 17-NOV-1999 (first entry)  
 XX  
 DE Human secreted protein clone ljl1442.1.  
 XX  
 KW Human; secreted protein; biological activity; nutritional; cytokine;  
 KW cell proliferation; differentiation; immune stimulating; vaccine;  
 KW haematopoiesis regulation; tissue growth; haemostatic; thrombolytic;  
 KW anti-inflammatory; tumour inhibition.  
 OS Homo sapiens.  
 XX  
 PN WC0946287-A1.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PE 11-MAR-1999; 99WO-US05243.  
 XX  
 PR 11-MAR-1998; 98US-0077521.  
 PR 14-MAY-1998; 98US-0079124.  
 PR 10-MAR-1999; 99US-0266105.  
 XX  
 PA (GEMV ) GENETICS INST INC.  
 XX  
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
 PI Merberg D, Treacy M, Agostino MJ, Steininger RJ;  
 XX  
 DR WPI; 1999-551362/46.  
 DR N-PSDB; AA221096.  
 XX  
 PT Polynucleotides encoding secreted human proteins, derived from human  
 PT fetal brain, human adult blood, human adult bladder, or human adult  
 PT neutral tissue cDNA libraries.  
 XX  
 PS Claim 17; Page 104; 118pp; English.  
 CC  
 CC AA221093 to AA221102 encode new human secreted proteins and AAY29861 to  
 CC AAY29873 represent the secreted proteins encoded by the polynucleotide  
 CC sequences. AA221103 to AA221112 represent probes for the secreted  
 CC proteins. The polynucleotides and proteins are predicted to have  
 CC biological activities which would make them suitable for treating,  
 CC preventing or ameliorating medical conditions in humans and animals,  
 CC although no supporting data is given. Suggested activities include  
 CC nutritional activity, cytokine and cell proliferation/differentiation  
 CC activity, immune stimulating (e.g. as vaccines) or suppressing activity,  
 CC haematopoiesis regulating activity, tissue growth activity,  
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory  
 CC activity, cachectin/tumour invasion suppressor activity, and tumour  
 CC inhibition activity. The polynucleotides and proteins can also be used  
 CC as nutritional sources or supplements. Such uses include use as a protein  
 CC or amino acid supplement, use as a carbon source, use as a nitrogen  
 CC source and use as a source of carbohydrate. They may also have utility  
 CC in compositions used for bone, cartilage, tendon, ligament, and/or nerve  
 CC tissue growth or regeneration, as well as for wound healing and tissue  
 CC repair and replacement, and in the treatment of burns, incisions and  
 CC ulcers. The proteins which induce cartilage and/or bone growth in  
 CC circumstances where bone is not normally formed, have application in  
 CC the healing of bone fractures and cartilage damage or defects in humans  
 CC and other animals.  
 SQ Sequence 299 AA;  
 CC  
 Query Match 100.0%; Score 1382; DB 20; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-86;  
 Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MARIPTLKFVYVIVAVLLPVLAYSATTAAROEENVOQTVAPOOQRHSFKGECPCAGSHRS 60  
 Db 41 maripkltklfvviavvllpvlaystatargeevpqqtvpqqrhskgcecpagshrs 100  
 QY 61 EHTGACNPCTEGVDYTNASNNPSCFPCTVCKSDOKHKSSCTMTRTDYCOCKEGTFRNEN 120  
 Db 101 ehtgacnpctegvdytnasnnpescfctvcsdqkhksctmttldvcqcgegtfirnen 160  
 QY 121 SPEMCRKSRCPGSEVOVSNCTSMDDIQVEEFGANATVETPAAEETMNTSPGTPAPAAE 180  
 Db 161 spemcrksrpsgevsqsnctswddiqveefganatvecpaaeetmtspgtpapaae 220  
 QY 181 ETMNTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPASSHY 240  
 Db 221 etmtspgtpapaaeetmtspgtpapaaeetmtspgtpapaaeetmtspgtpasshy 280  
 QY 241 LSCITVGIIVLIVLIVFV 259  
 Db 281 lscitvgliivlilivfv 299  
 RESULT 9  
 AAY05744  
 ID AAY05744 standard; Protein; 299 AA.  
 AC AAY05744;  
 XX  
 DT 19-JUL-1999 (first entry)  
 XX  
 DE Tumour necrosis factor receptor TR5.  
 XX  
 KW Tumour necrosis factor receptor; TR5; TRID; DCRI; agonist;  
 KW antagonist; screening; human; cancer; AIDS; Alzheimer's disease;  
 KW inflammation; arthritis; septicemia; autoimmune disease;  
 KW psoriasis; inflammatory bowel disease; transplant rejection;  
 KW graft versus host disease; infection; stroke; ischaemia;  
 KW acute respiratory disease syndrome; restenosis; brain injury;  
 KW bone disease; atherosclerosis; therapy.  
 OS Homo sapiens.  
 XX  
 PN EP911633-A1.  
 XX  
 PD 28-APR-1999.  
 XX  
 PF 02-OCT-1998; 98EP-0203332.  
 PR 08-OCT-1997; 97US-0061334.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 PI McDonnell PC, Young PR, Zou J;

XX WP1: 1999-246560/21.  
XX  
XX Identifying agonists and antagonists of tumor necrosis factor  
PT related receptors TR1, TR3 and TR5, and of ligand TL3, useful for  
PT treatment of cancer, AIDS, Alzheimer's disease, bone disease etc  
XX  
XX Disclosure: Page 13-14; 23pp; English.  
XX  
XX The present sequence represents tumour necrosis factor receptor  
CC (TNFR) TR5, also known as TR1D or DCR1. The invention relates  
CC to TNFR related polypeptides TR1, TR3 and TR5 (see AAY0542-44) and  
CC their ligand TL3 (see AAY05745). TR1, TR3, TR5 and TL3 are used in  
CC claimed methods of identifying agonists and antagonists, i.e.  
CC compounds that bind to the receptors or ligand, and which activate  
CC (agonist) or inhibit activation of (antagonists) TR1, TR3, TR5 or  
CC TL3. A screening kit for identifying agonists, antagonists,  
CC ligands, receptors, substrates, enzymes etc. for TR1, TR3, TR5 or  
CC TL3 polypeptides is provided. The agonists and antagonists are  
CC useful for treatment of chronic and acute inflammation, arthritis,  
CC septicemia, autoimmune disease e.g. inflammatory bowel disease,  
CC psoriasis, transplant rejection, graft versus host disease,  
CC infection, stroke, ischemia, acute respiratory disease syndrome,  
CC restenosis, brain injury, AIDS, bone diseases, cancer (e.g.  
CC lymphoproliferative disorders), atherosclerosis and Alzheimer's  
CC disease, etc., caused by imbalance of TR1, TR3, TR5 or TL3.  
XX  
SQ Sequence 299 AA:  
  
Query Match 100.0%; Score 1382; DB 20; Length 299;  
Best Local Similarity 100.0%; Pred. No. 2,9e-86;  
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MARIPTLKFVVIYAVLPLVLAYSATTAROEYVPOOTVAPQOORHSFKGECPPAGSHRS 60  
Db 41 maripkltkfvyvivaavlplvlaystatargeevpqqlvapgqrhstkgcecpagshrs 100  
  
QY 61 EHTGACNPCTEGVDYTNASNNPSCFCTVCKSDOKRHSCTMTTRDVCQCKEGTFRNEN 120  
Db 101 ehtgacnpctegvdyltnasnepsfcfctvcksdqkhksccumtrdvcqckegfrrnen 160  
  
QY 121 SPENCRCRSPSGEVQVSNCTSMWDIOCVEEFGANATVEPPAAEETMTNTSGTPAPAAE 180  
Db 161 spencrcrscpsgevgvsnctswddiqveefganatvetppaaeeumtntspgcpapaae 220  
  
QY 181 ETTMNTSPCTPAPAAEETMTSGTPAPAAEETMTSGTPAPAAEETMTSGTPASSHY 240  
Db 221 etmtntspgtpapaaeeumtntspgcpapaaeeumtntspgtpapaaeeumtntspgcpashy 280  
  
QY 241 LSCITVIGIIVLIVLIVFV 259  
Db 281 lscitvgiivlilvllivfv 299  
  
RESULT 10  
AAY00933  
ID AAY00933 standard; Protein: 299 AA.  
XX  
XX AAY00933:  
XX  
XX 02-JUN-1999 (first entry)  
XX  
XX Human TRAIL-R3 protein sequence.  
XX  
XX  
KW Human; DR5; DR5s; TRAIL-R3; apoptosis related condition; cancer; therapy;  
KW autoimmune disease; viral infection; degenerative disorder;  
KW amyotrophic lateral sclerosis; retinitis pigmentosa; ischemic injury;  
KW cerebellar degeneration; myelodysplastic syndrome.  
XX  
XX Homo sapiens.  
XX  
XX FN W09909165-A1.

XX 25-FEB-1999.  
PD  
XX  
XX 14-AUG-1998; 98WO-US16945.  
XX  
XX 15-AUG-1997; 97US-0055906.  
XX  
XX (IDUN-) IDUN PHARM INC.  
XX  
XX Alnemrl ES;  
XX  
XX WP1: 1999-181035/15.  
XX  
XX N-PSDB: AAX27280.  
XX  
XX Newly isolated polynucleotide encoding a mammalian TRAIL receptor  
PT protein - useful in for screening for (antagonists that modulate  
PT the apoptotic activity mediated by DR5 or TRAIL-R3 proteins  
XX  
XX Claim 16; Page 62-63; 71pp; English.  
XX  
XX This sequence is the human TRAIL receptor TRAIL-R3 of the invention. An  
CC antibody against the TRAIL receptors is useful for detecting mammalian  
CC DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in  
CC bioassays for screening for (antagonists of DR5 or TRAIL-R3 proteins.  
CC (Ant)agonists identified by the assay are useful for modulating the  
CC apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis  
CC related conditions which are treated in this way, include cancer  
CC (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus  
CC erythematosus and immune-mediated glomerulonephritis), viral infections  
CC (e.g. herpes virus, poxvirus and adenovirus), degenerative disorders  
CC (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral  
CC sclerosis, retinitis pigmentosa, cerebellar degeneration, myelodysplastic  
CC syndromes (e.g. aplastic anaemia) and ischemic injury (e.g. myocardial  
CC infarction and stroke). The polynucleotides can also be used to treat  
CC these diseases. Antisense oligonucleotides to the DNA sequences can be  
CC used to form a composition that is useful for inhibiting expression of a  
CC human DR5 or TRAIL-R3 protein.  
XX  
SQ Sequence 299 AA:  
  
Query Match 100.0%; Score 1382; DB 20; Length 299;  
Best Local Similarity 100.0%; Pred. No. 2,9e-86;  
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MARIPTLKFVVIYAVLPLVLAYSATTAROEYVPOOTVAPQOORHSFKGECPPAGSHRS 60  
Db 41 maripkltkfvyvivaavlplvlaystatargeevpqqlvapgqrhstkgcecpagshrs 100  
  
QY 61 EHTGACNPCTEGVDYTNASNNPSCFCTVCKSDOKRHSCTMTTRDVCQCKEGTFRNEN 120  
Db 101 ehtgacnpctegvdyltnasnepsfcfctvcksdqkhksccumtrdvcqckegfrrnen 160  
  
QY 121 SPENCRCRSPSGEVQVSNCTSMWDIOCVEEFGANATVEPPAAEETMTNTSGTPAPAAE 180  
Db 161 spencrcrscpsgevgvsnctswddiqveefganatvetppaaeeumtntspgcpapaae 220  
  
QY 181 ETTMNTSPCTPAPAAEETMTSGTPAPAAEETMTSGTPAPAAEETMTSGTPASSHY 240  
Db 221 etmtntspgtpapaaeeumtntspgcpapaaeeumtntspgtpapaaeeumtntspgcpashy 280  
  
QY 241 LSCITVIGIIVLIVLIVFV 259  
Db 281 lscitvgiivlilvllivfv 299  
  
RESULT 11  
AAY94671  
ID AAY94671 standard; Protein: 299 AA.  
XX  
XX AAY94671:  
XX  
XX 04-MAY-1999 (first entry)  
XX  
XX

Query Match	Best Local Similarity	100.0%;	Score 1382;	DB 20;	Length 299;	
Matches 259;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
QY 1	MARIKRLKFEVYVYIAVILLPVLA	SATTA	ROBEV	QQYATPA	POQORHSFGEGEC	PAGSHRS 60
DB 41	maripkrlkifvnylavillpvlay	altatargev	pqvtapqqrtnis	ifgcecpagshrs 100		
QY 61	EHTGACNPCTEGSVDTMA	SNNEP	SCFPCTVCK	SDSKHKSSCTMT	RTDTCQCKEGTF	RNNEN 120
DB 101	ehlgtcnpctegvdytlmsnmep	sfcfpcrvcksdqkhksscm	trtdiveqckegflrnn 160			
QY 121	SPEMKRCKSRCSGGEVO	SNCTSM	PDIOQVEEFG	ANAYETPA	AEETMNTSPGTPAPAAE 180	
DB 161	spemrkcsrccpsggevsnctsw	ddiqvееfganatlvetp	aaeetmnltspgtppaae 220			
QY 181	ETMNTSPGTPAPAAE	ETMTSPGTPAPAAE	ETMTSPGTPAPAAE	ETMTSPGTPAPAAE	ETMTSPGTPASSHY 240	
DB 221	etmnltspgtppaaeetmnlts	pgtppaaeetmnltspgtppaaeetmnltspgtppasshy 280				
QY 241	LSCTIVGIIIVLIVLLIVFY 259					
DB 281	lsctivgiivlilvllivfy 299					

RESULT 12

AAW88409

AAW88409 standard: Protein: 299 AA.

XX	AAW88409;	
AC		
XX	26-APR-1999	(first entry)
XX		
XX	Human Apo-2Dcr protein (amino acids -40 to 259) .	
DE		
XX		
KW	Apo-2Dcr: human; apoptosis; tumour necrosis factor receptor; neurodegeneration; autoimmune disease; inflammation; cancer; therapy.	
KW		
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..40
FT		/note= "-40 to -1 region of Apo-2Dcr"
FT	Peptide	41..69
FT		/note= "predicted signal peptide"
FT	Domain	41..201
FT		/note= "extracellular domain, this domain is specifically claimed in Claim 5"
FT	Domain	108..149
FT		/note= "cysteine-rich domain"
FT	Domain	150..189
FT		/note= "cysteine-rich domain"
FT	Peptide	202..216
FT		/note= "tandem repeat peptide"
FT	Peptide	217..231
FT		/note= "tandem repeat peptide"
FT	Peptide	232..246
FT		/note= "tandem repeat peptide"
FT	Peptide	247..261
FT		/note= "tandem repeat peptide"
FT	Peptide	262..276
FT		/note= "tandem repeat peptide"
FT	Region	265..299
FT		/note= "hydrophobic C-terminal region"
FT	Modified-site	117
FT		/note= "N-glycosylation"
FT	Modified-site	180
FT		/note= "N-glycosylation"
FT	Modified-site	196
FT		/note= "N-glycosylation"
FT	Modified-site	209
FT		/note= "N-glycosylation"
FT	Modified-site	224
FT		/note= "N-glycosylation"
PN	WO9858062-A1.	
XX		
PD	23-DEC-1998.	
XX		
PF	12-JUN-1998;	98WO-US12456.
XX		
PR	18-JUN-1997;	97US-0878168.
XX		
PA	(GETH ) GENENTECH INC.	
XX		
PI	Ashkenazi AJ, Baker KP, Chuntharapai A, Gurney A;	
PI	Kim KJ, Wood WI;	
XX		
DR	WPI: 1999-095340/08.	
XX		
DR	N-PSDB; AAW84347.	
XX		
PT	New Apo-2Dcr polypeptide - used for modulation and diagnosis of apoptosis, e.g. in neurodegeneration	
XX		
PS	Claim 9: Page 53-54; 88pp; English.	
XX		
CC	This polypeptide comprises human Apo-2Dcr, a novel member of the tumour necrosis factor receptor family that binds to Apo-2 ligand. Its amino acid sequence was deduced from the nucleotide sequence of an isolated cDNA clone (see AAW84347); an alternative translation	
CC		

CC initiation site in this clone will encode a polypeptide (see  
 CC AAW8408) lacking the first 40 amino acid residues of this sequence.  
 CC Apo-2Dcr shows more sequence identity to DR4 (60%) and Apo-2 (50%)  
 CC than to other apoptosis-linked receptors. The polypeptide can be  
 CC obtained by expression in host cells using the vector deposited as  
 CC ATCC 209087. The invention provides vectors and host cells for  
 CC recombinant production of Apo-2Dcr polypeptides, antibodies, and  
 CC transgenic and knockout animals (useful e.g. for screening and  
 CC developing drugs that protect against excessive apoptosis).  
 CC Apo-2Dcr, or chimeras comprising Apo-2Dcr or its (claimed)  
 CC extracellular domain fused to a heterologous polypeptide are used  
 CC to modulate apoptosis of mammalian cells (claimed) and/or NF-kappa  
 CC activation by Apo-2 ligand, and may be expressed in vivo or ex vivo  
 CC for gene therapy. They can be used in methods for the modulation  
 CC and diagnosis of apoptosis e.g. in cases of neurodegeneration,  
 CC autoimmune diseases and inflammation. Most human tumour cells do  
 CC not express Apo-2Dcr transcripts, but normal tissues do, suggesting  
 CC that Apo-2Dcr may permit selective killing of cancer cells by Apo-2  
 CC ligand, possibly by protecting normal, but not cancerous, cells.  
 CC  
 XX Sequence 299 AA:

Query Match 100.0%; Score 1382; DB 20; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-86;  
 Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARIPTLKFVYVIVAVLLPVLAYSATTAARQEVVPOQTVAPOQQRHSRKGECPCAGSHRS 60  
 DB 41 maripkllkfvyvivaavllpvlaysatatargeevpqgtvapqqrhskfgeecpcagshrs 100  
 QY 61 EHTGACNCTEGVDYTNASNNPSCFCTVCKSDOKHKSCTMTDNYCQCKEGFFRDN 120  
 DB 101 ehtgacnctegvdytnasnnpescfctvcksdokhksctmttrdtycqckegffrden 160  
 QY 121 SPEMCRKSRCPGSGEVQVSNCTSMWDIOCVEEFGANATVETPAAEETMNTSPGTPAPAAE 180  
 DB 161 spemcrksrpsgevgvsnctswddiqveefganatvecpaaeetmntspgtpapaae 220  
 QY 181 ETMTNTPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPASSHY 240  
 DB 221 etmntspgtpapaaeetmtspgtpapaaeetmtspgtpapaaeetmtspgtpasshy 280  
 QY 241 LSCITVIGIIVLILIVFY 259  
 DB 281 lscitvigiivlilivfy 299

## RESULT 13

AAAB01343  
 ID AAB01343 standard; Protein: 299 AA.

XX AAB01343;  
 AC  
 DT 25-SEP-2000 (first entry)  
 DE Death receptor.  
 XX  
 KW U1144; death receptor; apoptosis; programmed cell death; FAS;  
 KW TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;  
 KW human.  
 XX Homo sapiens.  
 OS  
 PN W0200034335-A2.  
 XX  
 PD 15-JUN-2000.  
 XX  
 PF 03-DEC-1999; 99WO-0526035.  
 XX  
 PR 04-DEC-1998; 98US-0205018.  
 XX  
 PA (SCHE ) SCHERING CORP.

XX  
 PI Leong C, Phillips JH;  
 XX  
 DR WPI, 2000-423383/36.  
 XX

PT Purified or recombinant polypeptide for modulating apoptosis comprises  
 PT a sequence which binds to an antibody specific for U1144 or its  
 PT fragments  
 XX

PS Disclosure; Page 75-76; 76pp; English.

CC A pure or recombinant polypeptide which binds to a polyclonal antibody  
 CC specific for the mature U1144 is useful for screening molecules which  
 CC block induction of apoptosis or interfere with antiapoptotic activity.  
 CC The polypeptide is also useful for modulating apoptosis and useful in  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, such as cancer or degenerative conditions and for  
 CC regulation of viral infection and replication. At least five  
 CC different death receptors are known, which include the CD95  
 CC (Fas/Apo-1), the TNF receptor-1, TNF receptor apoptosis-mediated  
 CC protein (TRAMP), death receptor-6 (DR-6), and TNF-related  
 CC apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.  
 CC  
 XX Sequence 299 AA:

Query Match 100.0%; Score 1382; DB 21; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-86;  
 Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARIPTLKFVYVIVAVLLPVLAYSATTAARQEVVPOQTVAPOQQRHSRKGECPCAGSHRS 60  
 DB 41 maripkllkfvyvivaavllpvlaysatatargeevpqgtvapqqrhskfgeecpcagshrs 100  
 QY 61 EHTGACNCTEGVDYTNASNNPSCFCTVCKSDOKHKSCTMTDNYCQCKEGFFRDN 120  
 DB 101 ehtgacnctegvdytnasnnpescfctvcksdokhksctmttrdtycqckegffrden 160  
 QY 121 SPEMCRKSRCPGSGEVQVSNCTSMWDIOCVEEFGANATVETPAAEETMNTSPGTPAPAAE 180  
 DB 161 spemcrksrpsgevgvsnctswddiqveefganatvecpaaeetmntspgtpapaae 220  
 QY 181 ETMTNTPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPASSHY 240  
 DB 221 etmntspgtpapaaeetmtspgtpapaaeetmtspgtpapaaeetmtspgtpasshy 280  
 QY 241 LSCITVIGIIVLILIVFY 259  
 DB 281 lscitvigiivlilivfy 299

## RESULT 14

AAW93578  
 ID AAW93578 standard; Protein: 259 AA.

XX AAW93578;  
 AC  
 DT 18-JUN-1999 (first entry)  
 DE Human hApo9 protein.  
 XX  
 KW Tumour necrosis factor receptor; signal transducer molecule; TNF; Apo4;  
 KW developmental abnormality; gestational abnormality; prostate cancer;  
 KW Apo6; Apo8; TNFR-1; TNFR-3; diagnosis; treatment; therapy; disease;  
 KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;  
 KW apoptosis; human.  
 XX Homo sapiens.  
 OS  
 PN W09911791-A2.  
 XX  
 PD 11-MAR-1999.  
 XX



```
OY 1 MARIPKILKEVVIVAVILLPVLAYSATTARQEEVPOQTVAPQOQRHSFKGEECPAGSHRS 60
Db 1 maripkilkfivvIvavIlpvLaysattarqeevpgltvapqgrhsfkgeecpagshrs 60
OY 61 EHTGACNPTCEGVDTYTNASNNEPSCFCTYCKSDOKHKSCTMTMRDVTWCCKEGRFRNEN 120
Db 61 ehTgacnpctegvdytnasnnepscfcTctvcksdqkhksscTmtrdvtwcgckegLfrnvn 120
OY 121 SPENCRCSCRCPSGSEVOYSNCTSMDDIQVEEFGANATVETPAAEETMNTSPGTPAPAAE 180
Db 121 spencrkscrcpsgsgevsncTswddiqveefganatvEtPaaEetmntspgtpapaaE 180
OY 181 ETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPASSHY 240
Db 181 etmntspgtpapaaEetmntltspgtpapaaEetmntltspgtpapaaEetmntltspgtpasshy 240
OY 241 LSCPIVGIIVLIVLIVPV 259
Db 241 lsctIvgIivIivIivfv 259
```

Search completed: August 13, 2002, 08:31:29  
Job time: 123 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2002, 08:29:26 ; Search time 28.27 Seconds  
(without alignments)  
880.337 Million cell updates/sec

Title: US-09-826-212-2

Perfect score: 1382

Sequence: 1 MARIKPTLKFVVIVAVLLP.....YLSCTVIGIIVLIVLIVFV 259

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

PIR\_71:\*  
1: pirl:\*  
2: pirl:\*  
3: pirl:\*  
4: pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	201.5	14.6	427	1	G0HUN
2	200.5	14.5	425	1	A26431
3	192	13.9	651	2	JC7705
4	188.5	13.6	461	2	JC4302
5	184.5	13.4	416	1	JN0006
6	178	12.9	801	2	T29018
7	169.5	12.3	461	1	A35356
8	166.5	12.0	271	2	S12783
9	166.5	12.0	272	2	T37552
10	166	12.0	272	2	I48700
11	164.5	11.9	314	2	I37383
12	163.5	11.8	335	2	A40036
13	163	11.8	327	2	A46484
14	157	11.4	326	1	GOVZML
15	156	11.3	324	2	F36791
16	153.5	11.1	324	2	JC2385
17	149.5	10.8	595	2	A42086
18	147.5	10.7	455	1	G0H071
19	146	10.6	474	2	B38634
20	145	10.5	459	2	I48854
21	144	10.4	454	1	G0MS71
22	143.5	10.4	98	2	H81072
23	141.5	10.2	292	2	S24169
24	141.5	10.2	348	2	T28623
25	141.5	10.2	349	2	D72175
26	141.5	10.2	349	2	D36858
27	141.5	10.2	493	2	JC5486
28	140.5	10.2	325	2	B43692
29	139.5	10.1	1367	1	S48478

30	134.5	9.7	93	2	S04157	outer membrane pro
31	133.5	9.7	577	2	A60501	thrombomodulin pre
32	133	9.6	888	2	T46726	secreted acid phos
33	132	9.6	307	1	GSEF3	salivary glue prot
34	132	9.6	607	2	S27776	80K protein (allel
35	132	9.6	3020	2	A43932	much 2 precursor,
36	130	9.4	1506	2	T30886	intermembrane muc
37	129.5	9.4	88	2	S02720	outer membrane pro
38	129.5	9.4	461	1	G0RTM1	tumor necrosis fac
39	129	9.3	393	2	S62335	IL1-7 protein - tr
40	127.5	9.2	135	2	T49996	ALG4 - Arabidops
41	127.5	9.2	1459	2	T32271	hypothetical prote
42	127	9.2	1802	2	S69703	HKR1 protein precu
43	126	9.1	138	2	D96715	protein F4N2.10 [l
44	126	9.1	514	2	A31643	cell adhesion 80K
45	126	9.1	571	2	T43456	hypothetical prote

#### ALIGNMENTS

RESULT 1

G0HUN

nerve growth factor receptor precursor, low affinity [validated] - human

N:Alternate names: NGF receptor

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1988 #sequence.revision 31-Mar-1988 #text.change 08-Dec-2000

C:Accession: A25218; A60204; S21689; I57638

R:Johnson, D.; Lananhan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, Cell 47, 545-554, 1986

A:Title: Expression and structure of the human NGF receptor.

A:Reference number: A25218; MUID:87051725

A:Accession: A25218

A:Molecule type: mRNA

A:Residues: 1-427 <UOH>

A:Cross-references: GB:M14764; NID:g189204; PIDN:AAB59544.1; PID:g189205

R:Marano, N.; Dietzschold, B.; Farley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob, J. Neurochem. 48, 225-232, 1987

A:Title: Purification and amino terminal sequencing of human melanoma nerve growth fa

A:Reference number: A60204; MUID:87085574

A:Accession: A60204

A:Molecule type: Protein

A:Residues: 29-31,'T',33-42,'TP',45-46,'TX',50-51,'XX',54-56 <MAR>

A:Experimental source: melanoma cell line A875

A>Note: this sequence has been corrected by a note added in proof to follow the nucle

R:Vissavajhala, P.; Leszyk, J.D.; Lin-Geerke, J.; Ross, A.H. Arch. Biochem. Biophys. 294, 244-252, 1992

A:Title: Structural domains of the extracellular domain of human nerve growth factor

A:Reference number: S21689; MUID:92198017

A:Accession: S21689

A>Status: preliminary

A:Molecule type: protein

A:Residues: 183-208 <VIS>

R:Sehgal, A.; Patil, N.; Chao, M. Mol. Cell. Biol. 8, 3160-3167, 1988

A:Title: A constitutive promoter directs expression of the nerve growth factor recept

A:Reference number: I57638; MUID:89096903

A:Accession: I57638

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-22 <RES>

A:Cross-references: GB:M21621; NID:g189206; PIDN:AAA6363.1; PID:g189207

C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom

C:Comment: The cysteine-rich region of the extracellular domain may form part or all

C:Comment: This protein is thought to form a high-affinity receptor when it associate

C:Comment: This receptor undergoes both N- and O-linked glycosylation.

C:Genetics:

A:Gene: GDB:NGFR

A:Cross-references: GDB:120234; OMIM:162010

A:Map position: 17q21-17q22

C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology

C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor

F:1-28/Domain: signal sequence #status predicted <SIG>

F:29-427/Product: nerve growth factor receptor #status experimental <MAT>  
 F:29-250/Domain: extracellular #status predicted <EXT>  
 F:32-65/Domain: NGF receptor repeat homology <NG>  
 F:67-108/Domain: NGF receptor repeat homology <NG2>  
 F:109-147/Domain: NGF receptor repeat homology <NG3>  
 F:149-169/Domain: NGF receptor repeat homology <NG4>  
 F:197-248/Region: serine/threonine-rich  
 F:251-272/Domain: transmembrane #status predicted <TRM>  
 F:273-427/Domain: intracellular #status predicted <INT>  
 F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.6%, Score 201.5; DB 1; Length 427;  
 Best Local Similarity 24.4%; Pred. No. 2.9e-05;  
 Matches 64; Conservative 25; Mismatches 92; Indels 81; Gaps 9;

Oy 51 EECPPAG--SHRSEHTGACN-----PCEGVDTNANNEPSCPPRYC 91  
 Db 30 EACPFGLYTHSGECKKACLGVAQPCGANOTVCEPCLDSVTSFSDVSAFEPCKPCTEC 89  
 Oy 92 KSDOKHKSSCTWTRDYVCOCKEGRFRENESP--EMCR-----KCSRC 131  
 Db 90 VGLQSMSPCVAEADAVCAVCAGYQDEETGRCACRVCESGLVFSQDKQNTVCBEC 149  
 Oy 132 PSG-----EVOYNSCTSMDDIOCEEFGANATVETPPAAEETMNT 170  
 Db 150 PDGTYSDANHYDPCLPCTVCEEDTERQLRECTRMADACEEIPGRMITSFTRP-PEGSDST 208  
 Oy 171 SPGTPAPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTT 230  
 Db 209 APSTOEPPA-----PEODLIASIVAG-----VVTVMGSSQPVYTRG--TT 248  
 Oy 231 SPGTPASSHYLSCTIVGIIVLI 252  
 Db 249 DNLIPVYCSITLAAYVGLVAYI 270

## RESULT 2

A26431  
 nerve growth factor receptor precursor, low affinity - rat  
 N:Alternate names: NGF receptor  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A26431; PH1229  
 R:Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.  
 Nature 325, 593-597, 1987  
 A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.  
 A:Reference number: A26431; MUID:87115859  
 A:Accession: A26431  
 A:Molecule type: mRNA  
 A:Residues: 1-425 <RAD>  
 R:Metzls, M.; Timusk, T.; Allikmets, R.; Saarma, M.; Persson, H.  
 Gene 121, 247-254, 1992  
 A:Title: Regulatory elements and transcriptional regulation by testosterone and retinoid  
 A:Reference number: PH1229; MUID:93077038  
 A:Accession: PH1229  
 A:Molecule type: DNA  
 A:Residues: 1-20 <MEP>  
 A:Cross-references: GB:X61269  
 C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma  
 C:Comment: The cysteine-rich region of the extracellular domain may form part or all of  
 C:Comment: This protein is thought to form a high-affinity receptor when it associates  
 C:Genetics:  
 A:Introns: 20/3  
 C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
 C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;  
 F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-427/Product: nerve growth factor receptor #status predicted <MAT>  
 F:30-251/Domain: extracellular #status predicted <EXT>  
 F:33-66/Domain: NGF receptor repeat homology <NG1>  
 F:66-109/Domain: NGF receptor repeat homology <NG2>  
 F:110-148/Domain: NGF receptor repeat homology <NG3>

F:150-190/Domain: NGF receptor repeat homology <NG4>  
 F:198-249/Domain: serine/threonine-rich  
 F:252-273/Domain: transmembrane #status predicted <TRM>  
 F:274-425/Domain: intracellular #status predicted <INT>  
 F:61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.5%; Score 200.5; DB 1; Length 425;  
 Best Local Similarity 23.9%; Pred. No. 3.4e-05;  
 Matches 68; Conservative 32; Mismatches 107; Indels 77; Gaps 9;

Oy 17 VILPVLAYSATTAROEVEVPOOTVAPQOORHSKGECPA---GSHRSEHTGA---CNPC 69  
 Db 17 LLLILGVSSGCAK-----ETCSTGLYTHS--GECCKACNLGSEVADPCGANOTVCEPC 68  
 Oy 70 TEGVDYTNASNNPSCPCVTCKSDOKHKSSCTWTRDYV----- 109  
 Db 69 LDNTFSDVYSATPECPKCTECLGLQSMSPCVAEADAVCAVCAGYQDEETGRCACSV 128  
 Oy 110 -----QCKEGRFNE--NSPDMCKRCSRCPSGEVQVNSCTSMDDIQ 148  
 Db 129 CEVSGGLVFSQDKQNTVCBECTYSDANHYDPCLPCTVCEEDTERQLRECTRMADAE 188  
 Oy 149 CVEEFGANATVETPPAAEETMNTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPA 208  
 Db 189 CEELPGRMIPKSTP-PEGSDSTAPSTOEPEVPEODLVPSIVA----- 230  
 Oy 209 AEFMTTSPGTPAPAAEETMTTSPGTPASSHLSCTIVGIIVLI 252  
 Db 231 --DMVTVMGSSQPVYTRG--TTDNLIPYCSITLAAYVGLVAYI 271

## RESULT 3

JC7705  
 death receptor-6 - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001  
 C:Accession: JC7705  
 R:Bridgman, J.T.; Bode, J.; Goetz, F.W.; Johnson, A.L.  
 Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001  
 A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.  
 A:Reference number: JC7705; MUID:21308433; PMID:11414698  
 A:Accession: JC7705  
 A:Molecule type: mRNA  
 A:Residues: 1-651 <BRI>  
 A:Cross-references: GB:AF349908  
 C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belo  
 C:Comment: activates a cell death and/or survival signaling cascade.  
 C:Genetics:  
 A:Gene: dr-6  
 C:Keywords: ovary  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>  
 F:332-350/Domain: transmembrane #status predicted <TRM>  
 F:410-475/Domain: death domain #status predicted <DED>  
 F:551-651/Region: conserved cytoplasmic #status predicted

Query Match 13.9%; Score 192; DB 2; Length 651;  
 Best Local Similarity 23.9%; Pred. No. 0.00015;  
 Matches 68; Conservative 35; Mismatches 110; Indels 72; Gaps 12;

Oy 14 IVAVLPLVLAYSATTAROEVEVPOQTVV-----PQOORHSFGECPAGSHSEH 62  
 Db 5 VLAVALPLVLVLGTRADAPKLTREONAVSLPAGKYLHDKRTNOBLIDCKCPAGTYSKH 64  
 Oy 63 -----TGACNCPTEGVDTNANNEPSCFPC--TVCKSDOKHKSSCTWTRDYVCOCKEGRF 116  
 Db 65 CTKSLRRCSPCPGPT-FTKHENGIERCHPCRKRCCLPMIKTCTALTDRCTCLSTF 123  
 Oy 117 R-----NENSPMKCKRCSRCPSGEV--OVSNCTSMDDIOCEE 153  
 Db 124 QINDTCVPTVCYGVGWGRKGTETEDVRCKRPLRGTFSDVPSVMCKTFTD--C--F 178

Oy	154	GANATVETPAAEETNTSGCTGAPAAEETMTNSPGTAPAAEETMTTSP-----	202
Dd	179	GKNMYVVYRGTRESQNVCCXSPASLCPNLSLTSS---DAADDETYEAAPTALPLKGLNSS	234
Oy	203	-----GTAPPAAEETMTTSPGTAPAAEETMTTSPGTAPASSHYLS	242
Dd	235	VFDLSSPPAP-----RVSNGTAEPTVDINDTSANGTCVAGPGLSL	273

## RESULT 4

tumor necrosis factor receptor p55 precursor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 23-Jul-1999  
C:Accession: J04302; PC4093  
R:Suter, B.; Paull, U.  
Gene 163, 263-266, 1995  
A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor  
A:Reference number: J04302; MUID:96011645  
A:Accession: J04302  
A:Molecule type: mRNA  
A:Residues: 1-461 <SUT>  
A:Cross-references: GB:U09994; NID:g1141752; PIDN:AAC48499.1; PID:g1141753  
A:Accession: PC4093  
A:Molecule type: protein  
A:Residues: 1-7 <SUT>  
A:Experimental source: kidney cell line 15  
C:Genetics:  
A:Gene: tnfr  
C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C:Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>  
F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>  
F:44-82/Domain: NGF receptor repeat homology <NGF>  
F:84-126/Domain: NGF receptor repeat homology <NGF>  
F:211-231/Domain: transmembrane #status predicted <TM>  
F:361-447/Domain: signal transduction #status predicted <ST>  
F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	13.6%	Score 188.5	DB 2	Length 461
Best Local Similarity	22.8%	Pred. NO.0.00018		
Matches 69	Conservative 30	Mismatches 94	Indels 109	Gaps 11

QY	42	000RHSFEGGCPAG--SHREHNGAONPCEGY-----	-DTNA	78
Db	37	REKRESL-----CPOGXSHPNQNSICCTKCHKGYTLHNDCLGPGDLIDCRECDNGFTTAS	92	
QY	79	SNNEPSCPCTVCSKD--QRIKSSCTMTPTDPTVOCCKEGTFENENSPEM--CRKCSRPSG	134	
Db	93	ENHLTQCLSCSKSEMSQVEISPCTYDTRDVCGRNNOYRKVSEITLFOCLNCSICPNG	153	
QY	135	EVO-----VNCSTSW-----DDIOCEVEEGANATVETPAAEETMN-----	165	
Db	153	TVQLPCLKEKODTICNCHSGFGLRDKKECVSCVCKNADCKNICPATSTRNDFODTGTVL	212	
QY	170	-----TSPGTAPAAE-ETMTNTPG-----	188	
Db	213	LPLVIFGCLAFLEVLGACLACRYRMKPKLYSIICGKSTPVRKEGEPLLATAPSGFTT	272	
QY	189	-TPAAPAEETMTSP-----GTPAAPAEETMTTSGTPAAPAEETMTTSPGTA	236	
Db	273	FSPIPSFSPTTTFSPVPSPFSDISSPTPTPCOWSMIKVTSPPKEIAPAPQAGPILPMPPA	332	
QY	237	SS 238		
Db	333	ST 334		

RESULT  
JN0006

nerve growth factor receptor, low affinity precursor - chicken  
 N:Alternate names: NGF receptor  
 C:Species: Gallus gallus (chicken)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999  
 C:Accession: J00006, A60504  
 R:Laage, T.H.; Westkamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; R  
 Neuron 2, 1123-1134, 1989  
 A:Title: Structure and developmental expression of the nerve growth factor receptor 1  
 A:Reference number: J00006, M0UD:90165579

A: Molecule type: mRNA  
A: Residues: 1-416 <L>R>  
A: Experimental source: embryonic chick brain  
R: Heier, J.G., Falceme-Naine, S., Wheeler, E.F., Bothwell, M.  
Dev. Biol. 137, 287-304, 1990  
A: Title: Structure and developmental expression of the chicken NGF receptor  
A: Reference number: A60504; MUID: 90152140

A:status: preliminary: not compared with conceptual translation  
A:molecule type: mRNA  
A:Residues: 21-35, 'Y', 37-172, 'K', 174-275, 'S', 277-395, 'R', 397-416 <HD>  
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma  
C:Comment: The cysteine-rich region of the extracellular domain may form part or all  
C:Comment: This protein is thought to form a high-affinity receptor when it associates  
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-416/Product: nerve growth factor receptor #status predicted <MAY>  
F:21-233/Domain: extracellular #status predicted <EXT>  
F:24-57/Domain: NGF receptor repeat homology <NG1>  
F:59-100/Domain: NGF receptor repeat homology <NG2>  
F:101-139/Domain: NGF receptor repeat homology <NG3>  
F:141-181/Domain: NGF receptor repeat homology <NG4>  
F:189-237/Region: serine/threonine-rich  
F:240-261/Domain: transmembrane #status predicted <MEM>  
F:265-416/Domain: intracellular #status predicted <INT>  
F:52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	13.4%;	Score	184.5;	DB 1,	Length	416;	
Best Local Similarity	23.4%;	Pred. No.	0.00029;				
Matches	69;	Conservative	36;	Mismatches	93;	Gaps	14

```

Oy 15 VAVILLPVLTASSTAROEVEVPOQIVAPQOQSHSKGECC-----PAGSHREHT 63
    1 : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 5 VPILLILLPAGPTWGSKKC-----LTKMTTSGECKRACNIGGEVPOPCYNQI--- 54
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Oy 64 GACNCTEGVDVYTNASNNPESCFCCTVC-----KSDQ----- 95
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 55 -VCEPCDLDSVTYSIDVSTATPECKPCTQCVGLHSMABCVESDADVACAYFODELGS 113
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Oy 96 -KHKRSCMT-----TRDYVC-OCKEETPNE-NSPMKRKGRCRSGEVOVNCI 142
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 114 CKESICIEVGGGLMPCPCDSODIYVCEEBPEBTFSEANFVDPCLPTICIEENEMVACECT 173
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Oy 143 SWDDIQCVEEFGANAYVETPAAEETMNTSPGPAPAAEETMNTSPGPAPAAEETMTTSP 202
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 174 ATSDAEC-RDLHPMTHTHTPSL-----AGSDSPETIRDPENT-----EGMATY- 216
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Oy 203 GTPAPAAEETMTSPGTPAPAAEETMTTSPGT-----PASHYLSTYIGVIL 252
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 217 -----LADIVYTWGSSQP-----VYSRTADNLIPVYCSILAAVGVGLVAYI 259
    : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

## RESULT

hypothetical protein ZK04.1 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 17-Mar-2000  
C:Accession: T29018  
R:Kirsten, J.  
submitted to the EMBL Data Library, April 1995  
A:Description: The sequence of *C. elegans* cosmid ZK4.







Db 122 KCKCKPDFCYDCSPGCEHCVCRCASCEHGLE--PCTATSNMTCRKQSPRN 168

## RESULT 14

GOVZML T2 protein - myxoma virus (strain Lausanne)

C:Species: myxoma virus

C:Date: 31-Dec-1992 #sequence\_revision 31-Dec-1992 #text\_change 18-Jun-1999

C:Accession: A40566

R:Upton, C.; Macen, J.L.; Schreiber, M.; McFadden, G.

A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis

A:Reference number: A40566; MUID:91335768

A:Accession: A40566

A:Molecule type: DNA

A:Residues: 1-326 <UPT>

A:Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310

C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

C:Keywords: glycoprotein

F:64-105/Domain: NGF receptor repeat homology <NG3>

F:106-147/Domain: NGF receptor repeat homology <NG3>

F:66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

## Query Match

11.4%; Score 157; DB 1; Length 326;

Best Local Similarity 24.7%; Pred. No. 0.01; Matches 42; Conservative 19; Mismatches 61; Indels 48; Gaps 6;

OY 53 CPAGSHNSEHTG-----ACNPTGEGVDYTNASNNPSCFECT-VCKSDQKHKSCTMTRD 106

Db 43 CPDGSYASRLCGPSDHYVCSPC-KNETFTASTNHAPACVSCRCRGTGHLSEQSCDKTRD 101

OY 107 TVCCKGEGTENENSPENCRC---SRCP-----SGEVOYNSCTSW----- 144

Db 102 RVCDGSAIGNICLKGQBCRCICAPKTKCPAGYGVSGHTRTDVLCCKPCRYTSDAVSST 161

OY 145 -----DDIOCVEEFGANATVETPAEETMNTSPGTP 175

Db 162 ETCSTSFNYISVERFNLVPVNDTCTTGTAGPNEVYKTSSEFSYLNHTDCDP 211

## RESULT 15

F36791

hypothetical protein ORF50 - Ictalurid herpesvirus 1 (strain auburn 1)

C:Species: Ictalurid herpesvirus 1

A:Note: host Ictalurus punctatus (channel catfish)

C:Date: 17-Aug-1992 #sequence\_revision 17-Aug-1992 #text\_change 31-Jan-2000

C:Accession: F36791

R:Davidson, A.J.

submitted to GenBank, January 1992

A:Description: Channel catfish virus: a new type of herpesvirus.

A:Reference number: A36804

A:Accession: F36791

A:Molecule type: DNA

A:Residues: 1-670 <DAV>

A:Cross-references: GB:M75136; NID:g331209; PIDN:AAA8153.1; PID:g331260

R:Davidson, A.J.

Virology 186, 9-14, 1992

A:Title: Channel catfish virus: a new type of herpesvirus.

A:Reference number: A39447; MUID:92087490

A:Contents: annotation

A:Note: neither protein nor nucleic acid sequence is given

C:Genetics:

A:Gene: 50

C:Superfamily: period clock protein; EGF homology

## Query Match

11.3%; Score 156; DB 2; Length 670;

Best Local Similarity 43.3%; Pred. No. 0.021; Matches 39; Conservative 15; Mismatches 30; Indels 6; Gaps 4;

OY 155 ANATVETPA-AEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETM 213

Db 152 ANITATPAGANDTANITTTATPA-GANDTANITTTATPAGANDTAVTTTSATPAGANDTAV 210

OY 214 TTSPGTPAPA---AEET-MTSPGTPASSH 239

Db 211 TTPATPAGANDTANDTAVTTTPAMPAGAN 240

Search completed: August 13, 2002, 08:30:04  
Job time: 38 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 13, 2002, 08:30:11 ; Search time 15.81 Seconds  
(without alignments)  
634.305 Million cell updates/sec

Title: US-09-826-212-2

Perfect score: 1382  
Sequence: 1 MARIKTLKFFVIVIVALLP.....YLSCTIVGIVLVLLIVFV 259

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1382	100.0	259	1 T10C_HUMAN	O14798 h tumor nec
2	634	45.9	386	1 T10D_HUMAN	Q9ubn6 homo sapien
3	472	34.2	468	1 T10A_HUMAN	O00220 homo sapien
4	448	32.4	440	1 T10B_HUMAN	O14763 homo sapien
5	201.5	14.6	427	1 TR16_HUMAN	P08138 homo sapien
6	200.5	14.5	425	1 TR16_RAT	P07174 rattus norv
7	194	14.0	332	1 TNR6_PIG	O77736 sus scrofa
8	188.5	13.6	461	1 TR1A_PIG	P50555 sus scrofa
9	187	13.5	323	1 TNR6_BOVIN	P51867 bos taurus
10	184.5	13.4	416	1 TR16_CHICK	P18519 gallus gall
11	171.5	12.4	471	1 TR1A_BOVIN	O19131 bos taurus
12	169.5	12.3	461	1 TRIB_HUMAN	P03333 homo sapien
13	166.5	12.0	271	1 TNR4_HUMAN	P15725 rattus norv
14	166.5	12.0	277	1 TNR4_HUMAN	P43468 homo sapien
15	166	12.0	272	1 TNR4_MOUSE	P47741 mus musculu
16	163.5	11.8	335	1 TNR6_HUMAN	P25445 homo sapien
17	163	11.4	327	1 TNR6_MOUSE	P25446 mus musculu
18	157	11.4	326	1 VT2_MYXVL	P29825 myxoma viru
19	156	11.3	670	1 VG50_HSV1	O00130 ictaluriid h
20	153.5	11.1	324	1 TNR6_RAT	O63199 rattus norv
21	152	11.0	5179	1 MOC2_HUMAN	Q02817 homo sapien
22	149.5	10.8	595	1 TNR8_HUMAN	P28908 homo sapien
23	147.5	10.7	455	1 TR1A_HUMAN	P19438 homo sapien
24	146	10.6	474	1 TRIB_MOUSE	P25119 mus musculu
25	144	10.4	454	1 TR1A_MOUSE	P25118 mus musculu
26	141.5	10.2	349	1 VC22_VARY	P34015 variola vir
27	140.5	10.1	325	1 VT2_SEVTA	P25943 shope fibro
28	139.5	9.7	577	1 AMYR_YEAST	P08640 saccharomyc
29	133.5	9.7	1453	1 TRBM_MOUSE	P15306 mus musculu
30	133.5	9.7	307	1 CA11_CHICK	P02457 gallus gall
31	132	9.6	307	1 SGS3_DROME	P02840 drosophila
32	129.5	9.4	88	1 H82_MEIGO	P11910 neisseria g
33	129.5	9.4	461	1 TR1A_RAT	P22934 rattus norv

34	128.5	9.3	1637	1 MRSP_STAU	P80544 staphylococ
35	128	9.3	1802	1 HKRL_YEAST	P41809 saccharomyc
36	126	9.1	514	1 CSA_DICDI	P08796 dictyostell
37	125	9.0	1723	1 AIM1_HUMAN	Q9Y4K1 homo sapien
38	124	9.0	450	1 CYL_PARDE	P13627 paracoccus
39	124	9.0	1959	1 AGRI_RAT	P25304 rattus norv
40	121.5	8.8	634	1 HWPI_CANAL	P46593 candida alb
41	121	8.8	283	1 TR14_HUMAN	Q92956 homo sapien
42	120.5	8.7	255	1 TNR9_HUMAN	O07011 homo sapien
43	119.5	8.6	1162	1 TCNA_TRYCR	P23253 trypanosoma
44	119	8.6	412	1 SEPL_HUMAN	Q14242 homo sapien
45	117.5	8.5	435	1 TNR3_HUMAN	P36941 homo sapien

## ALIGNMENTS

RESULT	ID	SEQUENCE	STANDARD	PRT	259 AA.
1	T10C_HUMAN	O14798: 014755:			
2	T10D_HUMAN	Q9ubn6: 000220:			
3	T10A_HUMAN	O14763: 000220:			
4	T10B_HUMAN	P08138: 000220:			
5	TR16_HUMAN	P07174: 000220:			
6	TR16_RAT	O77736: 000220:			
7	TNR6_PIG	P50555: 000220:			
8	TR1A_PIG	P51867: 000220:			
9	TNR6_BOVIN	P18519: 000220:			
10	TR16_CHICK	O19131: 000220:			
11	TR1A_BOVIN	P03333: 000220:			
12	TRIB_HUMAN	P15725: 000220:			
13	TNR4_HUMAN	P43468: 000220:			
14	TNR4_HUMAN	P47741: 000220:			
15	TNR4_MOUSE	P25445: 000220:			
16	TNR6_HUMAN	P25446: 000220:			
17	TNR6_MOUSE	P29825: 000220:			
18	VT2_MYXVL	O00130: 000220:			
19	VG50_HSV1	O63199: 000220:			
20	TNR6_RAT	Q02817: 000220:			
21	MOC2_HUMAN	P28908: 000220:			
22	TNR8_HUMAN	P19438: 000220:			
23	TR1A_HUMAN	P25119: 000220:			
24	TRIB_MOUSE	P25118: 000220:			
25	TR1A_MOUSE	P34015: 000220:			
26	VC22_VARY	P25943: 000220:			
27	VT2_SEVTA	P08640: 000220:			
28	AMYR_YEAST	P15306: 000220:			
29	TRBM_MOUSE	P02457: 000220:			
30	CA11_CHICK	P02840: 000220:			
31	SGS3_DROME	P11910: 000220:			
32	H82_MEIGO	P22934: 000220:			
33	TR1A_RAT				

RA Tschopp J.;  
 RL "Characterization of two receptors for TRAIL.";  
 RT FEBS Lett. 416:329-334(1997).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98211672; PubMed=9551946;  
 RA Morigiolapaya J., Cowper A.E., Xu X.-N., Morris G., McMichael A.J.,  
 RA Bell J.I., Screaton G.R.;  
 RT "Lymphocyte inhibitor of TRAIL (TNF-related apoptosis-inducing  
 RT ligand): a new receptor protecting lymphocytes from the death ligand  
 RT TRAIL.";  
 RL Immunol. 160:3-6(1998).  
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL. Lacks a  
 CC cytoplasmic death domain and hence is not capable of inducing  
 CC apoptosis. May protect cells against TRAIL mediated apoptosis by  
 CC competing with TRAIL-R1 and R2 for binding to the ligand.  
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.  
 CC -1- TISSUE SPECIFICITY: Higher expression in normal tissues than in  
 CC tumor cell lines. Highly expressed in peripheral blood  
 CC lymphocytes, spleen, skeletal muscle, placenta, lung and heart.  
 CC -1- PTM: N-GLYCOSYLATED AND O-GLYCOSYLATED.  
 CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.  
 CC -----  
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 CC -----  
 DR EMBL: AF020502; AAB71413.1; ALT\_INIT.  
 DR EMBL: AF014794; AAC05593.1; ALT\_INIT.  
 DR EMBL: AF012629; AAB67110.1; -  
 DR EMBL: AF012536; AAB67104.1; -  
 DR EMBL: AF016267; AAB81181.1; -  
 DR EMBL: AF033854; AAB87506.1; -  
 DR HSSP: P19438; TEXT.  
 DR MIM: 603613; -  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00020; TNFR\_c6; 1.  
 DR SMART: SM00208; TNFR: 1.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 KW Receptor; Apoptosis; Glycoprotein; Repeat; GPI-anchor; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 24 236  
 FT PROPEP 237 259  
 FT REPEAT 69 109  
 FT REPEAT 110 149  
 FT DOMAIN 162 236  
 FT REPEAT 162 176  
 FT REPEAT 177 191  
 FT REPEAT 192 206  
 FT REPEAT 207 221  
 FT REPEAT 222 236  
 FT REPEAT 222 236  
 FT DISULFID 69 85  
 FT DISULFID 88 101  
 FT DISULFID 91 109  
 FT DISULFID 111 125  
 FT DISULFID 128 141  
 FT DISULFID 131 149  
 FT LIPID 236 236  
 FT CARBOHYD 77 77  
 FT CARBOHYD 140 140  
 FT CARBOHYD 156 156  
 FT CONFLICT 119 119  
 FT SEQUENCE 259 AA; 27395 MW; FE3BF7FCEA50B8 CRC64;

Query Match 100.0%; Score 1382; DB 1; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 7, 4e-78;  
 Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MARIKTKLKVYVIVAVLLPVLVANSATTAROEVEVPOQTVAPOQQRHSGKEBCPAGSHRS 60  
 DB 1 MARIKTKLKVYVIVAVLLPVLVANSATTAROEVEVPOQTVAPOQQRHSGKEBCPAGSHRS 60  
 OY 61 EHTGACNCTGVDVDTNANNNPSCFCTVCKSDQKHSSCTMTDVCOCQKEGFRREN 120  
 DB 61 EHTGACNCTGVDVDTNANNNPSCFCTVCKSDQKHSSCTMTDVCOCQKEGFRREN 120  
 OY 121 SPMCKRCSRCPSGEVOVSNCTSMDDIOCEBFGANATVETPAAEETMTNTPSGTPAPAAE 180  
 DB 121 SPMCKRCSRCPSGEVOVSNCTSMDDIOCEBFGANATVETPAAEETMTNTPSGTPAPAAE 180  
 OY 181 ETMTNTPSGTPAPAAEETMTNTPSGTPAPAAEETMTNTPSGTPAPAAEETMTNTPSGTPASSHY 240  
 DB 181 ETMTNTPSGTPAPAAEETMTNTPSGTPAPAAEETMTNTPSGTPAPAAEETMTNTPSGTPASSHY 240  
 OY 241 LSCITVGIIVLIVLIVFV 259  
 DB 241 LSCITVGIIVLIVLIVFV 259  
 RESULT 2  
 T10D HUMAN STANDARD: PRT: 386 AA.  
 ID T10D HUMAN  
 AC Q9UBN6; Q9Y604;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 10D precursor (Decoy  
 DE receptor 2) (DCR2) (TNF-related apoptosis-inducing ligand receptor 4)  
 DE (TRAIL receptor-4) (TRAIL-R4) (TRAIL receptor with a truncated death  
 DE domain).  
 GN TNFRSF10D OR DCR2 OR TRAILR4 OR TRUND.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., SEQUENCE OF N-TERMINUS, AND VARIANT.  
 RP TISSUE-Fetal lung;  
 RC MEDLINE=98044290; PubMed=9382840;  
 RX Masters S.A., Sheridan J.P., Pitti R.M., Huang A., Skubatch M.,  
 RA Baldwin D., Yuan J., Gurney A., Goddard A.D., Godowski P.,  
 RA Askenazi A.;  
 RT "A novel receptor for Apo2L/TRAIL contains a truncated death domain.";  
 RT Curr. Biol. 7:1003-1006(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A., CHARACTERIZATION, AND VARIANTS S-35 AND L-310.  
 RP TISSUE-Forebrain fibroblast, and Peripheral blood lymphocytes;  
 RX MEDLINE=9809091; PubMed=9430226;  
 RA Degli-Esposti M.A., Dougall W.C., Smolak P.J., Waugh J.Y., Smith C.A.,  
 RA Goodwin R.G.;  
 RT "The novel receptor TRAIL-R4 induces NF-kappaB and protects against  
 RT TRAIL-mediated apoptosis, yet retains an incomplete death domain.";  
 RT Immunol. 7:813-820(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RP MEDLINE=98196860; PubMed=9537512;  
 RA Pan G., Ni J., Yu G.-L., Wei Y.-F., Dixit V.M.;  
 RT "TRUND, a new member of the TRAIL receptor family that antagonizes  
 RT TRAIL signalling.";  
 RT FEBS Lett. 424:41-45(1998).  
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL. Contains a  
 CC truncated death domain and hence is not capable of inducing  
 CC apoptosis but protects against TRAIL-mediated apoptosis. Reports  
 CC are contradictory with regards to its ability to induce the NF-  
 CC kappaB pathway (According to ref.1 it cannot but according to  
 CC ref.2 it can induce the NF-kappaB pathway).

```

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed, in particular in fetal
CC kidney, lung & liver and in adult testis and liver. Also expressed
CC in peripheral blood leukocytes, colon and small intestine, ovary,
CC prostate, thymus, spleen, pancreas, kidney, lung, placenta and
CC heart.
CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN (TRUNCATED).
CC -----
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CC -----
DR EMBL: AF029761; AAC03477.1; -
DR EMBL: AF021232; AAC32765.1; -
DR EMBL: AF021233; AAC32766.1; -
DR EMBL: AF023849; AAC52053.1; -
DR HSSP: P19438; 1NCF.
DR MIM: 603614; -.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 2.
DR SMART: SM00208; TNFR_2.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal;
KW Polymorphism.
FT STGNAL 1 55
FT CHAIN 56 386
FT DOMAIN 56 211 TUMOR NECROSIS FACTOR RECEPTOR
FT TRANSMEM 212 232 SUPERFAMILY MEMBER 10D.
FT REPEAT 233 386 EXTRACELLULAR (POTENTIAL).
FT REPEAT 98 139 POTENTIAL.
FT REPEAT 140 180 CYTOSOLASMIC (POTENTIAL).
FT DOMAIN 140 366 TNFR-CYS 1.
FT DOMAIN 225 228 TNFR-CYS 2.
FT DOMAIN 246 250 DEATH (TRUNCATED).
FT DISULFID 99 115 POLY-VAL.
FT DISULFID 118 131 POTENTIAL.
FT DISULFID 121 139 POTENTIAL.
FT DISULFID 141 155 POTENTIAL.
FT DISULFID 158 172 POTENTIAL.
FT CARBOHYD 127 180 POTENTIAL.
FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 35 35 P -> S (IN TRAIL-R4-B).
FT VARIANT 35 35 /FTID=VAR_011417.
FT VARIANT 310 310 S -> L (IN TRAIL-R4-B).
FT SEQUENCE 386 AA; 41823 MW; 77A93577CAAF2632 CRC64;
SQ

```

Query Match 45.9%; Score 634; DB 1; Length 386;  
 Best Local Similarity 51.8%; Pred. No. 2.9e-37;  
 Matches 132; Conservative 22; Mismatches 41; Indels 60; Gaps 3;

```

QY 5 PKILKPVYVAVLLPYLVANSATTAROEVEPQGFVAPQOQSHSKFGECPCAGSHRSEHTG 64
DB 35 PKILKPVYVAVLLPYLVANSATTAROEVEPQGFVAPQOQSHSKFGECPCAGSHRSEHTG 94
QY 65 ACNCTEGVDYTNASNNBPSCFPTCKSDOKHSSCTMTDTCVCKCEGFRFNNSEEM 124
DB 95 ACNCTEGVDYTNASNNBPSCFPTCKSDOKHSSCTMTDTCVCKCEGFRFNNSEEM 154
QY 125 CRKCS-SRCPGSEGVONCSWDIOCVEEFGANATVETPAEEMTNTSPGTPAPAAEETM 183
DB 155 CRTRCTGCPGRMVKVNSCTPRSDIKCKNESASSTGKTPAAEEVYITLLG----- 204
QY 184 NTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGTPASSHYLSC 243

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```

DB 205 -----MLASP-----YHYLLI 215
QY 244 TIVGIVLVILVIF 258
DB 216 IIVLVILVAVVGF 230

RESULT 3
T10A_HUMAN STANDARD; PRT; 468 AA.
ID T10A_HUMAN
AC 000220;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 10A precursor (Death
DE receptor 4) (TNF-related apoptosis-inducing ligand receptor 1) (TRAIL
DE receptor-1) (TRAIL-R1).
GN TNFRSF10A OR DR4 OR TRAILR1 OR APO2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97238921; Pubmed=9082980;
RA Pan G., O'Rourke K., Chinnaiyan A.M., Gentz R., Ebner R., Ni J.,
RA Dixit V.M.;
RT "The receptor for the cytotoxic ligand TRAIL.";
RL Science 276:111-113(1997).
RN [2]
RP FUNCTION.
RX MEDLINE=98090092; Pubmed=9430227;
RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;
RT "Death receptor 5, a new member of the TNFR family, and DR4 induce
RT FADD-dependent apoptosis and activate the NF-kappaB pathway.";
RL Immunity 7:821-830(1997).
-1- FUNCTION: Receptor for the cytotoxic ligand TRAIL; mediates
apoptosis in a caspase-dependent manner. Can trigger the nuclear
factor kappaB-pathway and can bind the cytoplasmic adapter
molecule FADD/MORT1 which engages initiator caspases such as
caspase 8 leading to subsequent activation of effector caspases
that execute apoptotic death of the cell.
-1- SUBUNIT: Can interact with TRADD and RIP.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- TISSUE SPECIFICITY: Widely expressed. High levels are found in
spleen, peripheral blood leukocytes, small intestine and thymus,
but also in K562 erythroleukemia cells, MCF7 breast carcinoma
cells and activated T-cells.
-1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U90875; AAC51226.1; -
DR HSSP: P19438; 1EXT.
DR MIM: 603611; -.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00020; TNFR_c6; 2.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.

```

FT SIGNAL 1 23 POTENTIAL.  
FT CHAIN 24 468 TUMOR NECROSIS FACTOR RECEPTOR  
FT DOMAIN 24 239 SUPERFAMILY MEMBER 10A.  
FT TRANSMEM 240 262 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 263 468 POTENTIAL.  
FT REPEAT 147 188 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 189 229 TNFR-CYS 1.  
FT DOMAIN 365 448 TNFR-CYS 2.  
FT DOMAIN 29 32 DEATH.  
FT DISULFID 132 145 POLY-ALA.  
FT DISULFID 148 164 POTENTIAL.  
FT DISULFID 167 180 POTENTIAL.  
FT DISULFID 170 188 POTENTIAL.  
FT DISULFID 190 204 POTENTIAL.  
FT DISULFID 207 221 POTENTIAL.  
FT DISULFID 211 229 POTENTIAL.  
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 468 AA; 50025 MM; 1E85DDC2C8760E7 CRC64;

Query Match 34.2%; Score 472; DB 1; Length 468;  
Best Local Similarity 58.7%; Pred.No.2.4e-22;  
Matches 91; Conservative 16; Mismatches 42; Indels 6; Gaps 3;

QY 3 RIPPTLKEVVIVAVLLPVLAVSATTAAROEVPQOTVAPOOQRHSFKGEGCPAGSHRSEH 62  
DB RHVHTFKFVV--VGVLLQVVPSSAATIKLHD--QSISTQGMWHSPLGELCPGSHRSEH 141

QY 63 TGACNPGCEGYDTNMANSPSCPCYCKSDQKHKSCTMTROTVCCKGCTRENENSP 122  
DB 142 PGACNRCRCEGYDTNMANSPNMLFACLPCTACKSDEERSPCCTTNTACCKGCTRENENSA 201

QY 123 EMCRCRSC-CPGSEGYOVNCTSMDDIOCVEEFGAN 156  
DB 202 EMCRCRSTGCPRGKVKYKDCITPMSDIECVKESGN 236

RESULT 4  
T10B\_HUMAN STANDARD: PRT: 440 AA.  
ID T10B\_HUMAN  
AC 014763: 015531: 015508: 015517: 014720: Q9BEVO:  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 10B precursor (Death receptor 5) (TNF-related apoptosis-inducing ligand receptor 2) (TRAIL receptor-2) (TRAIL-R2)  
GN TNFRSF10B OR DR5 OR TRAILR2 OR TRICK2 OR KILLER OR ZTNFR9.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RN [2]  
RP SEQUENCE FROM N.A. (LONG ISOFORM), AND SEQUENCE OF N-TERMINUS.  
RC TISSUE=foreskin fibroblast;  
RX MEDLINE=97459925; PubMed=9311998;  
RA Walczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Waugh J.Y., Bolani N., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A., Goodwin R.G., Rauch C.T.;  
RA "TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";  
RT EMBO J. 16:5386-5397(1997).  
RL [2]  
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS), AND ALTERNATIVE RP SPLICING.  
RX MEDLINE=97431692; PubMed=9285725;  
RA Screaton G.R., Mongkolsapaya J., Xu X.-N., Cowper A.E., McMichael A.J., Bell J.I.;  
RT "TRICK2, a new alternatively spliced receptor that transduces the cytotoxic signal from TRAIL.";  
RL Curr. Biol. 7:693-696(1997).  
RN [3]  
RP SEQUENCE FROM N.A. (LONG ISOFORM), AND CHARACTERIZATION.

RC TISSUE=Liver, and Spleen;  
RX MEDLINE=98039016; PubMed=9373179;  
RA Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N., Tschoep J.;  
RL "Characterization of two receptors for TRAIL.";  
RN FEBS Lett. 416:329-334(1997).  
RP [4]  
RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
RC TISSUE=ovary;  
RX MEDLINE=97467719; PubMed=9326928;  
RA Wu G.S., Burns T.F., McDonald E.R., Ili, Jang W., Meng R., Kranz I.D., Kao G., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R., Spinner N.B., Markowitz S., Wu G., el-Deiry W.S.;  
RT "Killer/DR5 is a DNA damage-inducible p53-regulated death receptor gene.";  
RL Nat. Genet. 17:141-143(1997).  
RN [5]  
RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
RX MEDLINE=97390508; PubMed=9242610;  
RA Pan G., Ni J., Wei Y.-F., Yu G.-I., Gentz R., Dixit V.M.;  
RT "An antagonist decoy receptor and a death domain-containing receptor for TRAIL.";  
RL Science 277:815-818(1997).  
RN [6]  
RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
RX MEDLINE=97467318; PubMed=9325248;  
RA MacFarlane M., Ahmed M., Srinivasula S.M., Fernandes-Alnemri T., Cohen G.M., Alnemri E.S.;  
RT "Identification and molecular cloning of two novel receptors for the cytotoxic ligand TRAIL.";  
RL J. Biol. Chem. 272:25417-25420(1997).  
RN [7]  
RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
RX MEDLINE=9809092; PubMed=9430227;  
RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;  
RT "Death receptor 5, a new member of the TNFR family, and DR4 induce FADD-dependent apoptosis and activate the NF-kappaB pathway.";  
RL Immunity 7:821-830(1997).  
RN [8]  
RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
RX MEDLINE=97390509; PubMed=9242611;  
RA Sheridan J.P., Walters S.A., Pletl R.M., Gurney A., Skubatch M., Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I., Goddard A.D., Godowski P., Ashkenazi A.;  
RT "Control of TRAIL-induced apoptosis by a family of signalling and decoy receptors.";  
RL Science 277:818-821(1997).  
RN [9]  
RP SEQUENCE FROM N.A. (LONG ISOFORM).  
RA Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yuasa Y.;  
RT "Genomic structure and mutation analyses of the DR5/TRAIL receptor 2 gene in colorectal carcinoma.";  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
RN [10]  
RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
CAO X., Zhang W., Wan T.;  
RA Cao X., Zhang W., Wan T.;  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
RN [11]  
RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
RA Farrah T., Vu T., Gilbert T., Gross J., O'Hara P.;  
RT "Homo sapiens homolog of tumor necrosis factor receptor.";  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
RN [12]  
RP SEQUENCE FROM N.A. (LONG ISOFORM).  
RC TISSUE=Cervix;  
RA Strausberg R.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [13]  
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183.  
RX MEDLINE=20017054; PubMed=10549288;  
RA Hymowitz S.G., Christinger H.W., Fuh G., Ullsch M., O'Connell M., Kelley R.F., Ashkenazi A., de Vos A.M.;  
RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a

RT complex with death receptor 5.";  
 RL MOL. Cell 4:563-571(1999).  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184.  
 RX PubMed-10542098.  
 RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,  
 RA Jones E.Y., Sreteron G.R.;  
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring  
 RT specificity in apoptotic initiation.";  
 RL Nat. Struct. Biol. 6:1048-1053(1999).  
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL; mediates  
 CC apoptosis in a caspase-dependent manner. Can trigger the nuclear  
 CC factor kappaB-pathway and can bind the cytoplasmic adapter  
 CC molecule FADD/MORT1 which engages initiator caspases such as  
 CC caspase 8 leading to subsequent activation of effector caspases  
 CC that execute apoptotic death of the cell.  
 CC -1- SUBUNIT: Homotrimer (Potential). Can interact with TRADD and RIP.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM/TRICK2B (SHOWN HERE)  
 CC AND A SHORT FORM/TRICK2A; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues;  
 CC very highly expressed in tumor cell lines such as Hela S3, K562,  
 CC HL-60, SM480, A549 and G361; highly expressed in heart, peripheral  
 CC blood lymphocytes, liver, pancreas, spleen, thymus, prostate,  
 CC ovary, uterus, placenta, testis, esophagus, stomach and throughout  
 CC the intestinal tract; not detectable in brain.  
 CC -1- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.  
 CC -1- DISEASE: Defects in TNFRSF10B may be a cause of squamous cell  
 CC carcinoma of the head and neck.  
 CC -1- SIMILARITY: CONTAINS 1 IIA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: AF016849; AAC51778.1; -  
 DR EMBL: AF018657; AAB70577.1; -  
 DR EMBL: AF018658; AAB70578.1; -  
 DR EMBL: AF016266; AAB81180.1; -  
 DR EMBL: AF022386; AAB71949.1; -  
 DR EMBL: AF012628; AAB67109.1; -  
 DR EMBL: AF020501; AAB71412.1; -  
 DR EMBL: AF016268; AAC01565.1; -  
 DR EMBL: AF012535; AAB67103.1; -  
 DR EMBL: AB014718; BAA33723.1; -  
 DR EMBL: AB014710; BAA33723.1; JOINED.  
 DR EMBL: AB014711; BAA33723.1; JOINED.  
 DR EMBL: AB014712; BAA33723.1; JOINED.  
 DR EMBL: AB014713; BAA33723.1; JOINED.  
 DR EMBL: AB014714; BAA33723.1; JOINED.  
 DR EMBL: AB014715; BAA33723.1; JOINED.  
 DR EMBL: AB014716; BAA33723.1; JOINED.  
 DR EMBL: AB014717; BAA33723.1; JOINED.  
 DR EMBL: AF153687; AAF75587.1; -  
 DR EMBL: AF192548; AAF07175.1; -  
 DR EMBL: BC001281; AAH01281.1; -  
 DR MIM: 603612; -  
 DR MIM: 601400; -  
 DR PDB: 1D0G; 22-OCT-99.  
 DR PDB: 1D4V; 01-NOV-99.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00531; death; 1.  
 DR Pfam: PF00020; TNFR\_c6; 2.  
 DR SMART: SM00005; DEATH; 1.  
 DR SMART: SM00208; TNFR; 2.  
 DR PROSITE: PSS0017; DEATH\_DOMAIN; 1.  
 DR PROSITE: PSS0052; TNFR\_NGFR\_1; 2.

DR PROSITE: PSS0050; TNFR\_NGFR\_2; 2.  
 KW Receptor: Apoptosis; Transmembrane; Repeat; Signal;  
 KW Alternative splicing; 3D-structure.  
 FT SIGNAL 1 55  
 FT CHAIN 56 440  
 FT DOMAIN 56 210 TUMOR NECROSIS FACTOR RECEPTOR  
 FT TRANSMEM 211 231 SUPERFAMILY MEMBER 10B.  
 FT DOMAIN 232 440 EXTRACELLULAR (POTENTIAL).  
 FT REPEAT 97 137 POTENTIAL.  
 FT REPEAT 138 178 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 192 206 TAPE.  
 FT DOMAIN 339 422 DEATH.  
 FT DOMAIN 250 253 POLY-GLY.  
 FT DISULFID 81 94  
 FT DISULFID 97 113  
 FT DISULFID 116 129  
 FT DISULFID 119 137  
 FT DISULFID 139 153  
 FT DISULFID 156 170  
 FT DISULFID 160 178  
 Query Match 32.48; Score 448; DB 1; Length 440;  
 Best Local Similarity 40.7%; Pred. No. 6,5e-21;  
 Matches 105; Conservative 23; Mismatches 68; Indels 62; Gaps 4;  
 QY 3 RIPTLKFVVYIVVLLPYLAYSATTAEROEVPQOTVAPQOQRHFRGECPPAGSHRSEH 62  
 DB 33 RVPKTL-VLVVAVALLVSAESALITQODLAPQORAPQOKRSPSGGLCPGHHSIED 90  
 QY 63 TGACNPCTEGVDYTNASNEPSCFPCITVCKSDQKHSCTWTRDVCCKEGTFRNENSP 122  
 DB 91 GRDIDCKYGGDDYTHNMNLDLFCRLCRDSCGEVELSPTTTRNTVOCCEGTREDESP 150  
 QY 123 EMCRC-K-SRCPGSEVOYSNCTSMDDIQCVEEFGANATVETPAAEETMTSPGPAPAAE 181  
 DB 151 EMCRCRCRCGCRGVKXVDCDTPWSDIECVH----- 180  
 QY 182 TMTNTPGTPAPAAEETMTSPGPAPAAEETMTSPGPAPAAEETMTSPGPASSHYL 241  
 DB 181 -----KESGTRHSG-EAPVETVTSPTSPASPCSL 211  
 QY 242 SCTIVGIVLVLLVLFV 259  
 DB 212 SGIIIGTVAAVLIVAV 229  
 RESULT 5  
 TR16\_HUMAN STANDARD; PRT; 427 AA.  
 AC P08138;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-  
 DE affinity nerve growth factor receptor) (NGF receptor) (Gp80-LINGER)  
 DE (p75 ICD) (Low affinity neurotrophin receptor p75NTR).  
 GN NGFR OR TNFRSF16.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87051725; PubMed=3022937;  
 RA Johnson D., Lanhahan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,  
 RA Botwell M., Chao M.;  
 RT "Expression and structure of the human NGF receptor.";  
 RL Cell 47:545-554(1986).  
 RN [2]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RX MEDLINE=89096903; PubMed=2850481;  
 RA Sehgal A., Patil N., Chao M.;

RT		"A constitutive promoter directs expression of the nerve growth factor receptor gene."
RH	MOL.	Cell. Biol. 8:3160-3167(1988).
CC	-1-	FUNCTON: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF, NT-3,
CC	AND NT-4.	CAN IMMEDIATE CELL SURVIVAL AS WELL AS CELL DEATH OF NEURAL CELLS.
CC	-1-	SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.
CC	INTERACTS WITH	p75NTR-ASSOCIATED CELL DEATH EXECUTOR.
CC	-1-	SUBCELLULAR LOCATION: Type I membrane protein.
CC	-1-	PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC	-1-	SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC	-1-	SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC	-----	
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CC	-----	
DR	EMBL;	M14764; AAB59544.1; .
DR	EMBL;	M21621; AAA36363.1; .
DR	PIR;	A25218; GOHUN.
DR	HSSP;	P07174; INGR.
DR	MIM;	162010; .
DR	InterPro;	IPRO00488; Death.
DR	InterPro;	IPRO01368; TNFR_C6.
DR	Pfam;	PF00531; death; 1.
DR	Pfam;	PF00020; TNFR_C6; 4.
DR	SMART;	SMO0005; DEATH; 1.
DR	SMART;	SMO0208; TNFR; 3.
DR	PROSITE;	PS00652; TNFR_NGFR_1; 3.
DR	PROSITE;	PS00500; TNFR_NGFR_2; 4.
DR	PROSITE;	PS50017; DEATH_DOMAIN; 1.
KW	Receptor;	Neurogenesis; Transmembrane; Glycoprotein; Repeat;
KW	Phosphorylation;	Signal; Apoptosis.
FT	SIGNAL	1 28
FT	CHAIN	29 427
FT	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 16, EXTRACELLULAR (POTENTIAL), POTENTIAL.	
FT	DOMAIN	29 250
FT	TRANSMEM	251 272
FT	DOMAIN	273 427
FT	REPEAT	31 64
FT	REPEAT	66 107
FT	REPEAT	108 146
FT	REPEAT	148 188
FT	DOMAIN	344 421
FT	DOMAIN	197 248
FT	DISULFD	32 43
FT	DISULFD	44 57
FT	DISULFD	47 64
FT	DISULFD	67 83
FT	DISULFD	86 99
FT	DISULFD	89 107
FT	DISULFD	109 122
FT	DISULFD	125 138
FT	DISULFD	128 146
FT	DISULFD	149 164
FT	DISULFD	167 180
FT	DISULFD	170 188
FT	CARBONYD	60
FO	SEQUENCE	427 AA; 45183 MW; BO9FA143FB30625B CXC64; N-LINKED (GLCNAC... ) (POTENTIAL);

Query Match	14.6%	Score 201.5	DB 1	Length 427
Best Local Similarity	24.4%	Pred. No. 6e-06		
Matches 64	Conservative 25	Mismatches 92	Indels 81	Gaps 9

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QY      51 EECFAG--SHSSEHTGACN-----PCTEGVDYTNASNNPSCFPCTVC 91
      | | | : | | | | | : | : : : | | | |
Db      30 EACFGLYTHSGECCKACNLGEGVAQPCGANQTVCEPCLDSTFSDVVSATEPECKPCTEC 89

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QY 92 KSQKXHKSSCMTIDPTVOCKEKGFRNNSP--EMCR-----KCSRC 131
Db 90 VGLQSMASAPCVBADDVACRCAYGYDDETTGRCACRCRCGSLVFCODKONTVCCEC 149
QY 132 PSG-----EVOVSNCTSMDDIQCEEFGANATVETPAAEEMNT 170
Db 150 PDGTYSDKANHYDPLCTVCEEDTBRQLRETRKAADACEEIPGRMTTRSTP--PESDST 208
QY 171 SPGTAPAPAAEETMTNSPCTPAPAAEETMTTSPGTAPAPAAEETMTTSPGTAPAPAAEETMTT 230
Db 209 APSTQEPFA-----PPEDDLIASTVAG-----VTTVMGSSQPVVTRG--TT 248
QY 231 SPGPASSHYSCTIYGIIVLI 252
Db 249 DNLIPVYCIIAAVYVGLAVYI 270

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RESULT	6
TR16_RAT	
ID	TR16_RAT
STANDARD:	PR1: 425 AA.
AC	P07174.
DT	01-APR-1988 (Rel. 07, Created)
DT	01-APR-1988 (Rel. 07, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Tumor necrosis factor receptor superfamily member 16 precursor (Low-affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)
GN	(p75 ICD) (Low affinity neurotrophin receptor p75NTR).
GN	NGFR OR TNFRSF16.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=87115859; PubMed=3027580;
RA	Radeke M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;
RT	"Gene transfer and molecular cloning of the rat nerve growth factor receptor.";
RL	Nature 325:593-597(1987).
RN	[2]
RP	SEQUENCE OF 1-22 FROM N.A.
RC	TISSUE=Liver;
RX	MEDLINE=93077038; PubMed=1446821;
RA	Wecsis M., Timmusk T., Allkmeets R., Saarna M., Persson H.;
RT	"Regulatory elements and transcriptional regulation by testosterone and retinoic acid of the rat nerve growth factor receptor promoter.";
RL	Gene 121:247-254(1992).
RN	[3]
RP	STRUCTURE BY NMR OF 334-418.
RX	MEDLINE=97449145; PubMed=9305641;
RA	Liepinsh E., Illeg L.L., Oetting G., Ibanez C.F.;
RT	"NMR structure of the death domain of the p75 neurotrophin receptor.";
RL	EMBO J. 16:4999-5005(1997).
CC	-1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF, NT-3, AND NT-4. CAN MEDIMATE CELL SURVIVAL AS WELL AS CELL DEATH OF NEURAL CELLS.
CC	-1- SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC	-1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC	-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC	-----
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CC	-----
DR	EMBL; X05137; CAA28783.1; -
DR	EMBL; X61269; -; NOT_ANNOTATED_CDS.
DR	PIR; A26431; A26431.

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DR PDB: 1NGR; 29-JUL-97.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death; 1.
DR Pfam: PF00020; TNFR_c6; 4.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 4.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
KW Phosphorylation; Signal; Apoptosis; 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 425
FT FT TUMOR NECROSIS FACTOR RECEPTOR
FT FT SUPERFAMILY MEMBER 16.
FT FT EXTRACELLULAR (POTENTIAL).
FT FT POTENTIAL.
FT FT CYTOPLASMIC (POTENTIAL).
FT FT REPEAT 274 425
FT FT TNFR-CYS 1.
FT FT REPEAT 32 65
FT FT TNFR-CYS 2.
FT FT REPEAT 109 147
FT FT TNFR-CYS 3.
FT FT REPEAT 149 189
FT FT TNFR-CYS 4.
FT FT DEATH.
FT FT DOMAIN 354 419
FT FT SER/THR-RICH.
FT FT DOMAIN 196 249
FT FT DISULFID 33 44
FT FT DISULFID 45 58
FT FT DISULFID 48 65
FT FT DISULFID 68 84
FT FT DISULFID 87 100
FT FT DISULFID 90 108
FT FT DISULFID 110 123
FT FT DISULFID 126 139
FT FT DISULFID 129 147
FT FT DISULFID 150 165
FT FT DISULFID 168 181
FT FT DISULFID 171 189
FT FT CARBOHYD 61 61
FT FT CARBOHYD 71 71
SQ SEQUENCE 425 AA; 45432 MW; B2E152D94D3827F8 CRC64;

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Query Match 14.5%; Score 200.5; DB 1; Length 425;
Best Local Similarity 23.9%; Pred. No. 6.9e-06;
Matches 68; Conservative 32; Mismatches 107; Indels 77; Gaps 9;

```

```

QY 17 VLLPVLAATATAROEVPQQTVAPOOQRHSFGGECPA---GSHRSEHGA---CNPC 69
DB 17 LLLILLGVSSGAK-----ETCSTGLYHS--GECKACNLGEGVAQPCGANQVCEPC 68
QY 70 TEGVDYTNASNNBPSCFCTVCKSDQKHKSSCTMTDRDVC----- 109
DB 69 LDNVFTSDVVASATPECKPCTECGLGLOMSAPCYEADAVRCAYGYQDEFTGHCACSV 128
QY 110 -----QCKEGTFRNE-NSPEMCRKCRKCPGSEGVSNCTSWDDIQ 148
DB 129 CEVGSGLVSCQDKONTVCCECEGEGYSDEANHVDPCLPTVCEDERQJRECTPWADAE 188
QY 149 CVDEFGANATVETPAAEETMTSPGPAPAAEETMTSPGPAPAAEETMTSPGPAPAA 208
DB 189 CEETPGKWIPIRSTP-PEGSSITAPSTOEPRVPEQDLVPESTVA----- 230
QY 209 AEETMTSPGPAPAAEETMTSPGPAPASSHYLSCTIVGIIIVL 252
DB 231 --DMVTTVMGSSQPVVTRG-TTDNLIPVYCSILAAVAVGLAVI 271

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RESULT 7
ID TNFR6_PIG STANDARD; PRT; 332 AA.
AC 077736;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

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DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE (CD95).
GN TNFRSF6 OR Ap1 OR FAS.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT Expression of apoptosis-associated genes in hibernating and stunned
RT myocardium of pig."
RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH (BT SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AJ001202; CAA04596.1; -.
DR HSSP: P25445; 1DDP.
DR DR InterPro: IPR000488; Death.
DR DR InterPro: IPR001368; TNFR_c6.
DR DR Pfam: PF00531; death; 1.
DR DR Pfam: PF00020; TNFR_c6; 3.
DR DR SMART: SM00005; DEATH; 1.
DR DR SMART: SM00208; TNFR; 3.
DR DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR DR PROSITE: PS50050; TNFR_NGFR_2; 2.
DR DR PROSITE: PS50017; DEATH_DOMAIN; 1.
KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 16
FT FT POTENTIAL.
FT FT TUMOR NECROSIS FACTOR RECEPTOR
FT FT SUPERFAMILY MEMBER 6.
FT FT EXTRACELLULAR (POTENTIAL).
FT FT POTENTIAL.
FT FT CYTOPLASMIC (POTENTIAL).
FT FT REPEAT 45 81
FT FT TNFR-CYS 1.
FT FT REPEAT 82 125
FT FT TNFR-CYS 2.
FT FT REPEAT 126 164
FT FT TNFR-CYS 3.
FT FT DEATH.
FT FT DOMAIN 227 311
FT FT CARBOHYD 38 38
FT FT CARBOHYD 116 116
SQ SEQUENCE 332 AA; 37592 MW; 5B8B03682756BF1B CRC64;

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Query Match 14.0%; Score 194; DB 1; Length 332;
Best Local Similarity 32.4%; Pred. No. 1.4e-05;
Matches 44; Conservative 24; Mismatches 50; Indels 18; Gaps 6;

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QY 28 TAROEVPQQTVAPOOQRHSFGGECPCAGSHR-----SEHTGA---CNPCTEGVDTYTNASN 81
DB 40 TKRESECP-----GQHRGEGPCGCPGPKRKRIADCTSPGAGAQCYPCSGEEDYTDKNHH 95
QY 82 EPCSCFCTVCKSDQKH---KSSCTMTDRDVCCKCKEGTFRNENSPMCRKCRKCPGSEGY 137

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FT CONFLICT 396 396 K -> R (IN REF. 2).  
 SQ SEQUENCE 416 AA; 44654 MW; 6BCEAB54F4D2D56 CRC64;  
 Query Match 13.4%; Score 184.5; DB 1; Length 416;  
 Best Local Similarity 23.4%; Pred. No. 6,4e-05;  
 Matches 69; Conservative 36; Mismatches 93; Indels 97; Gaps 14;  
 QY 15 VAVLLPVLAVSATTAAROEVEYPOQTVAPOOQRHSFKGECEPAGSHRSEHT 63  
 DB 5 VPLLILLPAGPTMGSKK-----LTKMYTSGECKKCNLGEVYQCGVNGT--- 54  
 QY 64 GACNPGTEGYDYNASNNPSCFCTVC-----KSDQ----- 95  
 DB 55 -VEPCIDSVTSDVTSATEPCKCTCQVGLHSMAPCVESDDAVCRACAYGFODELSGS 113  
 QY 96 -KHKSSCTM-----TRDTVC--CKEESTFRNE--NSPEMKKCRCPGSEGYVNSCT 142  
 DB 114 CKECISCEVGBGLMPCRDSDVYCECPBEGTSDENFVDPCLPTICEENEVYVNECT 173  
 QY 143 SMDDIQVEEFGANATVETPAAEETMTNTSPGTAPAAEETMTTSP 202  
 DB 174 ATSDAEC-RDLHPRTWTHHTSL-----AGSDSPERTDRPNT-----EGMATY- 216  
 QY 203 GTPAPAAEETMTTSPGTAPAAEETMTTSPGT-----PASSHYLSCTIVGIIVLI 252  
 DB 217 -----LADIVTYVMGSSQP-----VYSRGTADNLIIPVCSIIAAVYGLVAYI 259  
 RESULT 11  
 ID TRIA\_BOVIN STANDARD; PRT; 471 AA.  
 AC 019131;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor 1 precursor (p60) (TNF-R1) (TNF-R1)  
 DE (p55).  
 GN TNFRSF1A OR TNFR1.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Arteria;  
 RA Lee E.-K., Taylor M.J., Kehrl M.E.;  
 RT Cloning of cDNA encoding bovine tumor necrosis factor-receptor 1 (TNF-R1).  
 RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 RL (TNF-R1).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. THE ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING SIGNALING COMPLEX (DIS) PERFORMS CASPASE-8 PROTEOLYTIC ACTIVATION WHICH INITIATES THE SUBSEQUENT CASCADE OF CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING APOPTOSIS (BY SIMILARITY).  
 CC -1- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAFs, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
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 CC -----  
 CC EMBL: U90937; AB65143.1; -.  
 DR HSP; P19438; TNFR.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00531; death; 1.  
 DR Pfam: PF00020; TNFR\_c6; 3.  
 DR ProDom: PD000771; TNFR\_c6; 1.  
 DR SMART: SM00005; DEATH; 1.  
 DR SMART: SM00208; TNFR; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 3.  
 DR PROSITE: PS50017; DEATH DOMAIN; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Apoptosis.  
 FT SIGNAL 1 21  
 FT CHAIN 22 471  
 FT DOMAIN 22 210  
 FT TRANSMEM 211 233  
 FT DOMAIN 234 471  
 FT REPEAT 83 82  
 FT REPEAT 126 125  
 FT REPEAT 126 166  
 FT DOMAIN 167 195  
 FT DOMAIN 340 360  
 FT DOMAIN 372 457  
 FT DISULFID 44 56  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117  
 FT DISULFID 105 125  
 FT DISULFID 127 143  
 FT DISULFID 146 158  
 FT DISULFID 149 166  
 FT DISULFID 168 179  
 FT DISULFID 182 190  
 FT DISULFID 185 194  
 FT CARBOHYD 54 54  
 FT CARBOHYD 145 145  
 FT CARBOHYD 151 151  
 SQ SEQUENCE 471 AA; 51367 MW; 5243EF514DE81C4 CRC64;  
 Query Match 12.4%; Score 171.5; DB 1; Length 471;  
 Best Local Similarity 21.1%; Pred. No. 0.00044;  
 Matches 75; Conservative 32; Mismatches 118; Indels 131; Gaps 14;  
 QY 14 VAVLLPVLAVSATTAAROEVEYPOQTVAPOOQRHSFKGECEPAGSHRSEHTGACNPCTE 71  
 DB 6 VPGILLP-LVLPALLADVYRAGVGIVPHRBDLKRREPCQGGKYNHPQNTICTGCKHK 64  
 QY 72 GV-----DYTNASNNPSCFCTVCSD--QKHKSCMTTRDTV 108  
 DB 65 GTLYLNDPCPGGRDTCRCVCAFGTYALEHLARCLSCSRCDMEFVEISPCVVDRTV 124  
 QY 109 CCKEETFRN--ENSPMKKCRCPGSEGYV-----SNCTSMDD 146  
 DB 125 CGCKKQRYEYGEFGRLNCSLCPNGTVNIPCOERODTICHCNMGFELGAKCISCHD 184  
 QY 147 IQ-----CVEEFGA----- 155  
 DB 185 CKNNECEKLCPTRTSGKDSODPGTYVLLPVIYFGCLAFASVAVLACRYORMKPKLYS 244  
 QY 156 ----NATVEPAAEETMTNTSPG-----TPAPAAEETMTNTSP-----GTPAPAA 194  
 DB 245 IICGOSTLVKGEPELLVAPAGFNPPTTICSSPSSPSVSIPIYISCDRSNFGAVASPS 304  
 QY 195 EET-----MTTSPGTAPAAEETMTTSPGTAPAAEETMTTSPGTAPAAEETMTTSP 246  
 DB 305 SETAPPHLAKAPILPGPASTHTLCT-PGPPA-----STHLCTPPGPASTHTL--CTPV 353

RESULT 12  
 ID TRIB\_HUMAN STANDARD; PRT; 461 AA.  
 AC P20333;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor 2 precursor (Tumor necrosis factor binding protein 2) (TNFR2) (p80) (TNF-R2) (p75) (CD120B) (Etanercept).  
 GN TNFR2B OR TNFR2 OR TNFR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90260639; PubMed=2160731;  
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R., Dower S.K., Cosman D., Goodwin R.G.;  
 RT "A receptor for tumor necrosis factor defines an unusual family of cellular and viral proteins.";  
 RL Science 248:1019-1023(1990).  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9104591; PubMed=2172983;  
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., Kling M.W., Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;  
 RT "A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96299745; PubMed=8661109;  
 RA Bellingier C.P., White P.S., Matis J.M., Sulman E.P., Jensen S.J., Lepastier D., Stallard B.J., Goeddel D.V., Desauvage F.J.;  
 RT "Physical mapping and genomic structure of the human TNFR2 gene.";  
 RL Genomics 35:94-100(1996).  
 RN  
 RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=90349572; PubMed=2166946;  
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D., Ringold G.M.;  
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).  
 RN  
 RP SEQUENCE OF 27-31.  
 RX MEDLINE=90110215; PubMed=2153136;  
 RA Engelmann H., Novick D., Wallach D.;  
 RT "Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.";  
 RL J. Biol. Chem. 265:1531-1536(1990).  
 RN  
 RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.  
 RX MEDLINE=91056048; PubMed=2173696;  
 RA Loetscher H., Schlaeger E.J., Lamm H.-W., Pan Y.-C.E., Lesslauer W., Brockhaus M.;  
 RT "Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors from HL60 cells.";  
 RL J. Biol. Chem. 265:20131-20138(1990).  
 RN  
 RP CHARACTERIZATION.  
 RX MEDLINE=93016040; PubMed=1328224;  
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M., Lipari M.T., Goeddel D.V.;  
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor. Characterization of ligand binding, internalization, and receptor phosphorylation.";  
 RL J. Biol. Chem. 267:21172-21178(1992).

[8]  
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH  
 RP TRAF2.  
 RX MEDLINE=99221490; PubMed=10206649;  
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
 RT "Structural basis for self-association and receptor recognition of human TRAF2.";  
 RL Nature 398:533-538(1999).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW LEVEL ON THREONINE RESIDUES.  
 CC -1- PHARMACEUTICAL: Available under the name Enbrel (Immunex and Wyeth-Ayerst). Used to treat moderate to severe rheumatoid arthritis (RA). Enbrel consist of the extracellular ligand-binding portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to TNF-alpha and blocks its interactions with receptors.  
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".  
 CC -1- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;  
 CC WWW="http://www.enbrelinfo.com/".  
 CC -----  
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 CC -----  
 DR EMBL: M32315; AAA59929.1; -;  
 DR EMBL: M35857; AAA63262.1; -;  
 DR EMBL: U52165; AAC50622.1; -;  
 DR EMBL: U52156; AAC50622.1; JOINED.  
 DR EMBL: U52157; AAC50622.1; JOINED.  
 DR EMBL: U52158; AAC50622.1; JOINED.  
 DR EMBL: U52159; AAC50622.1; JOINED.  
 DR EMBL: U52160; AAC50622.1; JOINED.  
 DR EMBL: U52161; AAC50622.1; JOINED.  
 DR EMBL: U52162; AAC50622.1; JOINED.  
 DR EMBL: U52163; AAC50622.1; JOINED.  
 DR EMBL: U52164; AAC50622.1; JOINED.  
 DR EMBL: M55994; AAA36755.1; -;  
 DR PIR: A35356; A35356.  
 DR PIR: A36007; A36007.  
 DR PIR: A36475; A36475.  
 DR PIR: B35010; B35010.  
 DR PIR: A23666; A23666.  
 DR PDB: 1CA9; 12-APR-99.  
 DR MIM: 191191; -;  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00020; TNFR\_c6; 4.  
 DR ProDom: PD000771; TNFR\_c6; 1.  
 DR SMART: SM00208; TNFR; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 4.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;  
 KW Phosphorylation; Pharmaceutical; 3D-structure.  
 KW SIGNAL  
 FT CHAIN 23 461  
 FT DOMAIN 23 257  
 FT TRANSMEM 258 287  
 FT DOMAIN 288 461  
 FT REPEAT 39 76  
 FT REPEAT 77 118  
 FT REPEAT 119 162  
 FT REPEAT 163 201  
 FT DISULFID 40 53  
 FT DISULFID 54 67  
 FT DISULFID 57 75  
 FT DISULFID 78 93  
 FT  
 FT TUMOR NECROSIS FACTOR RECEPTOR 2.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT POTENTIAL.  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TNFR-CYS 1.  
 FT TNFR-CYS 2.  
 FT TNFR-CYS 3.  
 FT TNFR-CYS 4.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.  
 FT BY SIMILARITY.

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FT DISULFID 96 110 BY SIMILARITY.
FT DISULFID 100 118 BY SIMILARITY.
FT DISULFID 120 126 BY SIMILARITY.
FT DISULFID 134 143 BY SIMILARITY.
FT DISULFID 137 161 BY SIMILARITY.
FT DISULFID 164 179 BY SIMILARITY.
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 141 141 R -> P (IN REF. 4).
FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3).
FT CONFLICT 363 363 A -> T (IN REF. 4).
SQ SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;

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Query Match 12.3%; Score 169.5; DB 1; Length 461;  
 Best Local Similarity 25.2%; Pred. No. 0.00057;  
 Matches 74; Conservative 34; Mismatches 117; Indels 69; Gaps 15;

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OY 11 VVIVIVALLPYLAVSATTAROEVEPQQTVAQ-----QQRHSFGECPAGSH- 58
D 4 VAVMAALVAGLEMAAALPAQVAFTPYAPEPGSGTCRLREYDQTAQMCSCSPGQHA 63
OY 59 -----RSRHTGACNCTEGVDYTNASNNPSCFPC-TYCKSPQKHKSSCTMRDQVCOCK 112
D 64 KVFCTKTSDT-VCDSG-EDSTYTTQLMNVPECLSCGSRCSQVETQACTRQNRNICTCR 121
OY 113 EGFENNSPEMCRKCS---RCPSGEVOVSNCTSMDDIOCVBEFGANATVETPAAEETM- 168
D 122 PGWICALSKOECRCALCRKCRPGFVARBGTETSDVVC-----KPCAPGIFS 170
OY 169 NTSPECT-----PAPAAEETMNTS-----PCT---PAPAAEETMTSPG 203
D 171 NNTSSTDICRPHQICNVVAIPGNASRDVACTSTPSRMAPGAVHLPQVSTRSQHTQP- 229
OY 204 TPAPAAEETMTSPGTPAPAAEETMTSPGTPASHSYLSCTIVGIIIVLIVLI 256
D 230 TPBSTATSTFLPMGSPSPAGS-TGDFALPVG-----LIVGTVLADGLITI 276

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RESULT 13
TNRA_RAT
ID TNRA_RAT STANDARD; PRT: 271 AA.
AC P15725;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
  receptor) (OX40 antigen) (MRC OX40).
GN TNRSF4 OR TXGPIL OR OX40.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RA MEDLINE=90214614; PubMed=2157591;
RA Mallett S., Fossum S., Barclay A.N.;
RT "Characterization of the MRC OX40 antigen of activated CD4 positive T
  lymphocytes -- a molecule related to nerve growth factor receptor.";
RL EMBL J 9:1063-1068(1990).
CC -! FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -! SUBCELLULAR LOCATION: Type I membrane protein.
CC -! TISSUE SPECIFICITY: ACTIVATED T-CELLS.
CC -! SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
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CC -----
DR EMBL: J17037; CAA34897.1; -.
DR PIR: S08036; S08036.
DR PIR: S12783; S12783.
DR HSSE, P19438; TEXT.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR: 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS0050; TNFR_NGFR_2; 2.
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT CHAIN 1 19 POTENTIAL.
FT SIGNAL 20 271 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 20 210 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 211 235 POTENTIAL.
FT DOMAIN 236 271 CYTOPLASMIC (POTENTIAL).
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 102 TNFR-CYS 2.
FT REPEAT 103 123 TNFR-CYS 3 (INCOMPLETE).
FT REPEAT 124 164 TNFR-CYS 4.
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 271 AA; 29895 MW; C0646513B16B821 CRC64;

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Query Match 12.0%; Score 166.5; DB 1; Length 271;  
 Best Local Similarity 28.4%; Pred. No. 0.00054;  
 Matches 63; Conservative 25; Mismatches 93; Indels 41; Gaps 11;

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OY 52 ECPAGS---HRSRHT--GACNCTEGVDYTNASNNPSCFPCVVC--KSDQKHKSSCTMT 104
D 40 ECGPGHGWNSRCDHTRDYVCHRCPEG--FYNAVAVYDICKQCTQCNHSGSLKONCPT 97
OY 105 RDTVCOCKEGTF-RNENSPEMCRKCSRCPGSGVOVSN--CTSMDDIOCVBEFGANATVE 160
D 98 EDTVCOCKRGTGTPRODSSHKLGVDVCPGPPGHSFGSNQACKRW-----TNCITLS 147
OY 161 TPAAEETMTSPGTPAPAAEETMTSPGTPAPAEETM-TTSPGTPAPAEETMTTSS--P 217
D 148 GKQIHH-----PASNSLDIVCEDRSLLALLMETQRTTRPTTVSTTWVPTSTQLP 199
OY 218 GTPAPAEETMTSPGTPAPAEETMTSPGTPASSHSYLSCTIVGIIIVLIVLIVFV 259
D 200 SPTPLVA-----PEGPAAFAVILGLGLLAPLVLLALYL 234

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RESULT 14
TNRA_HUMAN
ID TNRA_HUMAN STANDARD; PRT: 277 AA.
AC P43489; Q13663;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
  receptor) (ACT35 antigen) (TAX-transcriptionally activated
  glycoprotein 1 receptor) (CD134 antigen).
GN TNRSF4 OR TXGPIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94170844; PubMed=7510240;
RA Latza U., Dueckop H., Schmittiger J., Ringeling J., Etzelbach F.,
RA Hummel M., Fonatsch C., Stein H.;
RT "The human OX40 homolog: cDNA structure, expression and chromosomal
  assignment of the ACT35 antigen.";
RL Eur. J. Immunol. 24:677-683(1994).
RN [2]
RP SEQUENCE FROM N.A.
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RX MEDLINE-95219871; PubMed-7704935.  
RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,  
RA Watson M.L., Seidlin M.F., Clifford K.N., Grabstein K., Alderson M.R.;  
RT "Identification of OX40 ligand and preliminary characterization of  
RT its activities on OX40 receptor."  
RL Circ. Shock 44:30-34(1994).  
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GRP34 CYTOKINE.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
CC -1- DATABASE: NAME-PROV: NOTE-CD guide CD134 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".  
CC -----  
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CC -----  
DR EMBL: X75962; CAAS3576.1; -  
DR EMBL: S76792; AAB3944.1; ALT\_INIT.  
DR HSSP: P25942; LCDP.  
DR MIM: 600315; -  
DR InterPro: IPR001368; TNFR\_c6.  
DR Pfam: PF00020; TNFR\_c6; 3.  
DR ProDom: PD000771; TNFR\_c6; 1.  
DR SMART: SM00208; TNFR; 3.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
KW Signal.  
FT SIGNAL 1 28  
FT CHAIN 29 277  
FT DOMAIN 29 214 POTENTIAL.  
FT TRANSMEM 215 235 TUMOR NECROSIS FACTOR RECEPTOR  
FT DOMAIN 236 277 SUPERFAMILY MEMBER 4  
FT REPEAT 30 65 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 66 107 TNFR-CYS 1.  
FT REPEAT 108 126 TNFR-CYS 2.  
FT REPEAT 127 167 TNFR-CYS 3 (INCOMPLETE).  
FT REPEAT 146 146 TNFR-CYS 4.  
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 277 AA; 29340 MM; 49F1525941550BF CRC64;  
Query Match 12.0%; Score 166.5; DB 1; Length 277;  
Best Local Similarity 26.2%; Pred. No. 0.00055;  
Matches 59; Conservative 36; Mismatches 83; Indels 47; Gaps 14;  
OY 52 ECPAGS-----HRESEHTGACNPCTEGVDYTNASNNPSCFPCVC--KSDOKHKSCGM 103  
DB 45 ECRONGAVSKCSRSQNT-VCRPGCGPF-YNDVYSSKP-CRPTCTCNLRSSGSRKQLCTA 101  
OY 104 TRDTVCQCKESTFRNENSPENCRKCRCPSEGVQVSN--CTSWDDICVEBFGANATVE 160  
DB 102 TQDVCRCRACT-CPLDSTYKPGVDCAPCPGPHFSPGDAQCPW-----TNCCTL- 149  
OY 161 TPAAEETMTSPGTAPAETMTMTSPGTAPAETMTMTSPGTAPAETMTMTSPGT 220  
DB 150 --AGHTLTQ-----PASNSSAIDCEDRDPPTQPOETO---GPRA---RPITVQPTGA 194  
OY 221 APAAEETMTSP-GTPASSHYLSCTIVGIV-----LIVLIVFV 259  
DB 195 WPRTSQSPSTRPVEYVPGRAVAATIGLGLVGLGLPLAILLALYL 239  
RESULT 15  
TNRA\_MOUSE STANDARD; PRT: 272 AA.  
ID TNRA\_MOUSE  
AC P47741;  
DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 4, precursor (OX40L  
DE receptor) (OX40 antigen).  
CN TNFRSF4 OR TKGPI OR OX40.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BAUB/C;  
RX MEDLINE-94044750; PubMed-8228223;  
RA Claeshead D.M., Buhlmann J.E., van den Eertwegh A.J.,  
RA Claeshead E., Noelle R.J., Fell H.;  
RT "Cloning of mouse OX40: a T cell activation marker that may mediate  
RT T-B cell interactions".  
RL J. Immunol. 151:5261-5271(1993).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-95255413; PubMed-7737295;  
RA Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
RA Barclay A.N.;  
RT "Gene structure and chromosomal localization of the mouse homologue  
RT of rat OX40 protein."  
RL Eur. J. Immunol. 25:926-930(1995).  
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GRP34 CYTOKINE.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: Z21674; CAA79772.1; -  
DR EMBL: X85214; CAAS9476.1; -  
DR HSSP: P19438; IEXT.  
DR MGD: MGI:104512; Tnftrsf4.  
DR InterPro: IPR001368; TNFR\_c6.  
DR Pfam: PF00020; TNFR\_c6; 3.  
DR ProDom: PD000771; TNFR\_c6; 1.  
DR SMART: SM00208; TNFR; 3.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
KW Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 272  
FT DOMAIN 20 211 POTENTIAL.  
FT TRANSMEM 212 235 TUMOR NECROSIS FACTOR RECEPTOR  
FT DOMAIN 237 272 SUPERFAMILY MEMBER 4  
FT REPEAT 26 65 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 62 103 TNFR-CYS 1.  
FT REPEAT 104 124 TNFR-CYS 2.  
FT REPEAT 125 165 TNFR-CYS 3 (INCOMPLETE).  
FT CARBOHYD 144 144 TNFR-CYS 4.  
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFILCT 15 15 A -> G (IN REF. 2).  
SQ SEQUENCE 272 AA; 30153 MM; 06B7BB4156F0D08E CRC64;  
Query Match 12.0%; Score 166; DB 1; Length 272;  
Best Local Similarity 25.8%; Pred. No. 0.00058;  
Matches 67; Conservative 37; Mismatches 106; Indels 50; Gaps 13;  
OY 16 AVLLPVLAYSATTARQEEPPQOTVAPQOQRHSFKG-----ECPAGS---HRESEHT--GA 65  
DB 10 ALLLALTLGLVTARLNCV-----KHYPGSHKCCRCRCOPGKGVSRCHDTROTTL 59





RESULT	2	
09QZM4		
ID	09QZM4	PRELIMINARY: PRT: 381 AA.
AC	09QZM4	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE	KILLER/DR5 TRAIL DEATH-INDUCING RECEPTOR.	
GN	TNFRSF10B.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_Taxid=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
FX	MEDLINE=99310501; PubMed=10383128;	
RA	Wu G.S., Burns T.F., Zhan Y., Alnemri E.S., El-Deiry W.S.;	
RT	"Molecular cloning and functional analysis of the mouse homologue of	
RT	the KILLER/DR5 tumor necrosis factor-related apoptosis-inducing ligand	
RT	(TRAIL) death receptor.";	
RL	Cancer Res. 59:2770-2775(1999).	
DR	EMBL; AF176833; AAD52656.1; .	
DR	HSSP; 014763; IDOG.	
DR	MGP; MG1:1341090; Tnftrsf10b.	
DR	InterPro; IPR001368; TNFR_c6.	
DR	Pfam; PF000531; death_1.	
DR	Pfam; PF00020; TNFR_c6; 2.	
DR	SMART; SM00005; DEATH; 1.	
DR	SMART; SM00208; TNFR; 2.	
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.	
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.	
DR	PROSITE; PS00050; TNFR_NGFR_2; 2.	
DR	Receptor	
SW	SEQUENCE 381 AA; 42164 MW; 222531758F4ADE0A CRC64;	
Query Match	20.7%; Score 285.5; DB 11; Length 381;	
Best Local Similarity	39.2%; Pred. No. 5,5e-16;	
Matches	58; Conservative 27; Mismatches 42; Indels 21; Gaps	
QY	11 VVIVYAVLLPVLYATYSATY-----ARQEEVPOQTVAPOQQRHSFGKECPAGSHRSEHTGA 65	
DB	40 LAVLDAAVEPVYANPAHNRPAGLQRPESPSR-----GPCLAGQYLSE--GN 84	
QY	66 CNPCTREGVDYTNASNNP-PSCFPTCYVSKDQKHKSCCTMTPTQYCOCKCKCTRENENSPKM 124	
DB	85 CKPCEGEGIDYTSNHSNLSDCILCYCKDKKVVETRCNITTYVCRCKGTFEDKDSPEI 144	
QY	125 CRKSCRPSGGEVQVQVNCSTWMDIQGVVE 152	
DB	145 CQSCNCCTDGEDEELTCTPRENRKCVSK 172	
RESULT	3	
ID	09JUL6	
AC	09JUL6	PRELIMINARY: PRT: 381 AA.
DT	01-OCT-2000 (TREMBLrel. 15, Created)	
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE	TRAIL RECEPTOR KILLER/DR5 HOMOLOGUE.	
GN	TNFRSF10B OR MK.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_Taxid=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=SPLEEN;	
RA	Nakamura Y., Tamari M., Watanabe O.;	
RT	"Mouse TRAIL receptor.";	

	RL	Submitted (Aug-1999) to the EMBL/Genbank/DDJB databases.	
	DR	EMBL; AB031081; BAA96462.1; -	
	DR	HSSP; O14763; IDOG	
	DR	MGD; MGI:1341090; Tnftrf10b.	
	DR	InterPro; IPR000488; Death.	
	DR	InterPro; IPR001368; TNFR_c6.	
	DR	Pfam; PF00020; TNFR_c6; 2.	
	DR	SMART; SM00005; DEATH; 1.	
	DR	SMART; SM00208; TNFR; 2.	
	DR	PROSITE; PS00017; DEATH_DOMAIN; 1.	
	DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.	
	DR	PROSITE; PS0050; TNFR_NGFR_2; 2.	
	KW	Receptor.	
	SQ	SEQUENCE 381 AA; 42223 MW; 2F7999EA2EB485B1 CRC64;	
		Query Match 20.1%; Score 282.5; DB 11; Length 385;	
		Best Local Similarity 37.8%; Pred. No. 9,8e-16;	
		Matches 57; Conservative 28; Mismatches 42; Indels 21; Gaps 4	
Oy	11	VVVIIVALLPLVLAYSATT-----AROEVPQOQTVAPOOOHRHFSGECPCAGSHRSEHTGA 65	
		: : :     :       :   :   :	
Dd	40	LAMIDAVFPVTANPAHNRPAQLGRREPSDR-----GPCLAGQYLSE--GN 84	
Oy	66	CNPCEBGVDYTNASNNE-PSCFFPYCVKSDQHKRSSCTMTPTDYCOCKGCFTRFNENSPM 124	
		:   :         :   :     :         :     :     :	
Dd	85	CKRCPEGIDYTSHSNNSLDSCILCYCKEDKAVETFCINITYTVCRCGPTEFKDSPRI 144	
Oy	125	CKRSKRCPSEGYOVSNCTSMWDIOCEE 152	
		:           :     :     :     :	
Dd	145	CGSCSNCITDGEELFTSCTPRENRKYVK 172	
	RESULT 4		
	09JUL5	PRELIMINARY; PRT; 385 AA.	
ID	09JUL5:		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	TRAIL RECEPTOR2 KILLER/DR5 HOMOLOGUE.		
GN	MK.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Nakamura Y., Tamari M., Watanabe O.;		
RT	"Mouse TRAIL receptor genomic.";		
RL	Submitted (Aug-1999) to the EMBL/Genbank/DDJB databases.		
DR	EMBL; AB031082; BAA96463.1; -		
DR	HSSP; O14763; IDOG.		
DR	InterPro; IPR000488; Death.		
DR	InterPro; IPR001368; TNFR_c6.		
DR	Pfam; PF00020; TNFR_c6; 2.		
DR	SMART; SM00005; DEATH; 1.		
DR	SMART; SM00208; TNFR; 2.		
DR	PROSITE; PS00017; DEATH_DOMAIN; 1.		
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.		
DR	PROSITE; PS0050; TNFR_NGFR_2; 2.		
KW	Receptor.		
SQ	SEQUENCE 385 AA; 42676 MW; 4FD089FCDCA134159 CRC64;		
	Query Match 20.1%; Score 277.5; DB 11; Length 385;		
	Best Local Similarity 37.8%; Pred. No. 2,6e-15;		
	Matches 56; Conservative 28; Mismatches 43; Indels 21; Gaps 4		
Oy	11	VVVIIVALLPLVLAYSATT-----AROEVPQOQTVAPOOOHRHFSGECPCAGSHRSEHTGA 65	
		: : :     :       :   :   :	
Dd	40	LAMIDAVFPVTANPAHNRPAQLGRREPSDR-----GPCIAGQYLSE--GN 84	



OY	66	CNPCEGVDTMASNNE-PSCPCCVCKSDOKHSSCMTDPTVOCKEGFRRNSPM	124
Dd	85	KCPKEGIDYTRSRSNHSLSDCILCTVCCKEDKVKYETRCNTITTTFCRCKAIGTFEDXDSPEI	144
OY	125	CRCSCRPSGEVOVSNCSTSMDDIOCEE	152
Dd	145	COSCSNCTDGEBELTSCTPRENRKCYSK	172
RESULT	5		
ID	057408	PRELIMINARY;	PRT; 368 AA.
AC	057408;		
DT	01-JUN-1998	(TREMBLrel. 06, Created)	
DT	01-JUN-1998	(TREMBLrel. 06, last sequence update)	
DT	01-DEC-2001	(TREMBLrel. 19, last annotation update)	
DE	SUGROUP E ALV RECEPTOR.		
OC	Melagris gallopavo (Common turkey).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.		
OX	NCHI_Taxid=9103;		
RN	[ ]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97471016; PubMed=9326659;		
RA	Ackins H.B., Brojatsch J., Naughton J., Rolfs M.M., Pesola J.M.,		
RT	Young J.A.;		
RT	"Identification of a cellular receptor for subgroup E avian leukosis		
RT	virus";		
RL	Proc. Natl. Acad. Sci. U.S.A. 94:11617-11622(1997).		
DR	EMBL; AF006002; AAB93987.1; -.		
DR	HSSP; O14763; IDOG.		
DR	InterPro; IPR001450; 4Fe4S_ferredoxin.		
DR	InterPro; IPR00488; Death.		
DR	InterPro; IPR001865; Ribosomal_S2.		
DR	InterPro; IPR001368; TNFR_c6.		
DR	Pfam; PF00531; death_1.		
DR	Pfam; PF00020; TNFR_c6; 2.		
DR	SMART; SMART0005; DEATH; 1.		
DR	SMART; SMART0208; TNFR; 2.		
DR	PROSITE; PS00196; 4FE4S_FERREDOXIN; UNKNOWN_1.		
DR	PROSITE; PS50017; DEATH_DOMAIN; 1.		
DR	PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.		
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.		
KW	PROSITE; PS50050; TNFR_NGFR_2; 2.		
KW	Receptor.		
SO	SEQUENCE	368 AA; 41020 MW; 5701AAC2A6D4F87E2 CRC64;	
Query Match	18.3%; Score 253; DB 13; Length 368;		
Best local similarity	34.7%; Pred. No. 2,6e-13;		
Matches	50; Conservative 27; Mismatches 59; Indels 8; Gaps		
OY	8	LKFVVIVAVILLPVLAYSATTAROEVEVPQOTVAPOOQRHSFGECBPAGSHSEHTGACN	67
Dd	6	LRFCEVLLILLAKVLHGSAAAVKRAVKSDYLKPDPY-----SKKCPMGTYLANDSSRCL	60
OY	68	PTEGEVDVTMANSNNPEPCPTVCCKSDOKHKSSCMTRDPTVOCKEGTFRANSP-EMKR	126
Dd	61	PEKKP-EETTERPDNDPKCGCTCRKHEDOVEPSCNSTMTTRACKNGTGFLCDLPDHCEMCO	119
OY	127	KC-SRPCSGEVVSNCTSGMDDIOC	149
Dd	120	KOOTRCRPGQVRIACTOQSILRC	143
RESULT	6		
ID	091A7	PRELIMINARY;	PRT; 368 AA.
AC	091A7;		
DT	01-OCT-2000	(TREMBLrel. 15, Created)	
DT	01-OCT-2000	(TREMBLrel. 15, last sequence update)	
DT	01-DEC-2001	(TREMBLrel. 19, last annotation update)	
DE	TVB51.		

GN TVE.  
 OS Gallus gallus (chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP MEDLINE=20193796; PubMed=10729132;  
 RA Adkins H.B., Brojatsch J., Young J.A.T.;  
 RT "Identification and Characterization of a TNFR-related Receptor for  
 RT Subgroups B/D/E Avian Leukosis Viruses Reveals Cysteine Residues  
 RT Required Specifically for Subgroup E Virus Entry.";  
 RL J. Virol. 74:3572-3578(2000).  
 DR EMBL: AF161713; AAF60221.1; -.  
 DR HSSP: O14763; IDOG.  
 DR InterPro: IPR001450; 4Fe4S\_ferredoxin.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00531; death; 1.  
 DR Pfam: PF00020; TNFR\_c6; 2.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 2.  
 DR PROSITE; PS00198; 4FE4S\_FERREDOXIN; UNKNOWN\_1.  
 DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; UNKNOWN\_1.  
 SO SEQUENCE 368 AA; 41531 MW; 0533CE531DEB47C6 CRC64;

Query Match	16.1%	Score 222:	DB 11:	Length 368:
Best Local Similarity	32.6%	Pred. 0.93e-11:		
Matches 47:	Conservative 24:	Mismatches 65:	Indels 8:	Gaps
Qy	8	LKFVVIVAVLLPVLAVSATTARQEEVYQQTVAPOQQRHSPKSGECPAGSHRSEHGACN	67	
Db	6	LRLCPVLLLFVAEVQDLSAAAVKKRADRSIDQKFDLYR----	RKCPMGTYEANDSIQCL	60
Qy	68	PCTEEVDYTNASNNPESCFPCTCKSDQKHSSCTMTPTDYCOCKEKGTFRNENSP-EMCR	122	
Db	61	PKCKN-EXTPEYDNPFPKGLGCRGCRGDEVEVSPCLPTNTQACAKNGTFCLPDHPCMCQ	119	
Qy	127	KC-SRCPSGEVOVSNCTSMDDIQC	149	
Db	120	KQTECPKQGVRLAPCTQHSLLC	143	
RESULT	7			
Q9PM79		PRELIMINARY;	PRT;	368 AA.
AC	09PM79			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	TVB53.			
GN	TVB.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archiosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97100985; PubMed=8945512;			
RA	Brojatsch J., Naughton J., Kolis M.M., Zingler K., Young J.A.;			
RT	"CA1, a TNFR-related protein, is a cellular receptor for cytopathic			
RL	avian leukosis-sarcoma viruses and mediates apoptosis.";			
RN	Cell 87:845-855(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Brojatsch J., Naughton J., Young J.A.T.;			
RT	Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF161712; AAD47256.1;			



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Db 235 VFDSLSSAP-----RVSNCTAETVDYNDTSANGTGVAGSLS 273
      :|||
RESULT 10
ID Q920W1 PRELIMINARY; PRT; 417 AA.
AC Q920W1;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE NERVE GROWTH FACTOR RECEPTOR.
GN NGFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A;
RX MEDLINE=9077793; PubMed=9857182;
RA Tuffreau C., Benejean J., Blondel D., Kieffer B., Flammang A.;
RT "Low-affinity nerve-growth factor receptor (P75NTR) can serve as a
RL receptor for rabies virus.";
EMBL J. 17:7250-7259(1998).
DR HSSP; AF105292; AAD17943.1; -.
DR HSSP; P07174; INGR.
DR MGD; MGI:97333; Ngfr.
DR InterPro; IPR000488; Death.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death.1.
DR SMART; SM00208; TNFR; 4.
DR SMART; SM00208; TNFR; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR.1; 3.
DR PROSITE; PS50050; TNFR_NGFR.2; 4.
KW Receptor.
SQ SEQUENCE 417 AA; 44686 MW; 5D7A4510DBA9B2 CRC64;

Query Match 14.4%; Score 198.5; DB 11; Length 417;
Best Local Similarity 24.7%; Pred. No. 9.2e-09;
Matches 71; Conservative 35; Mismatches 104; Indels 77; Gaps 11;

QY 14 IVAVLLPYLAISATTAHQEEVPOQTAVAPQOQRHSFKGECPA--GSHRSEHTGA----C 66
      :|||
Db 6 LLLLLLLLGVSFGAK-----ETCSTGMYTHS--GECCKACNNGEVAAQCGANQIVC 57
      :|||
QY 67 NPCIEGVYITNANNNPFCFCYCKSPQKHSSCTMTRDVY-----C 109
      :|||
Db 58 EPCLDSTVTFSDVSAATEKCKTECLGLQSMSPACVEADDAACRCRSYGYODEETGCEA 117
      :|||
QY 110 -----OCKEGTFRNE--NSPEMCRKSCSPGGEVOVNSCTGSM 145
      :|||
Db 118 CSVCGVSGGLVFCODKONTVCCECPCESTYSDEANHNHDPCLCTVCEPTEROLRECTPWA 177
      :|||
QY 146 DIQVEEFGANATVETPAAEETMTNTPGTAPAAEETMTNTPGTAPAAEETMTNTPGT 205
      :|||
Db 178 DAECEIPIGRMTRETP-PEGSDVTTPTGPEAPEPERDLASTVA-----DIVTTVMSSS 232
      :|||
QY 206 AAPAEETMTNTPGTAPAAEETMTNTPGTAPAAEETMTNTPGTAPAAEETMTNTPGT 252
      :|||
Db 233 QP-----VVTGRGT-----ADNLI-----PYCSTILAIVAGLVAYI 263
      :|||
RESULT 11
Q9PRG7 PRELIMINARY; PRT; 401 AA.
ID Q9PRG7

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AC Q9PRG7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE P75 NEUROTROPHIN RECEPTOR A-2.
GN P75NTRA.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Hutson L.D., Richards A.P., Bothwell M.;
RT "Life and death in the developing Xenopus retina: The role of the p75
RT neurotrophin receptor.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172400; AAD51031.1; -.
DR EMBL; AF172399; AAD51030.1; -.
DR HSSP; P07174; INGR.
DR InterPro; IPR000488; Death.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death.1.
DR SMART; SM00208; TNFR; 4.
DR SMART; SM00208; TNFR; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR.1; UNKNOWN_3.
DR PROSITE; PS50050; TNFR_NGFR.2; 3.
KW Receptor.
SQ SEQUENCE 401 AA; 43419 MW; D3BCAF7863EEEC CRC64;

Query Match 14.0%; Score 193; DB 13; Length 401;
Best Local Similarity 24.4%; Pred. No. 2.5e-08;
Matches 58; Conservative 34; Mismatches 104; Indels 42; Gaps 9;

QY 45 RHPFKGE---ECPASHRSEHTG---ACNPCTEGVDYTNANNNPFCFCYCKSPDQKH 97
      :|||
Db 26 OTTAKGECCTISQVGEYIKRGVNOYVCEPLDSVTTSDTSHTEACKPCTECGHRM 85
      :|||
QY 98 KSSCTMTRDVYCOCKEGTFERNENSPENCRKSCSPGGEVOVNSCTGSM 157
      :|||
Db 86 EAPCVESDDAVACAYGFTDKKSGQ-CKICKSCPEGFGMMMSCTNIDTIC-----EK 138
      :|||
QY 158 TVETPAAEETMTNTPGTAPAAE-----TMTNTPGTAPAAEETMTNTPGT 202
      :|||
Db 139 CPEGTYSDEDNDRDPCLTCTICDEDEIAKECTFTSDTYCYDPNPRVSVTPASSDPFYT 198
      :|||
QY 203 GTPAP---AAEETMTNTPGT-----PAPAAEETMTNTPGTAPAAEETMTNTPGT 253
      :|||
Db 199 GTSVPFDLSSSATTSKVSGLVPTGVAENLI-----PYCSTILAIVAGLVAYI 250
      :|||
RESULT 12
Q9CZ44 PRELIMINARY; PRT; 180 AA.
ID Q9CZ44
AC Q9CZ44;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE 2810028K06RIK PROTEIN.
GN TNFRSF1A2L2 2810028K06RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;

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Db      39 ECQGYGMVSHCRNSODT-ICHPCPEG--FYNEAVNYOACKPCYQCNRRSGSEPOQECTH 95
QY      104 TRDVTVCCKBETFRNENSPKCRKSCRCPSGEVQVSN---CTSMDDIOCVEEFGANATVE 160
Db      96 TRDVTVCRCRPGT-PLNGYKRGVDCAPCPQGHSEGNRRACRPW-----TNCYTL- 143
QY      161 TPAAEETMTSPGTPAPAAEE--TMNTSP-GTP-APAAEETMTSPGTPAPAAEETMTTS 216
Db      144 --ACKRTLQAPASSISDANVCEDRSSLATQPMETPSAPYRPPRTARTSTAMPRTA-----QG 195
QY      217 PGTPAPAAEETMTSPGTPASSHYLSCTI-VGIIVLIVLLI 256
Db      196 PSTP-----TLFASKG-PQLAIVLSIGLIGLIALLAALL 229

RESULT 15
Q9DF34      PRELIMINARY;      PRT;      357 AA.
AC      Q9DF34;
DT      01-MAR-2001 (TREMblrel. 16, Created)
DT      01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT      01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE      DEATH RECEPTOR.
OS      Brachydanio rerio (zebrafish) (zebra danio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC      Cypriniformes; Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      LONG Q., Huang H., Shafizadeh E., Liu N., Lin S.;
RT      "Stimulation of erythropoiesis by inhibiting a new hematopoietic death
RT      receptor in transgenic zebrafish.";
RL      Nat. Cell Biol. 0:0-0(2000).
DR      EMBL; AF302789; AAG21396.1; -.
DR      HSP; P19438; TEXT.
DR      InterPro; IPR001368; TNFR_c6.
DR      Pfam; PF00531; death; 1.
DR      SMART; SM00020; TNFR_c6; 3.
DR      SMART; SM00005; DEATH; 1.
DR      PROSITE; PS50017; DEATH_DOMAIN; 1.
DR      PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR      PROSITE; PS50050; TNFR_NGFR_2; 2.
KW      Receptor.
SQ      SEQUENCE      357 AA; 40662 MW; 1652B4840D9EEDBA CRC64;

Query Match      12.9%; Score 178.5; DB 13; Length 357;
Best Local Similarity 25.4%; Pred. No. 3.5e-07;
Matches 43; Conservative 31; Mismatches 58; Indels 37; Gaps 6;

QY      8 LKVVVIVAVLLPV-----LAYSATTAEOE-----EVPQQTVAPOQQRHS 47
Db      1 MRYITLVLALLNLTINARSHGDLAMARSVKNRLSRDVSCEGLEYHENICCL----- 55
QY      48 FKGEBCPAGSH-----RSEHTGACNPCTEGVDITMASNNEBSCFPCTVCKSDQKHKSSC 101
Db      56 ---NCPAGTYVVKACAAAEKGYCAPC-EFDYTEHDHGLKICSDCKRIDQETIEKC 110
QY      102 TMTBDTVQCKEGTF-RNENSPKCRKSCRCPSGEVQVSNCTSMDDIOC 149
Db      111 TSTONTKCKRNGSFCLPDQACEVYKCKSCCKEDETEKTSCTAISNTVC 159

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Search completed: August 13, 2002, 08:37:06  
 Job time: 390 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 13, 2002, 08:29:26 ; Search time 20.64 Seconds  
(Without alignments)  
306.503 Million cell updates/sec

Title: US-09-826-212-2  
Perfect score: 1382  
Sequence: 1 MARIPTKLFVVIVAVLLP.....YLSCTIVGIVLVLLVFPV 259

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1382	100.0	259	4	US-09-006-353A-2
2	1382	100.0	299	4	US-09-153-927-3
3	634	45.9	386	4	US-09-086-483A-2
4	472	34.2	467	4	US-09-086-483A-6
5	472	34.2	468	4	US-09-013-895A-2
6	448	32.8	440	3	US-08-883-036A-2
7	398.5	28.8	424	4	US-09-333-593A-8
8	380.5	27.5	412	4	US-09-333-593A-2
9	379.5	27.5	411	4	US-09-329-633A-2
10	379.5	27.5	411	4	US-09-079-029-1
11	236.5	17.1	303	4	US-09-333-593A-4
12	212	15.3	368	2	US-08-651-579-2
13	201.5	14.6	427	4	US-09-086-483A-4
14	201.5	14.6	427	4	US-09-041-886-2
15	201.5	14.6	427	4	US-09-006-353A-5
16	201.5	14.6	455	4	US-09-527-236A-4
17	184.5	13.4	224	3	US-08-974-022-50
18	184.5	13.4	224	4	US-08-795-445A-50
19	184.5	13.4	224	4	US-08-795-447A-50
20	184.5	13.4	224	4	US-08-974-186-50
21	184.5	13.4	224	4	US-08-795-446B-50
22	184.5	13.4	376	4	US-09-180-100-22
23	183.5	13.3	438	1	US-08-097-827-11
24	183.5	13.3	438	1	US-08-494-574-11
25	178.5	12.9	360	4	US-09-180-100-11
26	178.5	12.9	358	1	US-08-385-229-4
27	173.5	12.6	159	4	US-09-180-100-23

28	173.5	12.6	486	1	US-08-243-010-1	Sequence 1, Appl
29	169.5	12.3	461	1	US-08-385-229-2	Sequence 2, Appl
30	169.5	12.3	461	2	US-08-650-000-2	Sequence 2, Appl
31	169.5	12.3	461	4	US-09-042-785A-7	Sequence 7, Appl
32	169.5	12.3	461	4	US-08-477-347-3	Sequence 3, Appl
33	169.5	12.3	461	4	US-09-006-353A-4	Sequence 4, Appl
34	169.5	12.3	461	4	US-08-476-862-2	Sequence 2, Appl
35	169.5	12.3	461	6	5395760-2	Patent No. 5395760
36	169	12.2	144	4	US-09-180-100-21	Sequence 21, Appl
37	167.5	12.1	143	4	US-09-180-100-10	Sequence 10, Appl
38	167.5	12.1	335	4	US-08-815-469-6	Sequence 6, Appl
39	166.5	12.0	277	2	US-08-147-784-2	Sequence 2, Appl
40	166.5	12.0	277	4	US-08-195-967-2	Sequence 2, Appl
41	166.5	12.0	277	4	US-09-006-353A-12	Sequence 12, Appl
42	166.5	12.0	277	4	US-08-472-940-2	Sequence 2, Appl
43	165.5	12.0	669	4	US-09-013-885A-3	Sequence 3, Appl
44	164.5	11.9	314	1	US-08-444-231-19	Sequence 19, Appl
45	164.5	11.9	314	1	US-08-152-443A-19	Sequence 19, Appl

## ALIGNMENTS

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RESULT 1
US-09-006-353A-2
: Sequence 2, Application US/09006353A
: Patent No. 6261801
:
GENERAL INFORMATION:
: APPLICANT: WEI, YING-PEI
: APPLICANT: YU, GUO-LING
: APPLICANT: GENTZ, REINER
: APPLICANT: RUBEN, STEVEN
: TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: HUMAN GENOME SCIENCES, INC.
: STREET: 9410 KEY WEST AVENUE
: CITY: ROCKVILLE
: STATE: MD
: COUNTRY: US
: ZIP: 20850
:
COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/006.353A
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: BROOKES, ANDERS A
: REGISTRATION NUMBER: 36,373
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8512
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 259 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
US-09-006-353A-2

Query Match 100.0%; Score 1382; DB 4; Length 259;
Best Local Similarity 100.0%; Pred. No. 5.3e-102;
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MARIPTKLFVVIVAVLLPVLAVSATTAAROEVEPQQTAVADQQRHSFGKECPAGSHRS 60
Db 1 MARIPTKLFVVIVAVLLPVLAVSATTAAROEVEPQQTAVADQQRHSFGKECPAGSHRS 60
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QY 61 EHTGACNCTEGVDYTNASNNPSCFCTVCKSDOKHKSSCTMTBDYVCOCKEGTFRNEN 120
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Db 61 EHTGACNCTEGVDYTNASNNPSCFCTVCKSDOKHKSSCTMTBDYVCOCKEGTFRNEN 120
QY 121 SPENCRCRCSRCPGSEVOVSNCTSWDDIOCVBEFGANATVETPPAAEETMNTSPGTPAPAAE 180
      |||
Db 121 SPENCRCRCSRCPGSEVOVSNCTSWDDIOCVBEFGANATVETPPAAEETMNTSPGTPAPAAE 180
QY 181 ETMTNTPCTPPAPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPASSHY 240
      |||
Db 181 ETMTNTPCTPPAPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPASSHY 240
QY 241 LSCITVGIIVLIVLIVFV 259
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Db 241 LSCITVGIIVLIVLIVFV 259

RESULT 2
US-09-153-927-3
; Sequence 3, Application US/09153927A
; Patent No. 6297022
; GENERAL INFORMATION:
; APPLICANT: McDonnell, Peter C.
; APPLICANT: Young, Peter R.
; TITLE OF INVENTION: A Method of Identifying Agonists and
; TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3
; TITLE OF INVENTION: and TR5
; FILE REFERENCE: GH50031
; CURRENT APPLICATION NUMBER: US/09/153,927A
; CURRENT FILING DATE: 1998-09-16
; EARLIER APPLICATION NUMBER: 60/061,334
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Human
US-09-153-927-3

Query Match 100.0%; Score 1382; DB 4; Length 299;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARIPTLKEFVVIVAVLLPVLAASATTAROEVEVPOQTVAPOOQRHSFKGECPPAGSHRS 60
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Db 41 MARIPTLKEFVVIVAVLLPVLAASATTAROEVEVPOQTVAPOOQRHSFKGECPPAGSHRS 60
QY 61 EHTGACNCTEGVDYTNASNNPSCFCTVCKSDOKHKSSCTMTBDYVCOCKEGTFRNEN 120
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Db 101 EHTGACNCTEGVDYTNASNNPSCFCTVCKSDOKHKSSCTMTBDYVCOCKEGTFRNEN 160
QY 121 SPENCRCRCSRCPGSEVOVSNCTSWDDIOCVBEFGANATVETPPAAEETMNTSPGTPAPAAE 180
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Db 161 SPENCRCRCSRCPGSEVOVSNCTSWDDIOCVBEFGANATVETPPAAEETMNTSPGTPAPAAE 220
QY 181 ETMTNTPCTPPAPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPASSHY 240
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Db 221 ETMTNTPCTPPAPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPASSHY 280
QY 241 LSCITVGIIVLIVLIVFV 259
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Db 281 LSCITVGIIVLIVLIVFV 299

RESULT 3
US-09-086-483A-2
; Sequence 2, Application US/09086483A
; Patent No. 6214580
; GENERAL INFORMATION:
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APPLICANT: NI, et al.
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,483A
; FILING DATE: May-29-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,936
; FILING DATE: May-30-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/069,112
; FILING DATE: Dec-9-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 386 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-086-483A-2

Query Match 45.9%; Score 634; DB 4; Length 386;
Best Local Similarity 51.8%; Pred. No. 9.7e-43;
Matches 132; Conservative 22; Mismatches 41; Indels 60; Gaps 3;

QY 5 PKTLKEFVVIVAVLLPVLAASATTAROEVEVPOQTVAPOOQRHSFKGECPPAGSHRSHTG 64
      |||
Db 35 PKTLKEFVVIVAVLLPVLAASATTAROEVEVPOQTVAPOOQRHSFKGECPPAGSHRSHTG 94
QY 65 ACNPCTEGVDYTNASNNPSCFCTVCKSDOKHKSSCTMTBDYVCOCKEGTFRNENSPEN 124
      |||
Db 95 ACNPCTEGVDYTNASNNPSCFCTVCKSDOKHKSSCTMTBDYVCOCKEGTFRNENSPEN 154
QY 125 CRKC-SRCPSEGEVOVSNCTSWDDIOCVBEFGANATVETPPAAEETMNTSPGTPAPAAEETM 183
      |||
Db 155 CRCTCTGCPRRMVVXVSNCTPSRDIKCKNESAASTGTPAAEETVTTILG----- 204
QY 184 NTSPTPPAPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPASSHYLSC 243
      |||
Db 205 -----MLASP-----YHYLTI 215
QY 244 TVIGIIVLIVLIVF 258
      |||
Db 216 IYVLIIVLIVVVGTF 230

RESULT 4
US-09-086-483A-6
; Sequence 6, Application US/09086483A
; Patent No. 6214580
; GENERAL INFORMATION:
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APPLICATION NUMBER: US/08/883,036A  
FILING DATE: 26-JUN-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US --to be assigned--  
FILING DATE: 04-JUN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/829,536  
FILING DATE: 28-MAR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/815,255  
FILING DATE: 12-MAR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/799,861  
FILING DATE: 13-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2625-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 440 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-883-036A-2

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Query March 32.4%: Score 448; DB 3; Length 440;
Best Local Similarity 40.7%: Pred. No. 5.5e-28;
Matches 103; Conservative 23; Mismatches 68; Indels 62; Gaps
QY 3 RIPKTLKEVVYIVAVLLPVLAYSATTARQEEVPOQTVAPQOQRHSEKGECEPAGSHSEH 62
|:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:| |:|:|
Db 33 RVKPTL--VLVVAVALLLVYSAESALITQDDLA PQQRAAPQQRSSSESLCPGHHISD 90
QY 63 TGACPKTEGVDDYTMASNNNEBPCFCTYCKSKDQKHKSSCTMTDRDYCCCKEGTFRNEBP 122
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 91 GRDCISCTCYGGDYSTHWMDLLFLCLRCTRCDSEVELSPCTTTRNTYCCCEEGTFREDSBP 150
QY 123 EMCRCRC--SRCPSEGEVQVSNCTSMDDIOCVCEEGFANATVETPAAEETMTMSPGPAPAAEE 181
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 151 EMCRCRCRCRCRGAMKVGDCCTPMSIECVH----- 180
QY 182 TWMTSPGTPAPAAEETMTTSPGTPAPAAEETMTTSPGPAPAAEETMTTSPGTPASSHYL 241
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 -----KESQTKHSG--EAPAVEETVTSPTGPAPAPCSL 211
QY 242 SCTIVGIIIVLIVLIVFV 259
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 212 SGIIGTVTAAVVLIIVAV 229

RESULT 7
US-09-3333-593A-8
Sequence 8, Application US/09333593A
Patent No. 6313269
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH C.
APPLICANT: YOUNG, PETER R.
APPLICANT: MARSHALL, LISA A.
APPLICANT: ROSHAK, AMY K.
APPLICANT: TAN, KONG B.
APPLICANT: TRUENH, ALEMSEGED
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR.
FILE REFERENCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333, 593A
CURRENT FILING DATE: 1999-06-15

```

```

, PRIOR APPLICATION NUMBER: 08/916,625
, PRIOR FILING DATE: 1997-08-22
, PRIOR APPLICATION NUMBER: 08/853,684
, PRIOR FILING DATE: 1997-05-09
, PRIOR APPLICATION NUMBER: 60/041,230
, PRIOR FILING DATE: 1997-03-14
, NUMBER OF SEQ ID NOS: 8
, SOFTWARE: FastSeq for Windows Version 3.0
, SEQ ID NO 8
, LENGTH: 424
, TYPE: prt
, ORGANISM: HOMO SAPIENS
US-09-333-593A-8

```

[illegible]

```

RESULT      8
US-09-333-593A-2
: Sequence 2, Application US/0933593A
: Patent No. 613269
: GENERAL INFORMATION:
:   APPLICANT: DEEN, KEITH C.
:   APPLICANT: YOUNG, PETER R.
:   APPLICANT: MARSHALL, LISA A.
:   APPLICANT: ROSHAK, AMY K.
:   APPLICANT: TAN, KONG B.
:   APPLICANT: TRNENH, ALEMSSEGD
:   TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED RECEPTOR,
:   TITLE OF INVENTION: TR6
:   FILE REFERENCE: GH-50008-2
:   CURRENT APPLICATION NUMBER: US/09/333,593A
:   CURRENT FILING DATE: 1999-06-15
:   PRIOR APPLICATION NUMBER: 08/916,625
:   PRIOR FILING DATE: 1997-08-22
:   PRIOR APPLICATION NUMBER: 08/853,684
:   PRIOR FILING DATE: 1997-05-09
:   PRIOR APPLICATION NUMBER: 60/041,230
:   PRIOR FILING DATE: 1997-03-14
:   NUMBER OF SEQ ID NOS: 8
:   SOFTWARE: FastSeq for Windows Version 3.0
:   SEQ ID NO 2
:   LENGTH: 412
:   TYPE: PRT
:   ORGANISM: HOMO SAPIENS
US-09-333-593A-2

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[illegible]

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Db      33  RVPRKTLV-VLVVAVALLLIVSAESALITQODLAPQORRAAP00KRSPSGEGLCPPRHINSED  90
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Db      91  GRDICTSCYGGDYSTQWMDLLFCALRCIRCSGVEVLSPTTTRNTVCOCEGCFREEDSP  150
QY      123  EMCRCRC-SRCPGSEVOYNSNCISMDIOCYEE  152
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RESULT      9
US-09-329-633A-2
: Sequence 2, Application US/09329633A
: Patent No. 6252050
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Chuntarapai, Anan
: APPLICANT: Kim, K. Jin
: TITLE OF INVENTION: METHOD FOR MAKING MONOCLONAL ANTIBODIES AND
: TITLE OF INVENTION: CROSS-REACTIVE ANTIBODIES OBTAINABLE BY THE METHOD
: FILE REFERENCE: P14681 (REVISED)
: CURRENT APPLICATION NUMBER: US/09/329,633A
: CURRENT FILING DATE: 1999-06-10
: PRIOR APPLICATION NUMBER: US 60/089,253
: PRIOR FILING DATE: 1998-06-12
: NUMBER OF SEQ ID NOS: 2
: SEQ ID NO 2
: LENGTH: 411
: TYPE: PRT
: ORGANISM: human
: FEATURE:
: NAME/KEY: xaa
: LOCATION: 410
: OTHER INFORMATION: xaa = leu or met
US-09-329-633A-2

```

Query Match	27.5%	Score 379.5	DB 4	Length 411
Best Local Similarity	51.7%	Pred. No. 1.3e+22		
Matches	78	Conservative 17	Mismatches 53	Indels 3
			Gaps	2
QY	3	RIPKTLKEVVYIVAVLLPLVAYSATTAROEFPQOTVAPOOQRHSEKGECEPAGSHRSEH	62	
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Db	33	RVPKTL-VLVVAVALLLVSAESALITQODLAPQQRAPQQRSSBELCPGHHSID	90	
QY	63	TGACPCTEGYDYTNASNNBSCFPCTCYCKSSQQRKSSCTMTRDYVCOCKEGTFRNENS	122	
		:         :         :         :         :		
Db	91	GRDCISCTCYGGDYSTHWNDDLFTCLCTRCDSGEVELSPCTTRNTVCOCEGTFREEDSP	150	
QY	123	EMCRKC-SRCPSEGYNSCTSMDDIOCEE	152	
		:    :    :          :		
Db	151	EMCRKCTGCPGKAVKVGDCPTWSDIECVHK	181	

RESULT 10  
 US-09-079-029-1  
 : Sequence 1, Application US/09079029  
 : Patent No. 6343369  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Adams, Camilla W.  
 : APPLICANT: Ashkenazi, Avi J.  
 : APPLICANT: Chintalapati, Aan  
 : APPLICANT: Kim, Kyung J.  
 :  
 : TITLE OF INVENTION: Apo-2 Receptor  
 :  
 : NUMBER OF SEQUENCES: 14  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Genentech, Inc.  
 :  
 : STREET: 1 DNA Way  
 : CITY: South San Francisco  
 : STATE: California  
 :  
 : COUNTRY: USA  
 : ZIP: 94080

```

1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
3 COMPUTER: IBM PC compatible
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: WinPatIn (gentech)
6
7 CURRENT APPLICATION DATA:
8 APPLICATION NUMBER: US/09/079, 029
9
10 FILING DATE:
11
12 CLASSIFICATION:
13
14 ATTORNEY/AGENT INFORMATION:
15 NAME: Maichang, Diane L.
16 REGISTRATION NUMBER: 35,600
17 REFERENCE/DOCKET NUMBER: P1101R2
18
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: 650/225-5416
21
22 TELEFAX: 650/952-9881
23
24 INFORMATION FOR SEO ID NO: 1:
25
26 SEQUENCE CHARACTERISTICS:
27 LENGTH: 411 amino acids
28 TYPE: Amino Acid
29 TOPOLOGY: Linear
30
31 US-09-079-029-1

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[illegible]

```

RESULT 11
US-09-333-593A-4
Sequence 4, Application US/09333593A
Patent No. 6313269
GENERAL INFORMATION:
APPLICANT: DEEN, KEITH C.
APPLICANT: YOUNG, PETER R.
APPLICANT: MARSHALL, LISA A.
APPLICANT: ROSHAK, AMY K.
APPLICANT: TAN, KONG B.
APPLICANT: TRUENEN, ALEKSEGD
TITLE OF INVENTION: TUDMOR NECROSIS FACTOR RELATED RECEPTOR
TITLE OF INVENTION: TR6
FILE REFERENCE: GH-50008-2
CURRENT APPLICATION NUMBER: US/09/333,593A
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 08/916,625
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 08/853,684
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/041,230
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 303
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-333-593A-4

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Query Match 17.1%; Score 236.5; DB 4; Length 303;







GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: August 13, 2002, 08:31:29 ; Search time 51.8 Seconds  
(without alignments)  
40.741 Million cell updates/sec

Title: US-09-826-212-2\_COPY\_215\_233

Perfect score: 100  
Sequence: 1 TSPGPAPAEETMTTSPG 19

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Database :

A\_Geneseq\_032802:\*

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- 2: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1981.DAT:\*
- 3: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA1982.DAT:\*
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- 22: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	100	100.0	249	22 AAB82182	FLAG-TRID clone w1
2	100	100.0	259	19 AAW64668	Human TRID protein
3	100	100.0	259	20 AAY05726	Tumour necrosis fa
4	100	100.0	259	20 AAM93578	Human hAP09 protei
5	100	100.0	259	20 AAW88408	Human Apo-2Dcr pro
6	100	100.0	259	22 AAB20111	Human PRO366 polyp
7	100	100.0	259	22 AAB20111	Human immunostimu
8	100	100.0	259	22 AAB36696	Human tumour necro
9	100	100.0	259	22 AAB53091	Human angiogenesis
10	100	100.0	268	22 AAB82181	FLAG-TRID clone w1
11	100	100.0	299	19 AAW76331	Human tumour necro

12	100	100.0	299	20 AAY29864	Human secreted pro
13	100	100.0	299	20 AAY05744	Tumour necrosis fa
14	100	100.0	299	20 AAY00933	Human TRAIL-R3 pro
15	100	100.0	299	20 AAW94671	Human TNF-related
16	100	100.0	299	20 AAM88409	Human Apo-2Dcr pro
17	100	100.0	299	21 AAB01343	Death receptor, H
18	54	54.0	350	20 AAY00934	Human DR5 protein
19	54	54.0	440	19 AAB99284	Human TRAIL recept
20	54	54.0	440	19 AAW9260	Tumour necrosis fa
21	54	54.0	440	20 AAY05725	Tumour necrosis fa
22	54	54.0	440	21 AAB01340	TNF-related apopto
23	54	54.0	801	22 ABB52850	Escherichia coli p
24	53	53.0	536	21 AAB53136	Macaca mulatta rha
25	52	52.0	221	22 AAU50369	Propionibacterium
26	51	51.0	219	22 AAU48350	Propionibacterium
27	51	51.0	2066	22 AAE10146	Streptomyces nours
28	49	49.0	167	22 AAU32618	Novel human secret
29	49	49.0	761	22 ABB02677	Novel human diagno
30	49	49.0	907	22 ABB01455	Novel human diagno
31	48.5	48.5	258	21 AAY93386	Human PRO1305 (UNO
32	48.5	48.5	258	22 AAU29165	Human PRO polypept
33	48.5	48.5	258	22 AAB66135	Protein of the inv
34	48.5	48.5	602	21 AAY95660	Human Znt2 protei
35	48	48.0	152	22 AAU40239	Novel human diagno
36	48	48.0	189	22 ABB14657	Novel human diagno
37	48	48.0	238	22 ABB25281	Novel human diagno
38	48	48.0	259	22 ABB25407	Novel human diagno
39	48	48.0	1078	16 AAR71704	Collagen alpha 1 (
40	48	48.0	1078	21 AAY96125	Collagen type III
41	48	48.0	1196	21 AAR28916	Type III procollag
42	48	48.0	1466	22 ABB50291	Collagen type III
43	48	48.0	1469	22 ABB51591	Novel human diagno
44	47	47.0	191	22 ABB63572	Drosophila melanog
45	47	47.0	191	22 ABB67144	Drosophila melanog

## ALIGNMENTS

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ID	AAB82182	standard; Protein: 249 AA.
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AC	AAB82182;	
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DT	23-JUL-2001	(first entry)
XX		
DE	FLAG-TRID clone without a transmembrane domain.	
XX		
KW	FLAG-epitope tag; transmembrane domain; death domain; apoptosis;	
KW	cell suicide; tissue homeostasis; cell proliferation;	
KW	cell-cell signalling; Trail Receptor without Intracellular Domain; TRID.	
XX		
OS	Synthetic.	
XX		
FH	Key	Location/Qualifiers
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FT	Protein	/label= signal-peptide
FT		24..249
FT		/label= FLAG-TRID
FT	Peptide	27..34
FT		/label= FLAG-epitope
FT	Misc-difference	249
FT		/note= "Insertion site for candidate sequences"
XX		
PD	W0200114542-A1.	
XX		
PD	01-MAR-2001.	
XX		
PF	23-AUG-2000; 2000WO-US23112.	
XX		
PR	25-AUG-1999; 99US-0150747.	
XX		

PA (GENO-) GENOME THERAPEUTICS CORP.  
XX  
PI Denome SA, Swain PM, Tzellas N;  
XX  
DR WPI: 2001-374162/39.  
DR N-PSDB: AAH19326.  
XX  
XX  
PT Identifying a transmembrane domain of a membrane-spanning protein  
PT useful in defining processes in cell suicide and tissue homeostasis,  
PT comprises modifying the nucleic acid encoding a death domain-lacking  
PT membrane spanning protein -  
XX  
XX  
PS Disclosure: Fig 2; 38pp; English.  
XX  
XX The present invention relates to methods for identifying a transmembrane  
CC domain (TM) of a membrane-spanning protein. The method comprises  
CC modifying a nucleic acid encoding a death domain (DD)-lacking membrane  
CC spanning protein (e.g. TRAIL Receptor without Intracellular Domain; TRID)  
CC by replacing the nucleic acid encoding the TM of the DD-lacking  
CC membrane-spanning protein with a candidate nucleic acid sequence to  
CC produce a nucleic acid encoding a modified DD-lacking membrane spanning  
CC protein. The modified nucleic acid is then transfected into a host cell,  
CC which expresses a DD-containing receptor. The absence of apoptosis of the  
CC host cell is determined following exposure of the transfected cell to an  
CC apoptosis-inducing ligand. Candidate nucleic acids encoding TM prevent  
CC apoptosis of the host cell. The modified nucleic acid encoding the  
CC modified death domain-lacking membrane-spanning protein can also include  
CC a nucleic acid sequence encoding an epitope tag. The present sequence is  
CC a FLAG-TRID clone, which was used in the method of the present invention.  
CC This sequence comprises human TRID protein and the FLAG-epitope tag. The  
CC FLAG-epitope is a useful marker to purify proteins encoded by the  
CC modified DD-lacking membrane-spanning protein. The identified TM and  
CC membrane-spanning proteins may be used in defining processes involved in  
CC cell suicide and tissue homeostasis, and to evaluate, interfere and treat  
CC events, such as cell proliferation and cell-cell signalling pathways.  
XX  
SQ Sequence 249 AA;  
  
Query Match 100.0%; Score 100; DB 22; Length 249;  
Best Local Similarity 100.0%; Pred. No. 5.2e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TSPGTPAPAAETMTSPG 19  
|||  
Db 194 tspgtapaeeetmtspg 212  
  
RESULT 2  
ID AAM64668 standard; Protein; 259 AA.  
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XX AAM64668:  
XX  
XX 23-OCT-1998 (first entry)  
XX  
XX Human TRID protein.  
XX  
XX TRAIL receptor without intracellular domain; TRID; TNFR-5; human;  
KM tumour necrosis factor receptor-5; TNF-related apoptosis-inducing ligand;  
KM haematopoietic tissue; Immune system; ligand; apoptosis; treatment.  
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XX Homo sapiens.  
XX  
XX  
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XX Protein /label= signal  
XX 27..259  
XX /label= TRID  
XX 42..52  
XX /label= epitope  
XX 58..66  
XX /label= epitope  
XX Region

FT Region 68..76  
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FT 142..148  
FT /label= epitope  
XX  
XX WO9830693-A2.  
XX  
XX 16-JUL-1998.  
XX  
XX 13-JAN-1998; 98WO-US00152.  
XX  
XX 07-AUG-1997; 97US-0054885.  
XX 14-JAN-1997; 97US-0035496.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Ebner R, Feng P, Gentz RL, Ni J, Ruben SM, Wei Y;  
XX Yu G;  
XX WPI: 1998-399141/34.  
XX N-PSDB: AAV51348.  
XX  
XX Human TRAIL receptor without an intracellular domain polypeptide -  
XX used in the diagnosis of immune system-related disorder(s)  
XX  
XX Claim 1b; Fig 1: 90pp; English.  
XX  
XX This sequence represents a human TRID (TRAIL (TNF-related  
CC apoptosis-inducing ligand) receptor without an intracellular domain).  
CC TRID is a member of the tumour necrosis factor receptor (TNFR) family  
CC also known as TNFR-5. TRID is expressed in haematopoietic tissues and  
CC other normal human tissues. For a number of immune system-related  
CC disorders, substantially altered (whether increased or decreased) levels  
CC of TRID gene expression can be detected, therefore the TRID polypeptides,  
CC nucleic acids and antibodies are useful in the diagnosis of such immune  
CC system related disorders. Mutations of the TRID gene can also be  
CC detected. TRID can also be used to identify ligands which may be useful  
CC in the treatment of apoptosis related disorders. TRID is administered to  
CC humans at a parenteral dose of 0.01 to 1 mg/kg/day.  
XX  
SQ Sequence 259 AA;  
  
Query Match 100.0%; Score 100; DB 19; Length 259;  
Best Local Similarity 100.0%; Pred. No. 5.4e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TSPGTPAPAAETMTSPG 19  
|||  
Db 185 tspgtapaeeetmtspg 203  
  
RESULT 3  
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XX  
XX AAY05726:  
XX  
XX 19-JUL-1999 (first entry)  
XX  
XX Tumour necrosis factor receptor TRAIL-R3.  
XX  
XX TRAIL-3; tumour necrosis factor receptor; apoptosis; cancer;  
XX therapy.  
XX  
XX



OS	Mammalia.	
XX	Key	Location/Qualifiers
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FT	Protein	25..259
FT		/note="mature protein"
FT	Region	162..175
FT		/note="TAPE repeat"
FT	Region	176..191
FT		/note="TAPE repeat"
FT	Region	192..206
FT		/note="TAPE repeat"
FT	Region	207..221
FT		/note="TAPE repeat"
FT	Region	222..236
FT		/note="TAPE repeat"
FT	Domain	238..259
FT		/note="transmembrane domain"
PN	MO912963-A2.	
PD	18-MAR-1999.	
XX	11-SEP-1998;	98WO-U519029.
XX	06-MAY-1998;	98US-0084422.
PR	12-SEP-1997;	97US-0058631.
XX	(BIOJ ) BIOGEN INC.	
PA	Tschopp J;	
P1	WPI: 1999-276942/23.	
XX	N-PSDB; AAX25349.	
DR		
XX	Novel tumor necrosis factor receptor proteins TRAIL-R2 and TRAIL-R3	
PT	Disclosure; Page 28; 28pp; English.	
XX		
PS		
XX	The present sequence represents TRAIL-R3, a novel mammalian	
CC	cysteine-rich receptor of the tumor necrosis factor receptor family	
CC	The invention is related to novel receptors for TRAIL, i.e. TRAIL-R2	
CC	(see AA055725) and TRAIL-R3. TRAIL-R3 is highly glycosylated. It is	
CC	a putative glycosylphosphatidylinositol-anchored protein, which is	
CC	either cell-associated or processed and secreted. Secreted	
CC	TRAIL-R3 competes for the binding of TRAIL to TRAIL-R1 and/or	
CC	TRAIL-R2, thereby acting as an inhibitor of apoptosis. Expression	
CC	of TRAIL-R3 is restricted to peripheral blood lymphocytes and	
CC	skeletal muscle. It is likely that TRAIL-R3 acts as an important	
CC	regulator of TRAIL-R2 and -R3 induced cell death in vivo. A method	
CC	for preventing or reducing the advancement, severity or effects of	
CC	an immunological disease involves administering a TRAIL-R2 or	
CC	TRAIL-R3 blocking agent such as a soluble TRAIL-R (preferably	
CC	comprising a human immunoglobulin Fc domain) and an antibody. A	
CC	method of treating cancer involves administration of antibodies	
CC	against TRAIL-R3 or TRAIL-R2. A method of inducing cell death	
CC	involves administration of an agent capable of inhibiting the	
CC	binding of TRAIL-R2 or -R3 to its ligand.	
XX		
90	Sequence 259 AA;	

AAW93578	
ID AAW93578 standard; Protein; 259 AA.	
XX	
AC AAW93578;	
XX	
DT 18-JUN-1999 (first entry)	
XX	
DE Human hAPO9 protein.	
XX	
KM Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;	
KM developmental abnormality; gestational abnormality; prostate cancer;	
KM APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;	
KM cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;	
KM apoptosis; human.	
XX	
OS Homo sapiens.	
XX	
PN WO911791-A2.	
XX	
PD 11-MAR-1999.	
XX	
PX 04-SEP-1998; 98WO-US18393.	
PF	
PR 05-SEP-1997; 97US-0924634.	
XX	
PA (UNIT ) UNIT WASHINGTON.	
XX	
PI Chaudhary PM;	
XX	
DR WPt; 1999-205191/17.	
DR N-PSDB; AAX23412.	
XX	
PT New Tumor Necrosis Factor family receptor polypeptides and ligands -	
PT useful for diagnosis and treatment of prostate cancer and	
PT developmental or gestational abnormalities	
XX	
Claim 24; Fig 6; 156pp; English.	
XX	
PS This invention describes isolated Tumor Necrosis Factor (TNF) family	
CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active	
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL and TNRL3) or	
CC their active fragments. APO4 is useful for diagnosing prostate cancer	
CC by determining levels of APO4 in an individual. Prostate cancer can also	
CC be treated using APO4 selective binding agents linked to a therapeutic	
CC moiety. APO4 polypeptides are also useful for identifying selective	
CC binding agents, useful in diagnosis/treatment of disease by binding of	
CC agents to the polypeptide/active fragment which is extracellular, or	
CC expressed on the cell surface. The binding is preferably performed in	
CC vivo. APO4 polypeptides/active fragments are also useful for screening	
CC for agonists and antagonists by binding and observing the changer in APO4	
CC activity. Effective pharmacological agents useful in diagnosis or	
CC treatment of disease are also identified using APO4 polypeptides/active	
CC fragments and APO4 signal transducer molecules that specifically interact	
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4	
CC activity. The method is performed in vivo or in vitro. APO polypeptides	
CC are all useful as immunogens for preparing antibodies. APO4 is also	
CC useful for diagnosis/treatment of developmental or gestational	
CC abnormalities. APO8 was transfected to human Breast carcinoma cell line	
CC MCF-7, and induced apoptosis.	
XX	
SQ Sequence 259 AA:	



PR 01-MAR-2000; 2000MO-US05601.  
 PR 20-MAR-2000; 2000MO-US07377.  
 PR 21-MAR-2000; 2000MO-US07532.  
 PR 30-MAR-2000; 2000MO-US08439.  
 PR 17-MAY-2000; 2000MO-US13705.  
 PR 22-MAY-2000; 2000MO-US14042.  
 PR 30-MAY-2000; 2000MO-US14941.  
 PR 02-JUN-2000; 2000MO-US15264.  
 PR 10-NOV-2000; 2000MO-US30873.  
 XX  
 PA (GENTH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Geritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI; 2001-408281/43.  
 DR N-PSDB; AAF21393.  
 XX  
 PT Isolated, secretory and transmembrane PRO polypeptide used to detect  
 PT other PRO polypeptides, link bioactive molecules to cells expressing  
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 PT lung, breast, prostate, cervical  
 XX  
 PS Claim 12; Fig 300; 813pp; English.  
 XX  
 CC AAU12172-AAU12446 represent novel human secretory and transmembrane  
 CC PRO polypeptides. The PRO polypeptides are useful to detect other  
 CC PRO polypeptides, to link bioactive molecules to cells expressing  
 CC PRO polypeptides, to modulate biological activities of cells expressing  
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample.  
 CC Some of the 275 sequences are also useful to stimulate the release of  
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
 CC proliferation or differentiation of chondrocytes, the proliferation or  
 CC gene expression in pericyte cells, the release of proteoglycans from  
 CC cartilage, the proliferation of inner ear utricular supporting cells or  
 CC of T-lymphocytes, the release of a cytokine from peripheral blood  
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by  
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
 CC to factor VIIA. The PRO polypeptides can be used in assays to identify  
 CC molecules involved in binding interactions. The polynucleotides encoding  
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy.  
 CC  
 XX  
 SQ Sequence 259 AA;

Query Match 100.0%; Score 100; DB 22; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 5.4e-05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSPGTPAPAAETMTTSPG 19  
 |||  
 Db 185 tsptgtpapaaeetmttspg 203

RESULT 7  
 AAB20111  
 ID AAB20111 standard; Protein: 259 AA.  
 XX  
 AC AAB20111;  
 XX  
 DT 30-APR-2001 (first entry)  
 XX  
 DE Human immunostimulant PRO366 (Apo-2PCR).  
 XX  
 KW PRO366; UNO321; human; immune disease; autoimmune disease;  
 KW antirheumatic; antiarthritic; antiinflammatory; antianemic;  
 KW immunosuppressive; antithyroid; antidiabetic; neuroprotective;  
 KW hepatotropic; virocidic; dermatological; antiporiatic;

KW antisthmatic; antiallergic; immunostimulant; Apo-2PCR;  
 KW tumour necrosis factor receptor; apoptosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..29  
 FT /label= signal\_peptide  
 FT Protein 30..259  
 FT /label= Mature-Protein  
 FT Domain 240..257  
 FT /note= "transmembrane domain"  
 FT Region 85..92  
 FT /note= "TNFR/NGFR family cysteine-rich region"  
 FT Modified-site 126..130  
 FT /note= "cAMP- and cGMP-dependent protein kinase  
 FT phosphorylation site"  
 FT Modified-site 56..62  
 FT /note= "N-myristoylation site"  
 FT Modified-site 72..78  
 FT /note= "N-myristoylation site"  
 FT Modified-site 114..120  
 FT /note= "N-myristoylation site"  
 FT Modified-site 154..160  
 FT /note= "N-myristoylation site"  
 FT Modified-site 233..239  
 FT /note= "N-myristoylation site"  
 XX  
 XX W0200105972-A1.  
 XX  
 XX 25-JAN-2001.  
 PD  
 XX 15-MAR-2000; 2000MO-US06884.  
 PF  
 XX 20-JUL-1999; 99US-0144758.  
 PR  
 XX (GENTH ) GENENTECH INC.  
 PA  
 PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;  
 PI Hillan KJ, Mark MR, Masters SB, Pitti RM, Tumas D, Watanabe CK;  
 PI Wood WI;  
 XX  
 XX WPI; 2001-103149/11.  
 DR N-PSDB; AAF310053.  
 XX  
 PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
 PT diagnosing and treating immune-related disorders, such as multiple  
 PT sclerosis, rheumatoid arthritis and diabetes  
 XX  
 PS Claim 20; Fig 8; 127pp; English.  
 PS  
 XX The present sequence is that of PRO366 (UNO321), also designated  
 CC Apo-2PCR, a novel human Immunomodulator (27 KDa, PI 4.84), as  
 CC deduced from a human breast carcinoma cDNA clone (see AAF30053).  
 CC Apo-2PCR shows homology to apoptosis-linked receptors of the tumour  
 CC necrosis factor receptor family, such as DR4 and Apo-2. The invention  
 CC provides polynucleotides (see AAF30050-62) encoding novel human PRO  
 CC proteins (see AAB20108-20) including PRO366. Claimed compositions  
 CC comprising these proteins or their agonists are useful for increasing  
 CC infiltration of inflammatory cells into a tissue of a mammal,  
 CC stimulating or enhancing an immune response, or increasing the  
 CC proliferation of T-lymphocytes in a mammal in response to an antigen.  
 CC Claimed compositions comprising a PRO polypeptide or its antagonist  
 CC have the opposite effect. A claimed method for treating an immune  
 CC related disorder, such as a T cell disorder, involves administering  
 CC a PRO polypeptide, an agonist antibody or an antagonist antibody.  
 CC The disorder is selected from systemic lupus erythematosus,  
 CC rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis,  
 CC spondyloarthritis, systemic sclerosis, idiopathic inflammatory  
 CC myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis,  
 CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia,  
 CC thyroiditis, diabetes mellitus, immune-mediated renal disease,  
 CC demyelinated diseases (such as multiple sclerosis), autoimmune

CC chronic active hepatitis, primary biliary cirrhosis, granulomatous  
CC hepatitis, sclerosing cholangitis, inflammatory bowel disease  
CC (ulcerative colitis and Crohn's disease), gluten-sensitive  
CC enteropathy, Whipple's disease, (auto)immune-mediated skin diseases  
CC (such as bullous skin disease, erythema multiforme and psoriasis),  
CC allergic diseases (such as asthma, allergic rhinitis, atopic  
CC dermatitis, food hypersensitivity and urticaria), immunologic  
CC diseases of the lung and transplantation associated diseases (such  
CC as graft rejection and graft-versus-host disease) (all claimed).  
CC Claimed methods of diagnosing these disorders comprise detecting  
CC the level of expression of the PRO gene. Also claimed are a method  
CC of identifying a compound capable of inhibiting the expression or  
CC activity of the PRO polypeptide, vectors, host cells, antibodies,  
CC and a method of stimulating an immune response in a mammal using  
CC PRO366.  
XX  
SQ Sequence 259 AA:

Query Match 100.0%; Score 100; DB 22; Length 259;  
Best Local Similarity 100.0%; Pred. No. 5.4e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSPGTPAPAAEETMTSPG 19  
Db 185 tsptgpapaaeetmtspg 203  
|||||

RESULT 8  
AAB36696  
ID AAB36696 standard; Protein: 259 AA.  
XX  
AC AAB36696;  
XX  
DT 15-MAR-2001 (first entry)  
XX  
DE Human tumour necrosis factor receptor 5 (TRID) protein SEQ ID NO:2.  
XX  
XX Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; nontropic;  
KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;  
KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;  
KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;  
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;  
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;  
KW apoptotic cell death related disease; autoimmune disorder;  
KW cardiovascular disorder; viral infection.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO200071150-A1.  
XX  
PD 30-NOV-2000.  
XX  
PF 18-MAY-2000; 2000WO-US13515.  
XX  
PR 20-MAY-1999; 99US-0135164.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Wei Y, Ruben SM, Gentz RL, Ni J;  
XX  
DR WPI; 2001-041051/05.  
DR N-PSDB; AAC90774.  
XX  
XX Nucleic acid encoding a TRID polypeptide, also referred to as tumor  
PT necrosis factor receptor 5, useful in the diagnosis, treatment or  
PT prevention of cancer, autoimmune disorders and viral infection -  
XX  
XX Claim 15; Fig 1; 285pp; English.  
XX  
CC The present sequence represents the human TRID protein (tumour necrosis  
CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without  
CC intracellular domain, also referred to as tumour necrosis factor

CC receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive,  
CC nontropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant,  
CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic  
CC activities, and can be used in gene therapy. The TRID polynucleotides  
CC are useful for detecting complementary polynucleotides. TRID proteins and  
CC polynucleotides are useful in the treatment of tumours, resistance to  
CC parasite, bacteria and viruses, restenosis and graft versus host disease.  
CC They are also useful for inducing proliferation of T-cells, endothelial  
CC cells and certain haematopoietic cells, to regulate antiviral responses  
CC and to prevent certain autoimmune diseases after stimulation of TRID by  
CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID  
CC polypeptides are useful for treating and/or preventing diseases  
CC associated with increased or decreased apoptotic cell death. The TRID  
CC polynucleotides, proteins, antibodies, agonists and antagonists are  
CC useful in the diagnosis, treatment or prevention of: (a) cancer;  
CC (b) autoimmune disorders; (c) diseases associated with increased  
CC apoptosis; (d) cardiovascular disorders; and (e) viral infection.  
XX  
SQ Sequence 259 AA:

Query Match 100.0%; Score 100; DB 22; Length 259;  
Best Local Similarity 100.0%; Pred. No. 5.4e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSPGTPAPAAEETMTSPG 19  
Db 185 tsptgpapaaeetmtspg 203  
|||||

RESULT 9  
AAB53091  
ID AAB53091 standard; Protein: 259 AA.  
XX  
AC AAB53091;  
XX  
DT 28-FEB-2001 (first entry)  
XX  
DE Human angiogenesis-associated protein PRO366, SEQ ID NO:152.  
XX  
XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
KW myocardial infarction; diabetic retinopathy; Rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
KW gene therapy; transgenic animal.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO200053753-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 05-JAN-2000; 2000WO-US00219.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145698.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 05-OCT-1999; 99WO-US23089.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
XX

PA (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
PI Paoni NF, Pittl RM, Watanabe CK, Williams PM, Wood WT;  
XX WPI: 2001-090793/10.  
DR N-PSDB: AAC97488.  
XX  
XX New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
XX  
XX Claim 69; Fig 56; 293pp; English.  
XX  
XX The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells  
CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof.  
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
CC disease, or stroke. PRO nucleic acids are additionally useful in the  
CC recombinant production of PRO proteins, as hybridisation probes to  
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
CC animals useful for the development and screening of potential  
CC therapeutic agents. The present sequence represents a PRO protein of the  
CC invention.  
XX  
XX Sequence 259 AA;  
SO  
Query Match 100.0%; Score 100; DB 22; Length 259;  
Best Local Similarity 100.0%; Pred. No. 5,4e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TSPGTPAPAAEETMTTSPG 19  
|||||  
Db 185 tsptgpapaaeetmttspg 203  
RESULT 10  
AAB82181  
ID AAB82181 standard; Protein: 268 AA.  
XX  
XX AAB82181;  
XX  
XX 23-JUL-2001 (first entry)  
XX  
XX FLAG-TRID clone with a transmembrane domain.  
XX  
XX FLAG-epitope tag; transmembrane domain; death domain; apoptosis;  
KW cell suicide; tissue homeostasis; cell proliferation;  
KW cell-cell signalling; Trail Receptor without Intracellular Domain; TRID.  
XX

OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..23  
FT /label= Signal\_peptide  
FT Protein 24..268  
FT /label= FLAG-TRID\_protein  
FT Peptide 27..34  
FT /label= FLAG-epitope\_TAG  
FT Region 250..268  
FT /label= Transmembrane\_region  
XX  
XX WO200114542-A1.  
XX  
XX 01-MAR-2001.  
XX  
XX 23-AUG-2000; 2000WO-US23112.  
XX  
XX 25-AUG-1999; 99US-0150747.  
XX  
XX (GENO-) GENOME THERAPEUTICS CORP.  
XX  
XX Denome SA, Swain PM, Tzellas N;  
PI WPI: 2001-374162/39.  
DR N-PSDB: AAH19325.  
XX  
XX Identifying a transmembrane domain of a membrane-spanning protein  
PT useful in defining processes in cell suicide and tissue homeostasis,  
PT comprises modifying the nucleic acid encoding a death domain-lacking  
PT membrane spanning protein -  
XX  
XX PS  
XX Disclosure; Fig 1; 38pp; English.  
XX  
XX The present invention relates to methods for identifying a transmembrane  
CC domain (TM) of a membrane-spanning protein. The method comprises  
CC modifying a nucleic acid encoding a death domain (DD)-lacking membrane  
CC spanning protein (e.g. Trail Receptor without Intracellular Domain; TRID)  
CC by replacing the nucleic acid encoding the TM of the DD-lacking  
CC membrane-spanning protein with a candidate nucleic acid sequence to  
CC produce a nucleic acid encoding a modified DD-lacking membrane spanning  
CC protein. The modified nucleic acid is then transfected into a host cell,  
CC which expresses a DD-containing receptor. The absence of apoptosis of the  
CC host cell is determined following exposure of the transfected cell to an  
CC apoptosis-inducing ligand. Candidate nucleic acids encoding TM prevent  
CC apoptosis of the host cell. The modified nucleic acid encoding the  
CC modified death domain-lacking membrane-spanning protein can also include  
CC a nucleic acid sequence encoding an epitope tag. The present sequence is  
CC a FLAG-TRID clone, which was used in the method of the present invention.  
CC This sequence comprises human TRID protein and the FLAG-epitope tag. The  
CC FLAG-epitope is a useful marker to purify proteins encoded by the  
CC modified DD-lacking membrane-spanning protein. The identified TM and  
CC membrane-spanning proteins may be used in defining processes involved in  
CC cell suicide and tissue homeostasis, and to evaluate, interfere and treat  
CC events, such as cell proliferation and cell-cell signalling pathways.  
XX  
XX Sequence 268 AA;  
SQ  
Query Match 100.0%; Score 100; DB 22; Length 268;  
Best Local Similarity 100.0%; Pred. No. 5,5e-05;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TSPGTPAPAAEETMTTSPG 19  
|||||  
Db 194 tsptgpapaaeetmttspg 212  
RESULT 11  
AAW76331  
ID AAW76331 standard; Protein: 299 AA.  
XX  
XX AAW76331;  
AC

XX 11-JAN-1999 (first entry)  
 DT Human tumour necrosis related receptor TR5.  
 XX  
 DE  
 XX Tumour necrosis related receptor; TR5; human; inflammation;  
 KW arthritis; septicaemia; transplant rejection; autoimmune disease;  
 KW inflammatory bowel disease; graft versus host disease; infection;  
 KW stroke; ischaemia; acute respiratory disease syndrome; psoriasis;  
 KW restenosis; brain injury; AIDS; bone disease; cancer;  
 KW atherosclerosis; Alzheimer's disease; therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1..165  
 FT /label- sig-peptide  
 FT 66..299  
 FT /label- Mat\_protein  
 FT  
 XX EP867509-A2.  
 XX  
 XX 30-SEP-1998.  
 XX  
 XX 04-FEB-1998; 98EP-0300827.  
 XX  
 XX 28-JUL-1997; 97US-0901469.  
 XX 05-FEB-1997; 97US-0795910.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 XX  
 P1 Lyn SDP, Tan KB, Truneh A, Young PR;  
 XX  
 XX WPI: 1998-497862/43.  
 DR N-PSDB; AAV56990.  
 XX  
 XX New polynucleotide encoding TR5 polypeptide - used to diagnose,  
 PT prevent and treat e.g. Inflammation, arthritis, septicaemia,  
 PT autoimmune diseases, infections, stroke, ischaemia, ARDS, psoriasis,  
 PT restenosis, brain injury, AIDS and bone diseases  
 XX  
 PS Claim 5; Flg 1; 22pp; English.  
 CC This is the amino acid sequence of human tumour necrosis related  
 CC receptor TR5, as deduced from the sequence of an isolated cDNA  
 CC clone (see AAV56990). The protein is characterised as a GPI-linked  
 CC protein that has a membrane proximal O-glycosylation region. The  
 CC invention provides methods for the recombinant production of TR5  
 CC and its use in diagnostic and therapeutic methods. Treatment of a  
 CC subject in need of enhanced TR5 activity comprises administering an  
 CC agonist to the polypeptide and/or providing TR5 polynucleotide in a  
 CC form so as to effect production of the polypeptide activity in vivo.  
 CC Treatment of a subject with the need to inhibit TR5 polypeptide  
 CC activity comprises administering an antagonist to the polypeptide,  
 CC administering a nucleic acid that inhibits the expression of the  
 CC nucleotide sequence encoding the polypeptide and/or administering a  
 CC polypeptide that competes with the polypeptide for its ligand,  
 CC substrate or receptor. Diagnosing a disease or a susceptibility  
 CC to a disease related to expression or activity of TR5 polypeptide,  
 CC comprises determining the presence or absence of mutation in the  
 CC nucleotide sequence encoding the TR5 polypeptide in the genome of  
 CC the subject and/or analysing for the presence or amount of TR5  
 CC polypeptide expression in a sample. Identification of compounds  
 CC which bind to TR5 comprises contacting host cells with a candidate  
 CC compound and assessing the ability of it to bind to the cells. The  
 CC active agents can be used for the treatment of chronic and acute  
 CC inflammation, arthritis, septicaemia, autoimmune diseases (e.g.  
 CC inflammatory bowel disease, psoriasis), transplant rejection,  
 CC graft vs host disease, infection, stroke, ischaemia, acute  
 CC respiratory disease syndrome, restenosis, brain injury, AIDS, bone  
 CC diseases, cancer (e.g. lymphoproliferative disorders),  
 CC atherosclerosis and Alzheimer's disease.  
 CC  
 XX

SO Sequence 299 AA;  
 Query Match 100.0%; Score 100; DB 19; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TSPGTPAPAAEETMTSPG 19  
 ||||||||||||||||  
 Db 225 tsqgppapaaeetmtspg 243  
 RESULT 12  
 AAY29864  
 ID AAY29864 standard; Protein; 299 AA.  
 XX  
 AC AAY29864;  
 XX  
 DT 17-NOV-1999 (first entry)  
 XX  
 DE Human secreted protein clone j1442\_1.  
 XX  
 KW Human; secreted protein; biological activity; nutritional; cytokine;  
 KW cell proliferation; differentiation; immune stimulating; vaccine;  
 KW haematopoiesis regulation; tissue growth; haemostatic; thrombolytic;  
 KW anti-inflammatory; tumour inhibition.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9346287-A1.  
 XX  
 PD 16-SEP-1999.  
 XX  
 PF 11-MAR-1999; 99WO-US05243.  
 XX  
 PR 11-MAR-1998; 98US-0077521.  
 PR 14-MAR-1998; 98US-0079124.  
 PR 10-MAR-1999; 99US-0266105.  
 XX  
 PA (GENY ) GENETICS INST INC.  
 XX  
 PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
 PI Merdeig D, Treacy M, Agostino MO, Steininger RJ;  
 XX  
 DR WPI: 1999-551362/46.  
 DR N-PSDB; AA221096.  
 XX  
 XX Polynucleotides encoding secreted human proteins, derived from human  
 PT fetal brain, human adult blood, human adult bladder, or human adult  
 PT neural tissue cDNA libraries.  
 XX  
 PS Claim 17; Page 104; 118pp; English.  
 CC AA221093 to AA221102 encode new human secreted proteins and AAY29861 to  
 CC AAY29873 represent the secreted proteins encoded by the polynucleotide  
 CC sequences. AA221103 to AA221112 represent probes for the secreted  
 CC proteins. The polynucleotides and proteins are predicted to have  
 CC biological activities which would make them suitable for treating,  
 CC preventing or ameliorating medical conditions in humans and animals,  
 CC although no supporting data is given. Suggested activities include  
 CC nutritional activity, cytokine and cell proliferation/differentiation  
 CC activity, immune stimulating (e.g. as vaccines) or suppressing activity,  
 CC haematopoiesis regulating activity, tissue growth activity,  
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory  
 CC activity, cadherin/tumour invasion suppressor activity, and tumour  
 CC inhibition activity. The polynucleotides and proteins can also be used  
 CC as nutritional sources or supplements. Such uses include use as a protein  
 CC or amino acid supplement, use as a carbon source, use as a nitrogen  
 CC source and use as a source of carbohydrate. They may also have utility  
 CC in compositions used for bone, cartilage, tendon, ligament, and/or nerve  
 CC tissue growth or regeneration, as well as for wound healing and tissue  
 CC repair and replacement, and in the treatment of burns, incisions and

CC ulcers. The proteins which induce cartilage and/or bone growth in  
 CC circumstances where bone is not normally formed, have application in  
 CC the healing of bone fractures and cartilage damage or defects in humans  
 CC and other animals.

XX Sequence 299 AA;

Query Match 100.0%; Score 100; DB 20; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSPGTPAPAAEETMTSPG 19  
 |||||  
 Db 225 tsptgtpapaaeetmtspg 243

# RESULT 13

AAV05744  
 ID AAV05744 standard; Protein; 299 AA.

XX AAV05744;

DT 19-JUL-1999 (first entry)

DE Tumour necrosis factor receptor TR5.

XX Tumour necrosis factor receptor; TR5; TRID; DCRL; agonist;  
 KW antagonist; screening; human; cancer; AIDS; Alzheimer's disease;  
 KW inflammation; arthritis; septicemia; autoimmune disease;  
 KW psoriasis; inflammatory bowel disease; transplant rejection;  
 KW graft versus host disease; infection; stroke; ischaemia;  
 KW acute respiratory disease syndrome; restenosis; brain injury;  
 KW bone disease; atherosclerosis; therapy.

XX Homo sapiens.

PN EP911633-A1.

PD 28-APR-1999.

PF 02-OCT-1998; 98EP-0203332.

PR 08-OCT-1997; 97US-0061334.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PI McDonnell PC, Young PR, Zou J;

DR WPI; 1999-246560/21.

PT Identifying agonists and antagonists of tumor necrosis factor  
 PT related receptors TR1, TR3 and TR5, and of ligand TR3, useful for  
 PT treatment of cancer, AIDS, Alzheimer's disease, bone disease etc  
 PS Disclosure; Page 13-14; 23pp; English.

XX The present sequence represents tumor necrosis factor receptor  
 CC (TNFR) TR5, also known as TRID or DCRL. The invention relates  
 CC to TNFR related polypeptides TR1, TR3 and TR5 (see AAV05742-44) and  
 CC their ligand TR3 (see AAV05745). TR1, TR3, TR5 and TR3 are used in  
 CC claimed methods of identifying agonists and antagonists, i.e.  
 CC compounds that bind to the receptors or ligand, and which activate  
 CC (agonist) or inhibit activation of (antagonists) TR1, TR3, TR5 or  
 CC TR3. A screening kit for identifying agonists, antagonists,  
 CC ligands, receptors, substrates, enzymes etc. for TR1, TR3, TR5 or  
 CC TR3 polypeptides is provided. The agonists and antagonists are  
 CC useful for treatment of chronic and acute inflammation, arthritis,  
 CC septicemia, autoimmune disease e.g. inflammatory bowel disease,  
 CC psoriasis, transplant rejection, graft versus host disease,  
 CC infection, stroke, ischaemia, acute respiratory disease syndrome,  
 CC restenosis, brain injury, AIDS, bone diseases, cancer (e.g.  
 CC lymphoproliferative disorders), atherosclerosis and Alzheimer's

CC disease, etc., caused by imbalance of TR1, TR3, TR5 or TR3.

XX Sequence 299 AA;

Query Match 100.0%; Score 100; DB 20; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSPGTPAPAAEETMTSPG 19  
 |||||  
 Db 225 tsptgtpapaaeetmtspg 243

# RESULT 14

AAV00933  
 ID AAV00933 standard; Protein; 299 AA.

XX AAV00933;

DT 02-JUN-1999 (first entry)

DE Human TRAIL-R3 protein sequence.

XX Human; DR5; TRAIL-R3; apoptosis related condition; cancer; therapy;  
 KW autoimmune disease; viral infection; degenerative disorder;  
 KW amyotrophic lateral sclerosis; retinitis pigmentosa; ischaemic injury;  
 KW cerebellar degeneration; myelodysplastic syndrome.

XX Homo sapiens.

PN WO9909165-A1.

PD 25-FEB-1999.

PF 14-AUG-1998; 98WO-US16945.

PR 15-AUG-1997; 97US-0055906.

XX (IDUN-) IDUN PHARM INC.

PI Alnemri ES;

DR WPI; 1999-181035/15.

DR N-PSDB; AAX27280.

PT Newly isolated polynucleotide encoding a mammalian TRAIL receptor  
 PT protein - useful in for screening for (ant)agonists that modulate  
 PT the apoptotic activity mediated by DR5 or TRAIL-R3 proteins  
 PS Claim 16; Page 62-63; 71pp; English.

XX This sequence is the human TRAIL receptor TRAIL-R3 of the invention. An  
 CC antibody against the TRAIL receptors is useful for detecting mammalian  
 CC DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in  
 CC bioassays for screening for (ant)agonists of DR5 or TRAIL-R3 proteins.  
 CC (Ant)agonists identified by the assay are useful for modulating the  
 CC apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis  
 CC related conditions which are treated in this way, include cancer  
 CC (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus  
 CC erythematosus and immune-mediated glomerulonephritis), viral infections  
 CC (e.g. herpes virus, poxvirus and adenovirus), degenerative disorders  
 CC (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral  
 CC sclerosis, retinitis pigmentosa, cerebellar degeneration, myelodysplastic  
 CC syndromes (e.g. aplastic anaemia) and ischemic injury (e.g. myocardial  
 CC infarction and stroke). The polynucleotides can also be used to treat  
 CC these diseases. Antisense oligonucleotides to the DNA sequences can be  
 CC used to form a composition that is useful for inhibiting expression of a  
 CC human DR5 or TRAIL-R3 protein.

XX Sequence 299 AA;

Query Match 100.0%; Score 100; DB 20; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-05;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSPGTPAPAAEETWTSPG 19  
 |||||  
 DB 225 tspgtpapaaeetmtltspg 243

## RESULT 15

AAM94671  
 ID AAM94671 standard; Protein: 299 AA.

XX  
 AC AAM94671;

XX  
 DT 04-MAY-1999 (first entry)

XX  
 DE Human TNF-related apoptosis-inducing ligand binding protein.

XX  
 KW Human; TNF-related apoptosis-inducing ligand binding protein; clotting;

KW TRAIL-BP; tumour necrosis factor; T cell death; HIV; gene therapy;

KW thrombotic microangiopathy; thrombotic thrombocytopenic purpura;

KW haemolytic-uraemic syndrome; systemic lupus erythematosus.

XX  
 OS Homo sapiens.

XX  
 PN WO9900423-A1.

XX  
 PD 07-JAN-1999.

XX  
 PP 25-JUN-1998; 98WO-US13491.

XX  
 PR 26-JUN-1997; 97US-0883529.

XX  
 PA (IMMUNEX ) IMMUNEX CORP.

XX  
 PI Smith CA, Walczak H;

XX  
 DR WPI: 1999-095685/08.

XX  
 DR N-PSDB; AAX16692.

PT New isolated TRAIL binding protein - which binds to a tumour  
 PT necrosis factor-related apoptosis inducing ligand, used in the  
 PT diagnosis and treatment of TRAIL-mediated disorders

PS Claim 1: Fig 1; 47pp; English.

XX  
 CC The present sequence is human tumour necrosis factor (TNF)-related  
 CC apoptosis-inducing ligand (TRAIL) binding protein (BP). TRAIL-BP can be  
 CC used for inhibiting the biological activities of TRAIL or for purifying  
 CC TRAIL. TRAIL-BP proteins can be used for treating a TRAIL-mediated  
 CC disorder such as T cell death in HIV-infected patients. They can be used  
 CC for treating thrombotic microangiopathies such as thrombotic  
 CC thrombocytopenic purpura, haemolytic-uraemic syndrome, clotting of small  
 CC blood vessels or systemic lupus erythematosus. The TRAIL-BP nucleic  
 CC acids can also be used for gene therapy. They can also be used as  
 CC carriers for delivering attached agents to cells bearing TRAIL.

XX  
 SQ Sequence 299 AA;

Query Match 100.0%; Score 100; DB 20; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 6.1e-05;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSPGTPAPAAEETWTSPG 19  
 |||||  
 DB 225 tspgtpapaaeetmtltspg 243

Search completed: August 13, 2002, 08:31:30  
 Job time: 124 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: August 13, 2002, 08:30:04 ; Search time 28.27 Seconds  
(without alignments)  
64.581 Million cell updates/sec

Title: US-09-826-212-2\_COPY\_215\_233  
Perfect score: 100  
Sequence: 1 TSPCTPAPAAEETMTTSPG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52.0	801	2	T29018	hypothetical prote
2	52.0	878	2	T21621	hypothetical prote
3	51.0	2938	2	T30249	cell proliferation
4	50.0	292	2	S24189	mucin - rat
5	49.5	49.5	1	NDBE61	exonuclease (EC 3.
6	48.0	427	2	G71272	iron-sulfur cofact
7	48.0	433	2	S20963	homeotic protein H
8	48.0	650	2	T22002	hypothetical prote
9	48.0	846	2	T21700	hypothetical prote
10	48.0	1323	2	T30253	spalt protein - mo
11	48.0	1466	1	CGH07L	collagen alpha 1(I
12	47.0	284	2	S60743	secreted antigen P
13	47.0	284	2	F70888	probable pig prot
14	47.0	375	2	F75467	probable lipoprote
15	47.0	413	2	S76200	ferredoxin-NADP+
16	47.0	488	2	A27353	collagen alpha 1(I
17	47.0	495	2	AD2275	hypothetical prote
18	47.0	504	2	T13475	hypothetical prote
19	47.0	833	2	T22139	hypothetical prote
20	47.0	1049	1	CG807S	collagen alpha 1(I
21	47.0	1464	2	SS9856	collagen alpha 1(I
22	46.5	228	2	T10507	ribulose-phosphate
23	46.0	107	2	A72701	hypothetical prote
24	46.0	285	2	H70594	hypothetical prote
25	46.0	347	2	T14313	hypothetical prote
26	46.0	424	2	T33663	hypothetical prote
27	46.0	514	2	A31643	cell adhesion 80K
28	46.0	905	1	RGBY55	regulatory protein
29	46.0	998	2	T35745	probable ATP-bind1

30	46	46.0	2440	2	S39162	transcription coac
31	46	46.0	7463	2	T36248	CDA peptide synthe
32	45.5	45.5	223	1	MEVNSV	matrix protein - s
33	45.5	45.5	583	2	F69153	conserved hypotet
34	45.5	45.5	651	2	T15624	hypothetical prote
35	45.5	45.5	2105	2	T18968	hypothetical prote
36	45	45.0	340	2	C70743	probable serine-ty
37	45	45.0	348	2	I49262	cyclin cdk inhibit
38	45	45.0	429	2	A48377	glutamate-1-semial
39	45	45.0	454	2	A56954	yes-associated pro
40	45	45.0	478	2	A32555	major mezozoite su
41	45	45.0	348	2	T27542	hypothetical prote
42	45	45.0	632	2	S42731	collagen alpha 1 c
43	45	45.0	736	2	T25447	hypothetical prote
44	45	45.0	896	2	I56563	interleukin-3 rece
45	45	45.0	1176	2	A49848	nitrite reductase

## ALIGNMENTS

## RESULT 1

T29018  
hypothetical protein ZK84.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 17-Mar-2000

C:Accession: T29018

R:Kirsten, J.

Submitted to the EMBL Data Library, April 1995  
A:Description: The sequence of C. elegans cosmid ZK84.

A:Reference number: 220553

A:Accession: T29018

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-801 <KTR>

A:Cross-references: EMBL:U23181; PIDN:MAC48204.1; GSPDB:GN00020; CESP:ZK84.1

A:Experimental source: strain Bristol N2; clone ZK84

C:Genetics:

A:Gene: CESP:ZK84.1

A:Map position: 2

A:Introns: 22/2; 45/3; 108/1

C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo

Query Match 52.0%; Score 52; DB 2; Length 801;  
Best Local Similarity 76.9%; Pred. No. 26;  
Matches 10; Conservative 1; Mismatches 2; Gaps 0;

QY 6 PAPAETMTTSP 18  
|||||  
Db 585 PAPAETMTTSP 597

RESULT 2  
T21621  
hypothetical protein F32A7.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T21621

R:Kershaw, J.

Submitted to the EMBL Data Library, November 1996

A:Reference number: 219451

A:Accession: T21621

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-878 <WIL>

A:Cross-references: EMBL:Z83107; PIDN:CAR05498.1; GSPDB:GN00019; CESP:F32A7.5

A:Experimental source: clone F32A7

C:Genetics:

A:Gene: CESP:F32A7.5

A:Map position: 1

A:Introns: 74/3; 380/3; 439/3; 567/3; 728/3; 818/1

Query Match 52.0%; Score 52; DB 2; Length 878;  
Best Local Similarity 55.6%; Pred. No. 29;  
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 TSPGTPAPAAEETMTSP 18  
|:| | | | | | | | | |  
Db 354 TAPSPAPAPASATSP 371

## RESULT 3

T30249  
cell proliferation antigen Ki-67 - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
C:Accession: T30249  
R:Starborg, M.; Gell, K.; Brundell, E.; Hoog, C.  
J. Cell Sci. 109, 143-153, 1996  
A:Title: The murine Ki-67 cell proliferation antigen accumulates in the nucleolar and he  
1 for cell cycle progression.  
A:Reference number: 220787; MUID:96431717  
A:Accession: T30249  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-2938 <STA>  
A:Cross-references: EMBL:X82786; NID:91177527; PIDN:CAA58026.1; PID:91177528  
A:Experimental source: strain CBA; testis  
C:Genetics:  
A:Gene: Ki-67  
C:Keywords: cell cycle control; nucleus; tandem repeat

Query Match 51.0%; Score 51; DB 2; Length 2938;  
Best Local Similarity 62.5%; Pred. No. 1,4e+02;  
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 2 SPCGPAPAAEETMTS 17  
| | | | | | | | | |  
Db 1863 SPGTPAPQENEDCTA 1878

## RESULT 4

S24169  
mucin - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 10-Nov-1995  
C:Accession: S24169  
R:Huan, L.J.; Xu, G.; Forstner, G.; Forstner, J.  
Biochim. Biophys. Acta 1132, 79-82, 1992  
A:Title: A serine, threonine and proline-rich region near the carboxyl-terminus of a rat  
A:Reference number: S24169; MUID:92379096  
A:Accession: S24169  
A:Molecule type: mRNA  
A:Residues: 1-292 <HUA>

Query Match 50.0%; Score 50; DB 2; Length 292;  
Best Local Similarity 36.4%; Pred. No. 17;  
Matches 12; Conservative 2; Mismatches 5; Indels 14; Gaps 1;

OY 1 TSPGTPAPAAEETMTSPG 19  
| | | | | | | | | |  
Db 116 TSPSPSPSTSTLSPTVTATSTSTSPG 148

## RESULT 5

NDBR61  
exonuclease (EC 3.1.11.-) - human herpesvirus 1 (strain 17)  
N:Alternate names: gene UL12 protein (deoxyribonuclease)  
C:Species: human herpesvirus 1  
A:Note: host Homo sapiens (man)  
C:Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 16-Jun-2000  
C:Accession: A00781; C30083

R:McGeoch, D.J.; Dolan, A.; Frame, M.C.  
Nucleic Acids Res. 14, 3435-3448, 1986  
A:Title: DNA sequence of the region in the genome of herpes simplex virus type 1 cont  
A:Reference number: A93620; MUID:86205244  
A:Accession: A00781

A:Molecule type: DNA  
A:Residues: 1-626 <MCG>  
A:Cross-references: GB:X03839; NID:959841; PIDN:CAA27453.1; PID:959844  
R:McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; P  
J. Gen. Virol. 69, 1531-1574, 1988  
A:Title: The complete DNA sequence of the long unique region in the genome of herpes  
A:Reference number: A30083; MUID:86274327  
A:Accession: C30083  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-626 <MCG>

A:Cross-references: GB:X14112; NID:91944536; PIDN:CAA3325.1; PID:959513; GB:D00317  
C:Genetics:  
A:Gene: UL12  
A:Map position: 0.16-0.20  
C:Superfamily: herpesvirus exonuclease  
C:Keywords: exonuclease; hydrolase

Query Match 49.5%; Score 49.5; DB 1; Length 626;  
Best Local Similarity 64.7%; Pred. No. 44;  
Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

OY 2 SPCGPAPAAEETMTSP 18  
| | | | | | | | | |  
Db 604 SPG-PGPAAETTSSTSP 619

## RESULT 6

G71272  
iron-sulfur cofactor synthesis protein nifs2 TP0863 [similarity] - syphilis spirochet  
N:Contains: L-cysteine sulfotransferase (EC 2.8.1.-)  
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)  
C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 20-Jun-2000  
C:Accession: G71272  
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; G  
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uterback, T.; M  
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.  
Science 281, 375-388, 1998  
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.  
A:Reference number: A71250; MUID:98332770  
A:Accession: G71272  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-427 <COL>  
A:Cross-references: GB:AE001256; GB:AE000520; NID:93323171; PIDN:MAC65826.1; PID:9332  
C:Genetics:  
A:Experimental source: strain Nichols  
A:Gene: TP0863  
C:Superfamily: nitrogen fixation protein nifs  
C:Keywords: phosphoprotein; pyridoxal phosphate; sulfotransferase  
F:374/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted  
F:374/Active site: Cys (cysteine persulfide intermediate) #status predicted

Query Match 48.0%; Score 48; DB 2; Length 427;  
Best Local Similarity 52.9%; Pred. No. 47;  
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 TSPGTPAPAAEETMTS 17  
| | | | | | | | | |  
Db 209 TPPTGTPATGATATYS 225

## RESULT 7

S20963  
homeotic protein Hox B3 - mouse  
N:Alternate names: homeotic protein Hox 2.7

C:Species: Mus musculus (house mouse)  
 C:Date: 22-Nov-1993 #sequence\_revision 21-Jul-1995 #text\_change 20-Aug-1999  
 C:Accession: S20963; D42694  
 R:Sham, M.H.; Hunt, P.; Nonchev, S.; Papalopulu, N.; Graham, A.; Boncinelli, E.; Krumlauf  
 EMO J. 11, 1825-1836, 1992  
 A:Title: Analysis of the murine Hox-2.7 gene: conserved alternative transcripts with dif  
 A:Reference number: S20963; MUID:92258392  
 A:Accession: S20963  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-433 <SHA>  
 A:Cross-references: GB:X66177; GB:S35629; GB:S35738; NID:g112229; PIDN:CAA46951.1; PID:g  
 R:Nazaretti, A.; Kim, Y.; Nirenberg, M.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2883-2887, 1992  
 A:Title: Hox-1.11 and Hox-4.9 homeobox genes.  
 A:Reference number: A42694; MUID:92212934  
 A:Accession: D42694  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 213-238 <NAZ>  
 A>Note: sequence extracted from NCBI backbone (NCBIN:92310, NCBI:P:92316)  
 C:Superfamily: homeotic protein Hox B3; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:192-248/Domain: homeobox homology <HOX>

Query Match 48.0%; Score 48; DB 2; Length 433;  
 Best Local Similarity 60.0%; Pred. No. 48;  
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 3 PGTPAPAAEETMTTS 17  
 ||:|:|:|:|:|:|  
 Db 87 PGSPPSAAPTSTTS 101

RESULT 8  
 T22002  
 hypothetical protein F39H11.4 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T22002  
 R:White, S.  
 submitted to the EMBL Data Library, October 1996  
 A:Reference number: Z19500  
 A:Accession: T22002  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-650 <NIL>  
 A:Cross-references: EMBL:281079; PIDN:CAB03084.1; GSPDB:GN00019; CESP:F39H11.4  
 A:Experimental source: clone F39H11  
 C:Genetics:  
 A:Gene: CESP:F39H11.4  
 A:Map position: 1  
 A:Introns: 109/3; 154/1; 357/1; 420/3; 464/3; 566/2; 594/1; 628/3

Query Match 48.0%; Score 48; DB 2; Length 650;  
 Best Local Similarity 60.0%; Pred. No. 73;  
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 2 SPCTPAPAAEETMTT 16  
 :||:|:|:|:|:|:|  
 Db 346 APGAPAPAYGTTLT 360

RESULT 9  
 T21700  
 hypothetical protein F33E2.6 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T21700  
 R:Lennard, N.  
 submitted to the EMBL Data Library, January 1997

A:Reference number: Z19461  
 A:Accession: T21700  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-846 <NIL>  
 A:Cross-references: EMBL:284574; PIDN:CAB06541.1; GSPDB:GN00019; CESP:F33E2.6  
 A:Experimental source: clone F33E2  
 C:Genetics:  
 A:Gene: CESP:F33E2.6  
 A:Map position: 1  
 A:Introns: 99/3; 213/3; 332/3; 525/3

Query Match 48.0%; Score 48; DB 2; Length 846;  
 Best Local Similarity 56.2%; Pred. No. 95;  
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Oy 3 PGTPAPAAEETMTTSP 18  
 ||:|:|:|:|:|:|  
 Db 796 PGTEAPPTTEAPMTTP 811

RESULT 10  
 T30253  
 spalt protein - mouse (fragment)  
 N:Alternate names: zinc finger protein msal  
 C:Species: Mus musculus (house mouse)  
 C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000  
 C:Accession: T30253  
 R:Ott, T.; Kaestner, K.H.; Monaghan, A.P.; Schultz, G.  
 Mech. Dev. 56, 117-128, 1996  
 A:Title: The mouse homolog of the region specific homeotic gene spalt of Drosophila  
 A:Reference number: Z20791; MUID:96391179  
 A:Accession: T30253  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1323 <OTT>  
 A:Cross-references: EMBL:X97581; NID:g1296844; PIDN:CAA6196.1; PID:g1296845  
 C:Genetics:  
 A:Gene: msal  
 C:Function:  
 A:Description: may play an important role in the development of the nervous system

Query Match 48.0%; Score 48; DB 2; Length 1323;  
 Best Local Similarity 50.0%; Pred. No. 1.5e+02;  
 Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Oy 2 SPCTPAPAAEETMTSPG 19  
 ||:|:|:|:|:|:|  
 Db 530 SPQRPSASSECTSLSPG 547

RESULT 11  
 CGH07L  
 collagen alpha 1(III) chain precursor - human  
 N:Alternate names: procollagen alpha 1(III) chain  
 C:Species: Homo sapiens (man)  
 C:Date: 24-Apr-1984 #sequence\_revision 01-Sep-1995 #text\_change 21-Jul-2000  
 C:Accession: S05272; S04642; PE0011; S01726; S04887; A90399; A94562; I51868; S59511;  
 R:Prockop, D.J.  
 submitted to the EMBL Data Library, February 1989  
 A:Reference number: S05272  
 A:Accession: S05272  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1240, 'V', 1242-1466 <PRC>  
 A:Cross-references: EMBL:X14420; NID:g30057; PIDN:CAA32583.1; PID:g30058  
 R:Ala-Kokko, L.; Kontusari, S.; Baldwin, C.T.; Kuitvaniet, H.; Prockop, D.J.  
 Biochem. J. 260, 509-516, 1989  
 A:Title: Structure of cDNA clones coding for the entire prepro-alpha1(III) chain of h  
 erences.  
 A:Reference number: S04642; MUID:89350838

A:Accession: S04642  
A:Molecule type: mRNA  
A:Residues: 1-1196 <ALA>  
A:Cross-references: EMBL:X14420; NID:930057; PIDN:CAA32583.1; PID:930058  
A:Note: the complete sequence is not shown  
R:Benson-Chanda, V.; Su, M.W.; Well, D.; Chu, M.L.; Ramirez, F.  
Gene 78, 253-265, 1989  
A:Title: Cloning and analysis of the 5' portion of the human type-III procollagen gene  
A:Reference number: PE0011; MUID:89378752  
A:Accession: PE0011  
A:Molecule type: DNA  
A:Residues: 1-176 <BEN>  
A:Cross-references: GB:M2639; NID:9180813; PIDN:AA52040.1; PID:9180814  
R:Toman, P.D.; Ricca, G.A.; de Crombrughe, B.  
Nucleic Acids Res. 16, 7201, 1988  
A:Title: Nucleotide sequence of a cDNA coding for the amino-terminal region of human pre  
A:Reference number: S01726; MUID:88303360  
A:Accession: S01726  
A:Molecule type: mRNA  
A:Residues: 1-170 <TOM>  
A:Cross-references: EMBL:X07240; NID:930060; PIDN:CAA30229.1; PID:930061  
A:Note: the authors translated the codon CAG for residue 154 as His  
R:Janeczko, R.A.; Ramirez, F.  
Nucleic Acids Res. 17, 6742, 1989  
A:Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III) collagen.  
A:Reference number: S04887; MUID:89386015  
A:Accession: S04887  
A:Molecule type: mRNA  
A:Residues: 149-163, 'G', 164-240, 'D', 242-471, 'D', 473-487, 'L', 489, 'S', 491-613, 'Y', 615-634,  
A:Cross-references: EMBL:X15333; NID:929645; PIDN:CAA33387.1; PID:930045  
A:Note: the authors' translation of residues 905-932 is inconsistent with the nucleotide  
R:Sejer, J.M.; Kang, A.H.  
Biochemistry 16, 1158-1164, 1977  
A:Title: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptide  
A:Reference number: A90399; MUID:77134724  
A:Accession: A90399  
A:Molecule type: protein  
A:Residues: 'V', 169-225, 229-232, 'P', 234-292, 'D', 294-398 <SEY1>  
A:Experimental source: liver  
A:Note: sequence corrected by A94562; attachment of 2-O-alpha-D-glucosyl-O-beta-D-galact  
R:Sejer, J.M.  
submitted to the Atlas, December 1977  
A:Reference number: A94562  
A:Accession: A94562  
A:Molecule type: protein  
A:Residues: 'V', 169-225, 229-277, 'A', 279-292, 'D', 294, 'S', 296-398 <SEY2>  
A:Experimental source: liver  
A:Note: author submitted corrections to A90399  
R:Milicic, D.M.; Wiltz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H.  
Am. J. Hum. Genet. 53, 62-70, 1993  
A:Title: Parental somatic and germ-line mosaicism for a multexon deletion with unusual  
splicing.  
A:Reference number: I51868; MUID:93304430  
A:Accession: I51868  
A>Status: preliminary: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 186-194 <MIL>  
A:Cross-references: GB:S62925; NID:9386425; PIDN:AAD13937.1; PID:94261637  
R:Chiodo, A.A.; Silience, D.O.; Cole, W.G.; Bateman, J.F.  
Biochem. J. 311, 939-943, 1995  
A:Title: Abnormal type III collagen produced by an exon-17-skipping mutation of the COL3  
A:Reference number: S59511; MUID:96067614  
A:Accession: S59511  
A:Molecule type: mRNA  
A:Residues: 302-423 <CHR>  
A:Cross-references: GB:S79677; NID:91195576; PIDN:AAB35615.1; PID:91195577  
R:Sejer, J.M.; Kang, A.H.  
Biochemistry 17, 3404-3411, 1978  
A:Title: Covalent structure of collagen: amino acid sequence of five consecutive CNBr pe  
A:Reference number: A90414; MUID:79000343  
A:Accession: A90414  
A:Molecule type: protein  
A:Residues: 399-675, 'N', 677-727 <SEY3>

A:Experimental source: liver  
R:Lee, B.; Vitale, E.; Superti-Furga, A.; Steinmann, B.; Ramirez, F.  
J. Biol. Chem. 266, 5256-5259, 1991  
A:Title: G to T transversion at position +5 of a splice donor site causes skipping of  
A:Reference number: I55349; MUID:91161621  
A:Accession: I55349  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 537-605 <LEE>  
A:Cross-references: GB:M59312; NID:9180815; PIDN:AA52041.1; PID:9180816  
R:Sejer, J.M.; Mainardi, C.; Kang, A.H.  
Biochemistry 19, 1583-1589, 1980  
A:Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB5 from  
A:Reference number: A90438; MUID:80198282  
A:Accession: A90438  
A:Molecule type: protein  
A:Residues: 728-895, 'A', 897-964 <SEY4>  
A:Experimental source: liver  
R:Cole, W.G.; Chiodo, A.A.; Lamande, S.R.; Janeczko, R.; Ramirez, F.; Dahl, H.H.M.; C  
J. Biol. Chem. 265, 17070-17077, 1990  
A:Title: A base substitution at a splice site in the COL3A1 gene causes exon skipping  
A:Reference number: A38303; MUID:91009133  
A:Accession: A38303  
A:Molecule type: mRNA  
A:Residues: 861-1015 <COL>  
A:Cross-references: GB:J05617; GB:M55603; GB:M59227; NID:9180878; PIDN:AAB59383.1; PI  
A:Note: a mutant sequence with 942-977 spliced out from a patient with Ehlers-Danlos  
R:Mankoo, B.S.; Dalgleish, R.  
Nucleic Acids Res. 16, 2337, 1988  
A:Title: Human pro alpha1(III) collagen: cDNA sequence for the 3' end.  
A:Reference number: S02119; MUID:88189827  
A:Accession: S02119  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 950-1018, 'Y', 1020-1183, 'S', 1185-1466 <MAN>  
A:Cross-references: EMBL:X06700; NID:930053; PIDN:CAA29886.1; PID:930054  
R:Sejer, J.M.; Kang, A.H.  
Biochemistry 20, 2621-2627, 1981  
A:Title: Covalent structure of collagen: amino acid sequence of alpha1 (III)-CB9 from  
A:Reference number: A90446; MUID:81208139  
A:Accession: A90446  
A:Molecule type: protein  
A:Residues: 965-979, 'A', 981-984, 'PS', 987, 'QN', 990-1096, 'P', 1098-1152, 'AT', 1155, 'S', 11  
A:Experimental source: liver  
R:Loiold, H.R.; Brinker, J.M.; May, M.; PhilaJanietmi, T.; Morrow, S.; Rosenbloom, J.;  
Nucleic Acids Res. 12, 9383-9394, 1984  
A:Title: Molecular cloning and carboxyl-propeptide analysis of human type III procoll  
A:Reference number: A93551; MUID:85087944  
A:Accession: A93551  
A:Molecule type: mRNA  
A:Residues: 1065-1155, 'P', 1157-1466 <LOI>  
A:Cross-references: EMBL:X01655; EMBL:X01742; NID:929584; PIDN:CAA25821.1  
R:Miskulin, M.; Dalgleish, R.; Klueve-Beckerman, B.; Rennard, S.I.; Tolstoshev, P.; Br  
Biochemistry 25, 1408-1413, 1986  
A:Title: Human type III collagen gene expression is coordinately modulated with the c  
A:Reference number: I52393; MUID:86187804  
A:Accession: I52393  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1161-1200 <MIS>  
A:Cross-references: GB:M13146; NID:9180415; PIDN:AA52003.1; PID:9180416  
R:Emanuel, B.S.; Cannizzaro, L.A.; Sejer, J.M.; Myers, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985  
A:Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long  
A:Reference number: I59025; MUID:85216505  
A:Accession: I59025  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1165-1196 <EMA>  
A:Cross-references: GB:M11134; NID:9180417; PIDN:AA52004.1; PID:9180418  
R:Chu, M.L.; Well, D.; de Wel, W.; Bernard, M.; Sippola, M.; Ramirez, F.  
J. Biol. Chem. 260, 4357-4363, 1985  
A:Title: Isolation of cDNA and genomic clones encoding human pro-alpha1(III) collagen

QY	1	TSPGTPAPAAEETMTTSPG	19
		: :	
DB	100	TSPGLTSPGLTDPALTTSPG	118
RESULT	13		
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	probable plgC protein - Mycobacterium tuberculosis (strain H37RV)		
C:Species:	Mycobacterium tuberculosis		
C:Date:	17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999		
C:Accession:	F70888		
R:COLE, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon			
; Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd,			
Rejlanderam, M.A.; Rogers, J.; Rutler, S.; Seeger, K.; Skelton, S.; Squares, S.			
Nature 393, 537-544, 1998			
A:Authors:	Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.		
A>Title:	Deciphering the biology of Mycobacterium tuberculosis from the complete geno-		
A:Reference number:	A70500; MUID:98295987		
A:Accession:	F70888		
A:Status:	Preliminary; nucleic acid sequence not shown; translation not shown		
A:Molecule type:	DNA		
A:Residues:	1-284 <COL>		
A:Cross-references:	GB:A1022076; GB:AL123456; NID:g3256026; PIDN:CAI17874.1; PID:e125		
A:Experimental source:	strain H37RV		
A:Genetics:			
A:Gene:	pirc		
Query Match		47.0%;	Score 47; DB 2; Length 284;
Best Local Similarity		47.4%;	Pred. No. 42;
Matches	9; Conservative	2; Mismatches	8; Indels 0; Gaps 0;
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		: :	
DB	100	TSPGLTSPGLTDPALTTSPG	118
RESULT	14		
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	Probable lipoprotein - Deinococcus radiodurans (strain RI)		
C:Species:	Deinococcus radiodurans		
C:Date:	03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000		
C:Accession:	F75467		
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.			
; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;			
; Smith, H.O.; Venner, J.C.; Fraser, C.M.			
Science 286, 1571-1577, 1999			
A>Title:	Genome sequence of the radioresistant bacterium Deinococcus radiodurans RI.		
A:Reference number:	A75250; MUID:20036896		
A:Accession:	F75467		
A:Status:	Preliminary		
A:Molecule type:	DNA		
A:Residues:	1-375 <WHF>		
A:Cross-references:	GB:AE001939; GB:AE000513; NID:g6458563; PIDN:AAF10427.1; PID:g645		
A:Experimental source:	strain RI		
A:Genetics:			
A:Gene:	DR0848		
A:Map position:	1		
Query Match		47.0%;	Score 47; DB 2; Length 375;
Best Local Similarity		52.9%;	Pred. No. 56;
Matches	9; Conservative	2; Mismatches	6; Indels 0; Gaps 0;
QY	2	TSPGTPAPAAEETMTTSP	18
	:         :		
DB	67	TATPAPAPATPATPAP	83

RESULT	15
S76200	
ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - Synechocystis sp. (strain PCC 6	

C:Species: *Synechocystis* sp.  
 A:Variety: PCC 6803  
 C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
 C:Accession: S76200  
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
 DNA Res. 3, 109-136, 1996  
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*  
 S.  
 A:Reference number: S74322; MUID:97061201  
 A:Accession: S76200  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-413 <KAN>  
 A:Cross-references: EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BAA18459.1; PID:g165354  
 A:Experimental source: PCC 6803  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
 C:Genetics:  
 A:Gene: petH  
 C:Complex: monomer  
 C:Function:  
 A:Description: catalyzes electron transfer from reduced ferredoxin to NADP  
 A:Pathway: photosynthesis  
 A:Note: FAD cofactor  
 C:Superfamily: ferredoxin-NADP+ reductase; cytochrome-b5 reductase homology  
 C:Keywords: electron transfer; FAD; flavoprotein; NADP; oxidoreductase; photosynthesis  
 F:1-112/Domain: signal sequence #status predicted <SIG>  
 F:113-413/Product: ferredoxin-NADP+ reductase #status predicted <MAT>  
 F:121-260/Domain: FAD binding #status predicted <FAD>  
 F:143-398/Domain: cytochrome-b5 reductase homology <CBR>  
 F:261-413/Domain: NADP binding #status predicted <NADP>

Query Match 47.0%; Score 47; DB 2; Length 413;  
 Best Local Similarity 61.5%; Pred. No. 62;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 6 PAPAETMTTSP 18  
 ||| : ||||| :  
 Db 105 PAPSNTMTTTP 117

Search completed: August 13, 2002, 08:30:05  
 Job time: 39 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 13, 2002, 08:36:16 ; Search time 15.81 Seconds

(without alignments)  
46.532 Million cell updates/sec

Title: US-09-826-212-2\_COPY\_215\_233  
Perfect score: 100  
Sequence: 1 TSPGTPAPAAETMTTSPG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100	100.0	259	1 T10C_HUMAN	O14798 h tumor nec
2	54	54.0	440	1 T10B_HUMAN	O14763 homo sapien
3	49.5	49.5	626	1 EXON_HSV11	P04294 herpes simp
4	48	48.0	433	1 HXB3_MOUSE	P09026 mus musculu
5	48	48.0	559	1 FZD1_XENLA	Q919m5 xenopus lae
6	48	48.0	984	1 SX13_MOUSE	O04891 mus musculu
7	48	48.0	1466	1 CA13_HUMAN	P02461 homo sapien
8	47	47.0	284	1 ERP_MYCTU	Q50793 mycobacteri
9	47	47.0	413	1 FENR_STNY3	Q35318 synchocyst
10	47	47.0	1049	1 CA13_BOVIN	P04258 bos taurus
11	47	47.0	1464	1 CA13_MOUSE	P08121 mus musculu
12	47	47.0	2261	1 ABC1_HUMAN	Q95477 homo sapien
13	46.5	46.5	228	1 RPE_RHOCA	P51012 rhodobacter
14	46	46.0	514	1 CSA_DICT1	P08796 dictyosteli
15	46	46.0	706	1 Z151_CHICK	Q90625 gallus gall
16	46	46.0	905	1 SNF5_YEAST	P34880 saccharomyc
17	46	46.0	2442	1 CBP_HUMAN	Q92793 homo sapien
18	45.5	45.5	223	1 VMA7_SVCV	P04888 spring vire
19	45	45.0	275	1 TFE2D_ARPSF	O17488 artemia san
20	45	45.0	340	1 Y480_MYCTU	Q11146 mycobacteri
21	45	45.0	348	1 CDNC_MOUSE	P49919 mus musculu
22	45	45.0	429	1 GSA_XANCH	Q06741 xanthomonas
23	45	45.0	454	1 YAG5_HUMAN	P46937 homo sapien
24	45	45.0	652	1 YD84_HUMAN	Q92923 homo sapien
25	45	45.0	1176	1 MIR_NEUCR	P38681 neurospora
26	44.5	44.5	398	1 CIW4_MOUSE	O88434 mus musculu
27	44	44.0	252	1 BTE4_HUMAN	Q9bxx1 homo sapien
28	44	44.0	333	1 HXAI_RAT	O08656 rattus norv
29	44	44.0	412	1 SEPL_HUMAN	Q14242 homo sapien
30	44	44.0	427	1 DAMX_ECOLI	P11557 escherichia
31	44	44.0	525	1 Y487_TREPPA	O83500 treponema p
32	44	44.0	626	1 GPBA_HUMAN	P07359 homo sapien
33	44	44.0	781	1 YKG7_CAEEL	P46557 caenorhabdi

34	44	44.0	889	1 ENV_STVSP	P19503 simian immu
35	44	44.0	1670	1 CA34_HUMAN	O01955 homo sapien
36	43.5	43.5	839	1 APB1_RAT	O35430 rattus norv
37	43	43.0	137	1 GILZ_MOUSE	O92287 mus musculu
38	43	43.0	205	1 YJ11_MYCTU	O07722 mycobacteri
39	43	43.0	261	1 LPRF_MYCTU	P71798 mycobacteri
40	43	43.0	331	1 HXAI_MOUSE	P09022 mus musculu
41	43	43.0	351	1 OPSP_CHICK	P51475 gallus gall
42	43	43.0	384	1 VASP_CANFA	P50551 canis fami
43	43	43.0	427	1 GSA_PASMU	Q9cm99 pasteurella
44	43	43.0	431	1 HXB3_HUMAN	P14651 homo sapien
45	43	43.0	432	1 GSA_VIBCH	Q9ku97 vibrio chol

## ALIGNMENTS

RESULT 1  
T10C\_HUMAN STANDARD: PRT: 259 AA.  
ID T10C\_HUMAN 014798: 014755:  
AC 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 10C precursor (Decoy receptor 1) (DCR1) (Decoy TRAIL receptor without death domain) (TNF-related apoptosis-inducing ligand receptor 3) (TRAIL receptor-3) (TRAIL-R3) (TRAIL receptor without an intracellular domain) (Lymphocyte inhibitor of TRAIL) (Antagonist decoy receptor for TRAIL/Apo-2L).  
GN TNFRSF10C OR DCR1 OR TRAILR3 OR TRID OR LIT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97467318; PubMed=9325248;  
RA MacFarlane M., Ahmed M., Srinivasula S.M., Fernandes-Alnemri T., Cohen G.M., Alnemri E.S.;  
RT "Identification and molecular cloning of two novel receptors for the cytotoxic ligand TRAIL.";  
RT J. Biol. Chem. 272:25417-25420(1997).  
RN [2]  
RP SEQUENCE FROM N.A. AND CHARACTERIZATION.  
RX MEDLINE=97461602; PubMed=9314565;  
RA Degli-Esposti M.A., Smolak P.J., Walczak H., Waugh J., Huang C.-P., Dubose R.E., Goodwin R.G., Smith C.A.;  
RT "Cloning and characterization of TRAIL-R3, a novel member of the emerging TRAIL receptor family.";  
RT J. Exp. Med. 186:1165-1170(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97390508; PubMed=9242610;  
RA Pan G., Ni J., Wei Y.-F., Yu G.-L., Gentz R., Dixit V.M.;  
RT "An antagonist decoy receptor and a death domain-containing receptor for TRAIL.";  
RT Science 277:815-818(1997).  
RN [4]  
RP SEQUENCE FROM N.A. AND SEQUENCE OF N-TERMINUS.  
RX MEDLINE=97390509; PubMed=9242611;  
RA Sheridan J.P., Marsters S.A., Pitti R.M., Gurney A., Skubatch M., Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I., Goddard A.D., Godowski P., Ashkenazi A.;  
RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy receptors.";  
RT Science 277:818-821(1997).  
RN [5]  
RP SEQUENCE FROM N.A. AND CHARACTERIZATION.  
RX TISSUE=Liver, and Spleen;  
MEDLINE=98039016; PubMed=9373179;  
RA Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N.,

```

Query Match Similarity      100.0%: Score 100; DB 1; Length 259;
Best Local Similarity      100.0%: Pred. No. 3.2e-06;
Matches      19; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

OY      1      TSPGTPAPAAEETMTTSPG 19
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DB      185      TSPGTPAPAAEETMTTSPG 203

RESULT 2
ID      T10B_HUMAN      STANDARD:      PRT; 440 AA.
AC      014763; 015531; 015508; 015517; 014720; Q9BE00.
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      01-MAR-2002 (Rel. 41, Last annotation update)
DE      Tumor necrosis factor receptor superfamily member 10B precursor (Death
DE      receptor 5) (TNF-related apoptosis-inducing ligand receptor 2) (TRAIL
DE      receptor-2) (TRAIL-R2).
GN      TNFRSF10B OR DR5 OR TRAILR2 OR TRICK2 OR KILLER OR ZTNFR9.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A. (LONG ISOFORM), AND SEQUENCE OF N-TERMINUS.
RC      TISSUE=Forestin fibroblast;
RX      MEDLINE=974539925; PubMed=9311198;
RX      Walczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Waugh J.Y.,
RX      Bojani N., Tilmour M.S., Gerhart M.J., Schooley K.A., Smith C.A.,
RX      Goodwin R.G., Rauch C.T.;
RT      "TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";
RL      EMBO J. 16:5386-5397(1997).
RN      [2]
RP      SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS), AND ALTERNATIVE
RP      SPLICING.
RX      MEDLINE=97431692; PubMed=9285725;
RX      Screaton G.R., Mongkolsapaya J., Xu X.-N., Cowper A.E.,
RX      McMichael A.J., Bell J.I.;
RT      "TRICK2, a new alternatively spliced receptor that transduces the
RT      cytotoxic signal from TRAIL.";
RL      Curr. Biol. 7:693-696(1997).
RN      [3]
RP      SEQUENCE FROM N.A. (LONG ISOFORM), AND CHARACTERIZATION.
RP      TISSUE=Liver, and Spleen;
RX      MEDLINE=98039016; PubMed=9373179;
RX      Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N.,
RX      Tschopp J.;
RT      "Characterization of two receptors for TRAIL.";
RL      FEBS Lett. 416:329-334(1997).
RN      [4]
RP      SEQUENCE FROM N.A. (SHORT ISOFORM).
RP      TISSUE=OVARY;
RX      MEDLINE=97467719; PubMed=9326928;
RX      Wu G.S., Burns T.F., McDonald E.R. III, Jiang W., Meng R.,
RX      Kientz I.D., Kao G., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R.,
RX      Spinner N.B., Markowitz S., Wu G., el-Deiry W.S.;
RT      "KILLER/DR5 is a DNA damage-inducible p53-regulated death receptor
RT      gene.";
RL      Nat. Genet. 17:141-143(1997).
RN      [5]
RP      SEQUENCE FROM N.A. (SHORT ISOFORM).
RX      MEDLINE=97390508; PubMed=9242610;
RX      Pan G., Ni J., Wei Y.-F., Yu G.-T., Gentz R., Dixit V.M.;
RT      "An antagonist decoy receptor and a death domain-containing receptor
RT      for TRAIL.";
RL      Science 277:815-818(1997).
RN      [6]
RP      SEQUENCE FROM N.A. (SHORT ISOFORM).
RX      MEDLINE=97467318; PubMed=9325248;
RX      MacFarlane M., Ahmed M., Srinivasula S.M., Fernandes-Alnemri T.,
RX      Cohen G.M., Alnemri E.S.;

```

RT "Identification and molecular cloning of two novel receptors for the  
 RT cytotoxic ligand TRAIL.";  
 RL J. Biol. Chem. 272:25417-25420(1997).  
 RN [7]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RX MEDLINE=98090092; PubMed=9430227;  
 RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;  
 RT "Death receptor 5, a new member of the TNFR family, and DR4 induce  
 RT FADD-dependent apoptosis and activate the NF-kappaB pathway.";  
 RL Immunity 7:821-830(1997).  
 RN [8]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RX MEDLINE=97390509; PubMed=9242611;  
 RA Sheridan J.P., Masters S.A., Pitti R.M., Gurney A., Skubatch M.,  
 RA Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,  
 RA Goddard A.D., Godowski P., Ashkenazi A.;  
 RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy  
 RT receptors.";  
 RL Science 277:818-821(1997).  
 RN [9]  
 RP SEQUENCE FROM N.A. (LONG ISOFORM).  
 RA Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yuasa Y.;  
 RT "Genomic structure and mutation analyses of the DR5/TRAIL receptor 2  
 RT gene in colorectal carcinoma.";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RA Cao X., Zhang W., Man T.;  
 RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [11]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RA Parish T., Vu T., Gilbert T., Gross J., O'Hara P.;  
 RT "Homo sapiens homolog of tumor necrosis factor receptor.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [12]  
 RP SEQUENCE FROM N.A. (LONG ISOFORM).  
 RC TISSUE=Cervix;  
 RA Strausberg R.;  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183.  
 RX MEDLINE=20017034; PubMed=10549288;  
 RA Hymowitz S.G., Christinger H.W., Fuh G., Ullsch M., O'Connell M.,  
 RA Kelley R.F., Ashkenazi A., de Vos A.M.;  
 RT "Triggering cell death: the crystal structure of ApozL/TRAIL in a  
 RT complex with death receptor 5.";  
 RL Mol. Cell 4:563-571(1999).  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184.  
 RX PubMed=10542098;  
 RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,  
 RA Jones E.Y., Screaton G.R.;  
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring  
 RT specificity in apoptotic initiation.";  
 RL Nat. Struct. Biol. 6:1048-1053(1999).  
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL; mediates  
 CC apoptosis in a caspase-dependent manner. Can trigger the nuclear  
 CC factor kappaB-pathway and can bind the cytoplasmic adapter  
 CC molecule FADD/MORT1 which engages initiator caspases such as  
 CC caspase 8 leading to subsequent activation of effector caspases  
 CC that execute apoptotic death of the cell.  
 CC -1- SUBUNIT: Homotrimer (Potential). Can interact with TRADD and RIP.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM/TRICK2B (SHOWN HERE)  
 CC AND A SHORT FORM/TRICK2A; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues;  
 CC very highly expressed in tumor cell lines such as HeLa S3, K562,  
 CC HL-60, SW480, A549 and G361; highly expressed in heart, peripheral  
 CC blood lymphocytes, liver, pancreas, spleen, thymus, prostate,  
 CC ovary, uterus, placenta, testis, esophagus, stomach and throughout  
 CC the intestinal tract; not detectable in brain.  
 CC -1- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.  
 CC -1- DISEASE: Defects in TNFRSF10B may be a cause of squamous cell

CC carcinoma of the head and neck.  
 CC -1- SIMILARITY: CONTAINS 1 IA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: AF016849; AAC51778.1; -  
 DR EMBL: AF018657; AAB70577.1; -  
 DR EMBL: AF018658; AAB70578.1; -  
 DR EMBL: AF016266; AAB81180.1; -  
 DR EMBL: AF022386; AAB71949.1; -  
 DR EMBL: AF012628; AAB67109.1; -  
 DR EMBL: AF020501; AAB71412.1; -  
 DR EMBL: AF016268; AAC01565.1; -  
 DR EMBL: AF012535; AAB67103.1; -  
 DR EMBL: AB014718; BAA33723.1; -  
 DR EMBL: AB014710; BAA33723.1; JOINED.  
 DR EMBL: AB014711; BAA33723.1; JOINED.  
 DR EMBL: AB014712; BAA33723.1; JOINED.  
 DR EMBL: AB014713; BAA33723.1; JOINED.  
 DR EMBL: AB014714; BAA33723.1; JOINED.  
 DR EMBL: AB014715; BAA33723.1; JOINED.  
 DR EMBL: AB014716; BAA33723.1; JOINED.  
 DR EMBL: AB014717; BAA33723.1; JOINED.  
 DR EMBL: AF153687; AAF75587.1; -  
 DR EMBL: AF192548; AAF07175.1; -  
 DR EMBL: BC001281; AAH01281.1; -  
 DR MIM: 603612; -  
 DR MIM: 601400; -  
 DR PDB: 1D0G; 22-OCT-99.  
 DR PDB: 1D4V; 01-NOV-99.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00531; death; 1.  
 DR Pfam: PF00020; TNFR\_c6; 2.  
 DR SMART: SM00005; DEATH; 1.  
 DR SMART: SM00208; TNFR; 2.  
 DR PROSITE: PS50017; DEATH DOMAIN; 1.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 DR Receptor: Apoptosis; Transmembrane; Repeat; Signal;  
 KW Alternative splicing; 3D-structure.  
 FT SIGNAL 1 55  
 FT CHAIN 56 440  
 FT  
 FT DOMAIN 56 210 TUMOR NECROSIS FACTOR RECEPTOR  
 FT TRANSMEM 211 231 SUPERFAMILY MEMBER 10B  
 FT DOMAIN 232 440 EXTRACELLULAR (POTENTIAL).  
 FT REPEAT 97 137 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 138 178 TNFR-CYS 1.  
 FT REPEAT 192 206 TNFR-CYS 2.  
 FT REPEAT 339 422 TAPE.  
 FT DOMAIN 339 422 DEATH.  
 FT DOMAIN 250 253 POLY-GLY.  
 FT DISULFID 81 94  
 FT DISULFID 97 113  
 FT DISULFID 116 129  
 FT DISULFID 119 137  
 FT DISULFID 139 153  
 FT DISULFID 156 170  
 FT DISULFID 160 178  
 FT  
 Query March 54.0%; Score 54; DB 1; Length 440;  
 Best Local Similarity 76.9%; Pred. No. 4.4;  
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 7 APAAEETMTSPG 19  
 ||| |||:|:|

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Db      191 APAVEETVSSPG 203

RESULT 3
EXON_HSV11
ID      EXON_HSV11      STANDARD:      PRT:      626 AA.
AC      P04294;
DT      20-MAR-1987 (Rel. 04, Created)
DT      20-MAR-1987 (Rel. 04, Last sequence update)
DT      01-MAY-1992 (Rel. 22, Last annotation update)
DE      Alkaline exonuclease (EC 3.1.11.-).
CN      U12.
OS      Herpes simplex virus (type 1 / strain 17).
OC      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
CC      Alphaherpesvirinae; Simplexvirus.
OX      NCBI_TaxID=10299;

RN      RP
RP      SEQUENCE FROM N.A.
RX      MEDLINE=88274327; PubMed=2839594;
RA      McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
RA      McNab D., Perry L.J., Scott J.E., Taylor P.;
RT      "The complete DNA sequence of the long unique region in the genome of
RT      herpes simplex virus type 1".
RL      J. Gen. Virol. 69:1531-1574(1988).
RN      RP
RP      SEQUENCE FROM N.A.
RX      MEDLINE=86205244; PubMed=3010237;
RA      McGeoch D.J., Dolan A., Frame M.C.;
RT      "DNA sequence of the region in the genome of herpes simplex virus
RT      type 1 containing the exonuclease gene and neighbouring genes.";
RL      Nucleic Acids Res. 14:3435-3448(1986).
CC      -1- SIMILARITY: BELONGS TO THE HERPESVIRUSES ALKALINE EXONUCLEASE
CC      FAMILY.
CC      -----
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CC      -----
DR      EMBL: D10879; BAA01658.1; -;
DR      EMBL: X14112; CA32325.1; -;
DR      EMBL: X03839; CAA27453.1; -;
DR      PIR: A00781; NDBE61.
DR      PIR: C30083; C30083.
DR      InterPro: IPR001616; Herpes_alk_exo.
DR      Pfam: PF01771; Herpes_alk_exo.1.
DR      PRINTS: PR00924; ALKEXNUCLASE.
DR      Hydrolase; Nuclease; Exonuclease.
SQ      SEQUENCE 626 AA; 67508 MW; 7B86C941A0105035 CRC64;

Query Match      49.5%; Score 49.5; DB 1; Length 626;
Best Local Similarity 64.7%; Pred. No. 24;
Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY      2 SPGTPAPAAEETMTSP 18
      ||| |||| ||: ||
Db      604 SPG-PGPAAAETMTSSSP 619

RESULT 4
HXB3_MOUSE
ID      HXB3_MOUSE      STANDARD:      PRT:      433 AA.
AC      P09026; P10285; Q61680;
DT      01-NOV-1988 (Rel. 09, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      15-JUL-1999 (Rel. 38, Last annotation update)
DE      Homeobox protein Hox-B3 (Hox-2.7) (MH-23).
GN      HOXB3 OR HOXB-3 OR HOX-2.7.
OS      Mus musculus (Mouse).

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OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;

RN      RP
RP      SEQUENCE FROM N.A.
RX      MEDLINE=92258392; PubMed=1582411;
RA      Sham M.H., Hunt P., Nonchev S., Papalopulu N., Graham A.,
RA      Boncinelli E., Krumlauf R.;
RT      "Analysis of the murine Hox-2.7 gene: conserved alternative
RT      transcripts with differential distributions in the nervous system and
RT      the potential for shared regulatory regions.";
RL      EMBO J. 11:1825-1836(1992).
RN      RP
RP      SEQUENCE FROM N.A.
RX      MEDLINE=95196953; PubMed=7890121;
RA      Brown W.M., Taylor G.R.;
RT      "The 5'-sequence of the murine Hox-b3 (Hox-2.7) gene and its intron
RT      contain multiple transcription-regulatory elements.";
RL      Int. J. Biochem. 26:1403-1409(1994).
RN      RP
RP      SEQUENCE OF 152-361 FROM N.A.
RX      MEDLINE=88054465; PubMed=2890503;
RA      Lonai P., Arman E., Czosnek H., Ruddle F.H., Blatt C.;
RT      "New murine homeoboxes: structure, chromosomal assignment, and
RT      differential expression in adult erythropoiesis.";
RL      DNA 6:409-418(1987).
RN      RP
RP      SEQUENCE OF 181-265 FROM N.A.
RX      MEDLINE=89091992; PubMed=2463210;
RA      Graham A., Papalopulu N., Lorimer J., Mcvey J.H., Tuddenham E.G.D.,
RA      Krumlauf R.;
RT      "Characterization of a murine homeo box gene, Hox-2.6, related to the
RT      Drosophila Deformed gene.";
RL      Genes Dev. 2:1424-1438(1988).
CC      -1- FUNCTION: SEQUENCE-SPECIFIC TRANSCRIPTION FACTOR WHICH IS PART OF
CC      A DEVELOPMENTAL REGULATORY SYSTEM THAT PROVIDES CELLS WITH
CC      SPECIFIC POSITIONAL IDENTITIES ON THE ANTERIOR-POSTERIOR AXIS.
CC      -1- SUBCELLULAR LOCATION: Nuclear.
CC      -1- SIMILARITY: BELONGS TO THE ANTP FAMILY OF HOMEOBOX PROTEINS.
CC      -----
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CC      -----
DR      EMBL: X66177; CAA46951.1; -;
DR      EMBL: U02278; AAB60496.1; -;
DR      EMBL: M18168; AAA37840.1; -;
DR      PIR: S20963; S20963.
DR      PIR: C29585; C29585.
DR      HSSP: P02833; ISAN.
DR      TRANSFAC: T01724; -.
DR      MGD: MGI:96184; Hoxb3.
DR      InterPro: IPR001827; Antennapedia.
DR      InterPro: IPR001356; Homeobox.
DR      Pfam: PF00046; homeobox.1.
DR      PRINTS: PR00025; ANTENNAPEDIA.
DR      PRINTS: PR00024; HOMEOBOX.
DR      SMART: SM00389; HOX.1.
DR      PROSITE: PS00027; HOMEOBOX_1.1.
DR      PROSITE: PS00032; ANTENNAPEDIA.1.
DR      PROSITE: PS50071; HOMEOBOX_2.1.
KW      Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW      transcription regulation.
FT      DOMAIN 129 134      ANTP-TYPE HEXAPEPTIDE.
FT      DOMAIN 154 181      GLY-RICH.
FT      DNA_BIND 191 250      HOMEOBOX.
FT      CONFLICT 113 113      G->C (IN REF. 1).
FT      CONFLICT 119 119      A->S (IN REF. 1).
FT      CONFLICT 152 169      GCGGGGGGGGGGGGGG -> RLMMRPAAVVAANAARG

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RX MEDLINE=98201614; PubMed=9524265;  
 RA Kido S., Hirooka Y., Ogawa M., Sakai Y., Yoshimura Y., Also S.;  
 RT "Cloning and characterization of mouse mSox13 cDNA.";  
 RL Gene 208:201-206(1998).  
 RN [3]  
 RP SEQUENCE OF 405-460 FROM N.A.  
 RX MEDLINE=93181275; PubMed=8441686;  
 RA Wright E.M., Snopce B., Koopman P.;  
 RT "Seven new members of the Sox gene family expressed during mouse  
 development";  
 RL Nucleic Acids Res. 21:744-744(1993).  
 CC -1- FUNCTION: BINDS TO THE SEQUENCE 5'-AACAT-3'.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; MAY BE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: IN THE EMBRYO, HIGH LEVELS OF EXPRESSION ARE  
 CC FOUND IN THE ARTERIAL WALLS AT 13.5 DAYS POST COITUM (DPC). LOW  
 CC LEVELS ARE FOUND IN THE INNER EAR AT 13.5 DPC AND IN SOME CELLS IN  
 CC THE THYMUS AT 16.5 DPC. EXPRESSED IN THE TRACHEAL EPITHELIUM BELOW  
 CC THE VOCAL CORD AND IN THE HAIR FOLLICLES AT 18 DPC.  
 CC -1- SIMILARITY: CONTAINS 1 HMG BOX.  
 CC -----  
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 CC -----  
 DR EMBL: AJ000740; CAA04278.1; -  
 DR EMBL: AB006329; BAA25786.1; -  
 DR EMBL: Z18962; CAA79487.1; -  
 DR PIR: S30241; S30241.  
 DR HSSP: O05066; IHRV.  
 DR MGD: MGI:98361; Sox13.  
 DR InterPro: IPR000910; HMG\_12\_box.  
 DR SMART: PF00505; HMG\_box; 2.  
 DR Pfam: PF00505; HMG; 1.  
 KW DNA-binding; Nuclear protein; Alternative splicing.  
 FT DOMAIN 159 195 GLN-RICH.  
 FT DNAS BIND 397 465 HMG BOX.  
 FT VARSPIC 495 519 PGCSPKLHPVSRPSLVARGGLML -> OGAROSYTIIP  
 FT (IN ISOFORM 2).  
 FT VARSPIC 603 609 SMWSQ -> ELVYLD (IN ISOFORM 2).  
 FT VARSPIC 610 984 MISSING (IN ISOFORM 2).  
 FT CONFLICT 35 35 P -> L (IN REF. 2).  
 FT CONFLICT 41 42 AT -> TN (IN REF. 2).  
 FT CONFLICT 195 195 O -> QQ (IN REF. 2).  
 SQ SEQUENCE 984 AA; 108897 MW; 7F5506EDADEB98C5 CRC64;  
 Query Match 48.0%; Score 48; DB 1; Length 984;  
 Best Local Similarity 53.3%; Pred. No. 59;  
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Oy 1 TSPGTPAPAAETMT 15  
 Db 28 TOPGDPAPASODAAAT 42  
 RESULT 7  
 CA13\_HUMAN STANDARD; PRT; 1466 AA.  
 AC P02461; O15112;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Collagen alpha 1(III) chain precursor.  
 GN COL3A1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP Tissue-Skin fibroblast;  
 RX MEDLINE=89350838; PubMed=2764886;  
 RA Ala-Kokko L., Kontusaari S., Balowin C.T., Kuivaniemi H.,  
 RA Prockop D.J.;  
 RT "Structure of cDNA clones coding for the entire prepro alpha 1 (III)  
 RT chain of human type III procollagen. Differences in protein structure  
 RT from type I procollagen and conservation of codon preferences.";  
 RL Biochem. J. 260:509-516(1989).  
 RN [2]  
 RP SEQUENCE OF 149-1225 FROM N.A.  
 RX MEDLINE=89386015; PubMed=2780304;  
 RA Janeczko R.A., Ramirez F.;  
 RT "Nucleotide and amino acid sequences of the entire human alpha 1  
 RT (III) collagen.";  
 RL Nucleic Acids Res. 17:6742-6742(1989).  
 RN [3]  
 RP SEQUENCE OF 168-398.  
 RX MEDLINE=77134724; PubMed=557335;  
 RA Seyer J.M., Kang A.H.;  
 RT "Covalent structure of collagen: amino acid sequence of cyanogen  
 RT bromide peptides from the amino-terminal segment of type III collagen  
 RT of human liver.";  
 RL Biochemistry 16:1158-1164(1977).  
 RN [4]  
 RP REVISIONS.  
 RA Seyer J.M.;  
 RL Submitted (DEC-1977) to the PIR data bank.  
 RN [5]  
 RP SEQUENCE OF 399-727.  
 RX MEDLINE=79000343; PubMed=687591;  
 RA Seyer J.M., Kang A.H.;  
 RT "Covalent structure of collagen: amino acid sequence of five  
 RT consecutive CNBr peptides from type III collagen of human liver.";  
 RL Biochemistry 17:3404-3411(1978).  
 RN [6]  
 RP SEQUENCE OF 728-964.  
 RX MEDLINE=80198282; PubMed=6246925;  
 RA Seyer J.M., Mainardi C., Kang A.H.;  
 RT "Covalent structure of collagen: amino acid sequence of alpha 1  
 RT (III)-CB5 from type III collagen of human liver.";  
 RL Biochemistry 19:1583-1589(1980).  
 RN [7]  
 RP SEQUENCE OF 950-1466 FROM N.A.  
 RX MEDLINE=88189827; PubMed=3357782;  
 RA Mankoo B.S., Dalgleish R.;  
 RT "Human pro alpha 1(III) collagen: cDNA sequence for the 3' end.";  
 RL Nucleic Acids Res. 16:2337-2337(1988).  
 RN [8]  
 RP REVISION TO 1184.  
 RX MEDLINE=89098346; PubMed=3211760;  
 RA Molyneux K., Dalgleish R.;  
 RT "Human type III collagen 'variant' is a cDNA cloning artefact.";  
 RL Nucleic Acids Res. 16:11833-11833(1988).  
 RN [9]  
 RP SEQUENCE OF 1065-1466 FROM N.A.  
 RX MEDLINE=85087944; PubMed=6096827;  
 RA Loidl H.R., Brinker J.M., May M., Pihlajaniemi T., Morrow S.,  
 RA Rosendloom J., Myers J.C.;  
 RT "Molecular cloning and carboxyl-propeptide analysis of human type III  
 RT procollagen.";  
 RL Nucleic Acids Res. 12:9383-9394(1984).  
 RN [10]  
 RP SEQUENCE OF 965-1200.  
 RX MEDLINE=81208139; PubMed=7016180;  
 RA Seyer J.M., Kang A.H.;  
 RT "Covalent structure of collagen: amino acid sequence of alpha  
 RT 1(III)-CB9 from type III collagen of human liver.";  
 RL Biochemistry 20:2621-2627(1981).  
 RN [11]  
 RP SEQUENCE OF 1176-1466 FROM N.A.

RX MEDLINE=85157600; PubMed=2579949;  
 RA Chu M.-L., Weil D., de Wet W.J., Bernard M.P., Sipola M., Ramirez F.;  
 RT "Isolation of cDNA and genomic clones encoding human pro-alpha 1  
 RT (III) collagen. Partial characterization of the 3' end region of the  
 RT gene.";  
 RL J. Biol. Chem. 260:4357-4363(1985).  
 RN [12]  
 RP SEQUENCE OF 1161-1200 FROM N.A.  
 RX MEDLINE=86187804; PubMed=3754462;  
 RA Miskulin M., Dalglish R., Klueve-Beckerman B., Rennard S.I.,  
 RA Tolstoshev P., Brantly M., Crystal R.G.;  
 RT "Human type III collagen gene expression is coordinately modulated  
 RT with the type I collagen genes during fibroblast growth.";  
 RL Biochemistry 25:1408-1413(1986).  
 RN [13]  
 RP SEQUENCE OF 1-170 FROM N.A.  
 RX TISSUE-Placenta;  
 RA Toman D., Ricca G., de Crombrughe B.;  
 RT "Nucleotide sequence of a cDNA coding for the amino-terminal region  
 RT of human prepro alpha 1(III) collagen.";  
 RL Nucleic Acids Res. 16:7201-7201(1988).  
 RN [14]  
 RP SEQUENCE OF 1-176 FROM N.A.  
 RX MEDLINE=89378752; PubMed=2777083;  
 RA Benson-Chanda V., Su M.W., Weil D., Chu M.-L., Ramirez F.;  
 RT "Cloning and analysis of the 5' portion of the human type-III  
 RT procollagen gene (COL3A1).";  
 RL Gene 78:255-265(1989).  
 RN [15]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE=97255959; PubMed=9101290;  
 RA Kuivaniemi H., Tromp G., Prockop D.J.;  
 RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-  
 RT associated collagen (type IX), and network-forming collagen (type X)  
 RT cause a spectrum of diseases of bone, cartilage, and blood vessels.";  
 RL Hum. Mutat. 9:300-315(1997).  
 RN [16]  
 RP VARIANT AORTIC ANEURYSM ARG-303, AND VARIANT THR-668.  
 RX MEDLINE=93293988; PubMed=8514866;  
 RA Tromp G., Wu Y., Prockop D.J., Madhathari S.L., Kleinert C.,  
 RA Barley J.J., Zhang J., Noerregaard O., Darling R.C., Abbott W.M.,  
 RA Cole C.W., Jaakola P., Rynanen M., Pearce W.H., Yao J.S.T.,  
 RA Majamaa K., Smulens S.N., Gatalica Z., Ferrell R.E., Jimenez S.A.,  
 RA Jackson C.E., Michels V.V., Kaye M., Kuivaniemi H.;  
 RT "Sequencing of cDNA from 50 unrelated patients reveals that mutations  
 RT in the triple-helical domain of type III procollagen are an  
 RT infrequent cause of aortic aneurysms.";  
 RL J. Clin. Invest. 91:2539-2545(1993).  
 RN [17]  
 RP VARIANT THR-698.  
 RX MEDLINE=91045136; PubMed=2235526;  
 RA Zafarullah K., Kleinert C., Tromp G., Kuivaniemi H., Kontusaari S.,  
 RA Wu Y., Ganguly A., Prockop D.J.;  
 RT "G to A polymorphism in exon 31 of the COL3A1 gene.";  
 RL Nucleic Acids Res. 18:6180-6180(1990).  
 RN [18]  
 RP VARIANT AORTIC ANEURYSM ARG-786.  
 RX MEDLINE=91056145; PubMed=2243125;  
 RA Kontusaari S., Tromp G., Kuivaniemi H., Romanic A.M., Prockop D.J.;  
 RT "A mutation in the gene for type III procollagen (COL3A1) in a family  
 RT with aortic aneurysms.";  
 RL J. Clin. Invest. 86:1465-1473(1990).  
 RN [19]  
 RP VARIANT EDS-IV ARG-828.  
 RX MEDLINE=94016385; PubMed=8411057;  
 RA Richards A.J., Narcisi P., Lloyd J.C., Ferguson C., Pope F.M.;  
 RT "The substitution of glycine 661 by arginine in type III collagen  
 RT produces mutant molecules with different thermal stabilities and  
 RT causes Ehlers-Danlos syndrome type IV.";  
 RL J. Med. Genet. 30:690-693(1993).  
 RN [20]  
 RP VARIANT EDS-IV SER-957.

RX MEDLINE=89109135; PubMed=2492273;  
 RA Tromp G., Kuivaniemi H., Shikata H., Prockop D.J.;  
 RT "A single base mutation that substitutes serine for glycine 790 of  
 RT the alpha 1 (III) chain of type III procollagen exposes an arginine  
 RT and causes Ehlers-Danlos syndrome IV.";  
 RL J. Biol. Chem. 264:1349-1352(1989).  
 RN [21]  
 RP VARIANT EDS-IV VAL-960.  
 RX MEDLINE=95268429; PubMed=7749417;  
 RA Tromp G., de Paeppe A., Nuytincx L., Madhathari S.L., Kuivaniemi H.;  
 RT "Substitution of valine for glycine 793 in type III procollagen in  
 RT Ehlers-Danlos syndrome type IV.";  
 RL Hum. Mutat. 5:179-181(1995).  
 RN [22]  
 RP VARIANT EDS-IV GLU-1014.  
 RX MEDLINE=92316511; PubMed=1352273;  
 RA Richards A.J., Ward P.N., Narcisi P., Nicholls A.C., Lloyd J.C.,  
 RA Pope F.M.;  
 RT "A single base mutation in the gene for type III collagen (COL3A1)  
 RT converts glycine 847 to glutamic acid in a family with Ehlers-Danlos  
 RT syndrome type IV. An unaffected family member is mosaic for the  
 RT mutation.";  
 RL Hum. Genet. 89:414-418(1992).  
 RN [23]  
 RP VARIANT EDS-IV ASP-1050.  
 RX MEDLINE=90037070; PubMed=2808425;  
 RA Tromp G., Kuivaniemi H., Stolle C.A., Pope F.M., Prockop D.J.;  
 RT "Single base mutation in the type III procollagen gene that converts  
 RT the codon for glycine 883 to aspartate in a mild variant of  
 RT Ehlers-Danlos syndrome IV.";  
 RL J. Biol. Chem. 264:19313-19317(1989).  
 RN [24]  
 RP VARIANT EDS-IV VAL-1077.  
 RX MEDLINE=91374480; PubMed=1895316;  
 RA Richards A.J., Lloyd J.C., Ward P.N., de Paeppe A., Narcisi P.,  
 RA Pope F.M.;  
 RT "Characterisation of a glycine to valine substitution at amino acid  
 RT position 910 of the triple helical region of type III collagen in a  
 RT patient with Ehlers-Danlos syndrome type IV.";  
 RL J. Med. Genet. 28:458-463(1991).  
 RN [25]  
 RP VARIANT EDS-IV GLU-1173.  
 RX MEDLINE=93022543; PubMed=1357232;  
 RA Johnson P.H., Richards A.J., Pope F.M., Hopkinson D.A.;  
 RT "Query Match 48.0%; Score 48; DB 1; Length 1466;  
 RT Best Local Similarity 44.4%; Pred. No. 89;  
 RT Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
 QY 2 SPGTPAPAAEETMTSPG 19  
 Db 1117 APGSPRAGGAGATGSPG 1134  
 ID ERP MYCTU STANDARD: PRT: 284 AA.  
 AC 050793: 053586: Q53468:  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Exported repetitive protein precursor (Cell surface protein plrg)  
 DE (EXP53).  
 GN ERP OR PIRG OR RV3810 OR MT3917 OR MTV026.15.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MT103;  
 RX MEDLINE=96118692; PubMed=7496523;  
 RA Berthet F.-X., Raugier J., Lim E.M., Philipp W., Gicquel B.,

RA Portnoi D.;  
 RT "Characterization of the Mycobacterium tuberculosis erp gene encoding  
 a potential cell surface protein with repetitive structures.";  
 RL Microbiology 141:2123-2130(1995).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 Gordon S.V., Eiglmeier K., Gae S., Barry C.E. III, Tekala F.,  
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 Davies R., Devlin K., Feltham A., Gents J., Hamlin N., Holroyd S.,  
 Horsley R., Jagels K., Kirogh A., McLean J., Moule S., Murphy L.,  
 Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
 Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 Delcher A., Utterback T., Feldman J., Khouri H., Gill J., Mikula A.,  
 Bishal W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 laboratory strains.";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RP SEQUENCE OF 1-24 FROM N.A.  
 RC STRAIN=MT103;  
 RX MEDLINE=95095987; PubMed=7798150;  
 RA Lim E.M., Raubier J., Timm J., Torrea G., Murray A., Gicquel B.,  
 Portnoi D.;  
 RT "Identification of Mycobacterium tuberculosis DNA sequences encoding  
 exported proteins by using phoA gene fusions.";  
 RL J. Bacteriol. 177:59-65(1995).  
 [5]  
 RP CHARACTERIZATION;  
 RX MEDLINE=99008810; PubMed=9784137;  
 RA Berthel F.-X., Lagranderie M., Gounon P., Laurent-Winter C.,  
 Enseigne D., Chavaret P., Thouron F., Maranghi E., Pellicio V.,  
 Portnoi D., Marchal G., Gicquel B.;  
 RT "Attenuation of virulence by disruption of the Mycobacterium  
 tuberculosis erp gene.";  
 RL Science 282:759-762(1998).  
 CC -1- FUNCTION: SURFACE-EXPOSED PROTEIN REQUIRED FOR MULTIPLICATION AND  
 INTRACELLULAR GROWTH.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -1- SIMILARITY: TO M.LEPRAE 28 KDA ANTIGEN.  
 CC -----  
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 CC -----  
 CC EMBL: L38851; AAA96136.1; -;  
 DR EMBL: AL022076; CA11874.1; -;  
 DR EMBL: AE007185; AAK48283.1; -;  
 DR EMBL: S74657; AAB32855.1; -;  
 DR TIGR: MT3917; -;  
 DR TubercuList: RV3810; -;  
 KW Antigen; Transmembrane; Repeat; Signal; Complete proteome.  
 FT SIGNAL 1 22  
 FT CHAIN 23 284  
 FT DOMAIN 23 252  
 FT TRANSMEM 253 273  
 FT DOMAIN 274 284  
 FT POTENTIAL. CYTOPLASMIC (POTENTIAL).

FT DOMAIN 92 121 6 x 5 AA TANDEN REPEATS OF P-[GA]-L-T-S.  
 FT REPEAT 92 96 1-1.  
 FT REPEAT 97 101 1-2.  
 FT REPEAT 102 106 1-3.  
 FT REPEAT 107 111 1-4.  
 FT REPEAT 112 116 1-5.  
 FT REPEAT 117 121 1-6.  
 FT DOMAIN 144 173 6 x 5 AA APPROXIMATE TANDEN REPEATS OF  
 P-[ATG]-[LG]-X-X.  
 FT REPEAT 144 148 2-1.  
 FT REPEAT 149 153 2-2.  
 FT REPEAT 154 158 2-3.  
 FT REPEAT 159 163 2-4.  
 FT REPEAT 164 168 2-5.  
 FT REPEAT 169 173 2-6.  
 FT VARIANT 256 256 A -> V (IN ISOLATE MT103).  
 FT CONFLICT 5 5 R -> S (IN REF. 4).  
 FT CONFLICT 7 7 R -> S (IN REF. 4).  
 SQ SEQUENCE 284 AA; 27700 MW; 1164C7FE3E7ADE42 CRC64;  
 Query Match 47.0%; Score 47; DB 1; Length 284;  
 Best Local Similarity 47.4%; Pred. NO. 22;  
 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 TSPGPAPAEERTMTSPG 19  
 DB 100 TSPGLTSPGLDPAITSPG 118  
 ||||| : | : |||||  
 RESULT 9  
 FENR\_SVNV3  
 ID FENR\_SVNV3 STANDARD; PRT; 413 AA.  
 AC O55318; P74364;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ferredoxin-NADP reductase (EC 1.18.1.2) (FNR).  
 GN PFTH OR SLR1643.  
 OS Synechocystis sp. (strain PCC 6803).  
 CC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 OK NCBI\_TaxID=1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA van Thor J.J.;  
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; PubMed=8905231;  
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 Miyajima N., Hikosawa M., Sugiyama M., Sasamoto S., Kimura T.,  
 Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,  
 Okumura S., Shimpo S., Takeuchi C., Wada T., Matsubae A.,  
 Yamada M., Yasuda M., Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 entire genome and assignment of potential protein-coding regions";  
 RL DNA Res. 3:109-136(1996).  
 CC -1- CATALYTIC ACTIVITY: Reduced ferredoxin + NADP(+) - oxidized  
 ferredoxin + NADPH.  
 CC -1- COFACTOR: FAD.  
 CC -1- SUBCELLULAR LOCATION: MAY BE BOUND TO THE THYLAKOID MEMBRANE OR  
 ANCHORED TO THE THYLAKOID-BOUND PHCOBLISOMES.  
 CC -1- SIMILARITY: IN THE N-TERMINAL REGION, TO PHYCOBLISOME LINKER  
 PROTEIN CPD.  
 CC -1- SIMILARITY: WITH OTHER SPECIES FNR.  
 CC -----  
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CC -----
DR EMBL: X94297; CAA63961.1;
DR EMBL: D90914; BAA18459.1;
DR HSP: P21890; 1BxK
DR InterPro: IPR001685; Cpcd
DR InterPro: IPR001709; Flavyrid_cyt_redctse.
DR Pfam: PF01383; Cpcd; 1.
DR Pfam: PF00175; NAD_binding; 1.
DR PRINTS; PR00371; PNCRC.
DR ProDom: PD002828; Cpcd; 1.
DR Oxidoreductase; Flavoprotein; NADP; FAD; Thylakoid; Membrane;
KW Phycobilisome; Complete proteome.
KW DOMAIN 1
FT DISULFID 231 236 BY SIMILARITY.
FT NE_BIND 265 283 NADP (RIBOSE PART) (BY SIMILARITY).
FT CONFLICT 182 182 E -> K (IN REF. 1).
FT CONFLICT 243 243 D -> S (IN REF. 1).
FT CONFLICT 347 350 QHRV -> STGL (IN REF. 1).
SQ SEQUENCE 413 AA; 46359 MW; FF33709639FC0CA8 CRC64;

Query Match 47.0%; Score 47; DB 1; Length 413;
Best Local Similarity 61.3%; Pred. No. 33;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 PAPAEEETMTSP 18
    111 : :1111:1
Db 105 PAPESNKTMTTTP 117

RESULT 10
CAL3_BOVIN STANDARD; PRT; 1049 AA.
AC P04256;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Collagen alpha 1(III) chain.
GN COL3A1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE OF 1-242.
RX MEDLINE=80026026; Pubmed=488906;
RA Fietzek P.P., Allmann H., Rautenberg J., Henkel W., Wachter E.,
RA Kuhn K.;
RT "The covalent structure of calf skin type III collagen. I. The amino
RT acid sequence of the amino terminal region of the alpha 1(III) chain
RT (positions 1-222).";
RN Hoppe-Seyler's Z. Physiol. Chem. 360:809-820(1979).
[2]
RP SEQUENCE OF 243-422.
RX MEDLINE=80026027; Pubmed=488907;
RA Dewes H., Fietzek P.P., Kuhn K.;
RT "The covalent structure of calf skin type III collagen. II. The amino
RT acid sequence of the cyanogen bromide peptide alpha 1(III)CHL8,10,2
RT (positions 223-402).";
RN Hoppe-Seyler's Z. Physiol. Chem. 360:821-832(1979).
[3]
RP SEQUENCE OF 423-571.
RX MEDLINE=80026028; Pubmed=488908;
RA Bertz H., Fietzek P.P., Kuhn K.;
RT "The covalent structure of calf skin type III collagen. III. The
RT amino acid sequence of the cyanogen bromide peptide alpha 1(III)CH4
RT (positions 403-551).";
RN Hoppe-Seyler's Z. Physiol. Chem. 360:833-840(1979).
[4]
RP SEQUENCE OF 572-808.

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RX MEDLINE=80026029; Pubmed=488909;
RA Lang H., Glanville R.W., Fietzek P.P., Kuhn K.;
RT "The covalent structure of calf skin type III collagen. IV. The amino
RT acid sequence of the cyanogen bromide peptide alpha 1(III)CB5
RT (positions 552-788).";
RN Hoppe-Seyler's Z. Physiol. Chem. 360:841-850(1979).
[5]
RP SEQUENCE OF 809-947.
RX MEDLINE=80026030; Pubmed=488910;
RA Dewes H., Fietzek P.P., Kuhn K.;
RT "The covalent structure of calf skin type III collagen. V. The amino
RT acid sequence of the cyanogen bromide peptide alpha 1(III)CB9A
RT (position 789-927).";
RN Hoppe-Seyler's Z. Physiol. Chem. 360:851-860(1979).
[6]
RP SEQUENCE OF 948-1049.
RX MEDLINE=80026031; Pubmed=488911;
RA Allmann H., Fietzek P.P., Glanville R.W., Kuhn K.;
RT "The covalent structure of calf skin type III collagen. VI. The amino
RT acid sequence of the carboxyterminal cyanogen bromide peptide alpha
RT 1(III)CB9B (positions 928-1028).";
RN Hoppe-Seyler's Z. Physiol. Chem. 360:861-868(1979).
[7]
CC -1 FUNCTION: COLLAGEN TYPE III OCCURS IN MOST SOFT CONNECTIVE TISSUES
CC ALONG WITH TYPE I COLLAGEN.
CC -1 SUBUNIT: TRIMERS OF IDENTICAL ALPHA 1(III) CHAINS. THE CHAINS ARE
CC LINKED TO EACH OTHER BY INTERCHAIN DISULFIDE BONDS. TRIMERS ARE
CC ALSO CROSS-LINKED VIA HYDROXYLISINES.
CC -1 UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
DR PIR: A02862; CGB07S.
DR InterPro: IPR000087; Collagen.
DR InterPro: IPR001007; WMFC.
DR Pfam: PF01391; Collagen; 17.
DR PROSITE: PS01208; WMFC; PARTIAL.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Collagen.
FT DOMAIN 1 14 NONHELICAL REGION (N-TERMINAL).
FT DOMAIN 15 1040 TRIPLE-HELICAL REGION.
FT DOMAIN 1041 1049 NONHELICAL REGION (C-TERMINAL).
FT MOD_RES 95 95 HYDROXYLATION.
FT MOD_RES 107 107 HYDROXYLATION.
FT MOD_RES 119 119 HYDROXYLATION.
FT MOD_RES 938 938 HYDROXYLATION.
FT MOD_RES 950 950 HYDROXYLATION.
FT CARBOHYD 107 107 O-LINKED (GAL. . .).
FT CARBOHYD 950 950 O-LINKED (GAL. . .).
FT DISULFID 1040 1040 INTERCHAIN.
FT DISULFID 1041 1041 INTERCHAIN.
SQ SEQUENCE 1049 AA; 93651 MW; 8EEC33D1C66EC9A3 CRC64;

Query Match 47.0%; Score 47; DB 1; Length 1049;
Best Local Similarity 44.4%; Pred. No. 85;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 2 SPGTPAPAEEETMTSPG 19
    111 : :111
Db 961 APGSPGAGHGAGVSGSPG 978

RESULT 11
CAL3_MOUSE STANDARD; PRT; 1464 AA.
AC P08121; O61429; Q9CRN7;
DT 01-AUG-1988 (Rel. 08, Created)
DT 15-JUL-1998 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Collagen alpha 1(III) chain precursor.
GN COL3A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL X DBA; TISSUE=Embryo;
RX MEDLINE=95011609; PubMed=7926795;
RA Toman D., de Crombrughe B.;
RT "The mouse type-III procollagen-encoding gene: genomic cloning and
  complete DNA sequence."
RL Gene 147:161-168(1994).
RN [2]
RP SEQUENCE OF 1-488 FROM N.A.
RX MEDLINE=88167858; PubMed=3443309;
RA Wood L., Theriault N., Vogel G.;
RT "Complete nucleotide sequence of the N-terminal domains of the murine
  alpha-1 type-III collagen chain."
RL Gene 61:225-230(1987).
RN [3]
RP SEQUENCE OF 1-28 FROM N.A.
RX MEDLINE=85131189; PubMed=3972847;
RA Liau G., Mudryj M., de Crombrughe B.;
RT "Identification of the promoter and first exon of the mouse alpha 1
  (III) collagen gene."
RL J. Biol. Chem. 260:3773-3777(1985).
RN [4]
RP SEQUENCE OF 810-1464 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryonic head;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
  Aikawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
  Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
  Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
  Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
  Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
  Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
  Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
  Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,
  Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
  Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
  Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
  Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
  Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
  Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
  Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
  Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [5]
RP SEQUENCE OF 1442-1464 FROM N.A.
RC STRAIN=C57BL;
RX MEDLINE=91274355; PubMed=2054384;
RA Metcarranta M., Toman D., de Crombrughe B., Vuorio E.;
RT "Specific hybridization probes for mouse type I, II, III and IX
  collagen mRNAs."
RL Biochim. Biophys. Acta 1089:241-243(1991).
CC -1- FUNCTION: COLLAGEN TYPE III OCCURS IN MOST SORT CONNECTIVE TISSUES
  ALONG WITH TYPE I COLLAGEN.
CC -1- SUBUNIT: TRIMERS OF IDENTICAL ALPHA 1(III) CHAINS. THE CHAINS ARE
  LINKED TO EACH OTHER BY INTERCHAIN DISULFIDE BONDS. TRIMERS ARE
  ALSO CROSS-LINKED VIA HYDROXYLYSINES.
CC -1- PTM: PROLINES AT THE THIRD POSITION OF THE TRPEPTIDE REPEATING
  UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC O-LINKED GLYCAN CONSISTS OF GLC-GAL DISACCHARIDE (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 VWFC DOMAIN.
CC -----
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CC -----
DR EMBL; X52046; CAA36279.1; -

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DR EMBL; M18933; AAA37338.1; -
DR EMBL; K03037; -; NOT_ANNOTATED_CDS.
DR EMBL; AK019448; BAB31724.1; -
DR EMBL; X57983; CAA41048.1; -
DR PIR; A22287; A22287.
DR PIR; A27353; A27353.
DR PIR; S16373; S16373.
DR MGI; MGI:88453; Col3a1.
DR InterPro; IPR000087; Collagen.
DR InterPro; IPR000885; Fib_collagen_C.
DR InterPro; IPR001007; VWFC.
DR Pfam; PF01410; COLF1; 1.
DR Pfam; PF01391; COLLAGEN; 17.
DR ProDom; PD002078; Fib_collagen_C; 1.
DR SMART; SM00038; COLF1; 1.
DR SMART; SM00214; VWFC; 1.
DR PROSITE; PS01208; VWFC; 1.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Collagen; Signal.
FT SIGNAL 1 23
FT PROPEP 24 154
FT CHAIN 155 1203
FT PROPEP 1204 1464
FT DOMAIN 31 90
FT DOMAIN 155 169
FT CARBOHD 262 262
FT MOD_RES 262 262
FT MOD_RES 283 283
FT MOD_RES 859 859
FT MOD_RES 976 976
FT MOD_RES 1093 1093
FT MOD_RES 1105 1105
FT DISULFD 1196 1195
FT DISULFD 1196 1196
FT SEQUENCE 1464 AA; 138944 MW; 2104EC27A886090B CRC64;
SQ
Query Match 47.0%; Score 47; DB 1; Length 1464;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
QY 2 SPGTPAPAAEETMTTSPG 19
Db 453 SPGTPGPKGEDGKDGSPG 470
RESULT 12
ABCI_HUMAN STANDARD; PRT; 2261 AA.
AC 095477; Q9UN08; Q9UN07; Q9UN06; Q9N0V4; Q9UN09; Q96T85; Q96S56;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette
DE transporter 1) (ATP-binding cassette 1) (ABC-1) (Cholesterol efflux
DE regulatory protein).
GN ABCI OR ABC1 OR CERP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20345099; PubMed=10884428;
RA Santamarina-Pojo S., Peterson K.M., Knapper C.L., Qiu Y.,
RA Freeman L.A., Cheng J.-F., Osorio J., Remaley A.T., Yang X.-P.,
RA Handen Schild C.C., Prades C., Chimini G., Blackmon E.E.,
RA Francois T.L., Duverger N., Rubin E.M., Rosier M., Denefle P.,
RA Fredrickson D.S., Brewer H.B. Jr.;
RT "Complete genomic sequence of the human ABCI1 gene: analysis of the
  human and mouse ATP-binding cassette A promoter."

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Proc. Natl. Acad. Sci. U.S.A. 97:7987-7992(2000).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-SKIN;  
 RA Schwartz K., Lawn R.M., Wade D.P.;  
 RT "ABCA1 gene expression and apoA-I-mediated cholesterol efflux are  
 regulated by LXR.";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21251004; PubMed=11352567;  
 RA Qiu Y., Cavellier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;  
 RT "Human and mouse ABCA1 comparative sequencing and transgenesis  
 studies revealing novel regulatory sequences.";  
 RL Genomics 73:66-76(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Tanaka A.R., Abe-Dohmae S., Arakawa R., Sadanami K., Kidera A.,  
 RA Kioka N., Amachi T., Yokoyama S., Ueda K.;  
 RT "A new topological model of functional human ABCA1-signal peptide  
 cleavage and glycosylation of a large extracellular domain.";  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 21-2261 FROM N.A.  
 RX MEDLINE=99194549; PubMed=10092505;  
 RA Langmann T., Klucken J., Reil M., Liebisch G., Luciani M.F.,  
 RA Chmial G., Kaminski W.E., Schmitz G.;  
 RT "Molecular cloning of the human ATP-binding cassette transporter 1  
 (ABCA1): evidence for sterol-dependent regulation in macrophages.";  
 RL Biochem. Biophys. Res. Commun. 257:29-33(1999).  
 RN [6]  
 RP SEQUENCE OF 21-2261 FROM N.A.  
 RX MEDLINE=99364413; PubMed=10431238;  
 RA Rust S., Rosier M., Funke H., Reil J., Amoura Z., Plette J.-C.,  
 RA Delzenne J.-F., Brewer H.B., Duverger N., Denefle P., Assmann G.;  
 RT "Tangier disease is caused by mutations in the gene encoding  
 ATP-binding cassette transporter 1.";  
 RL Nat. Genet. 22:352-355(1999).  
 RN [7]  
 RP VARIANTS FHA THR-1091 AND 1893-GLU-ASP-1894 DEL.  
 RX MEDLINE=20001430; PubMed=10533863;  
 RA Marcel M., Brooks-Wilson A., Clee S.M., Roomp K., Zhang L.-H., Yu L.,  
 RA Collins J.A., van Dam M., Molhuizen H.O.F., Loubser O.,  
 RA Ouellete B.F.F., Senses C.W., Fichter K., Mott S., Denis M.,  
 RA Boucher B., Pimstone S., Genest J. Jr., Kastelein J.J.P., Hayden M.R.;  
 RT "Mutations in the ABC1 gene in familial HDL deficiency with defective  
 cholesterol efflux.";  
 RL Lancet 354:1341-1346(1999).  
 RN [8]  
 RP VARIANTS TD ARG-597 AND ARG-1477, AND VARIANT FHA LEU-693 DEL.  
 RX MEDLINE=99364411; PubMed=10431236;  
 RA Brooks-Wilson A., Marcel M., Clee S.M., Zhang L.-H., Roomp K.,  
 RA van Dam M., Yu L., Brewer C., Collins J.A., Molhuizen H.O.F.,  
 RA Loubser O., Ouellete B.F.F., Fichter K., Ashbourne-Excoffon K.J.D.,  
 RA Senses C.W., Scherer S., Mott S., Denis M., Martindale D.,  
 RA Frohlich J., Morgan K., Koop B., Pimstone S., Kastelein J.J.P.,  
 RA Hayden M.R.;  
 RT "Mutations in ABC1 in Tangier disease and familial high-density  
 lipoprotein deficiency.";  
 RL Nat. Genet. 22:336-345(1999).  
 RN [9]  
 RP VARIANTS TD SER-590; SER-935 AND VAL-937, AND VARIANTS ALA-399 AND  
 RP MET-883.  
 RX MEDLINE=99364412; PubMed=10431237;  
 RA Bodzioch M., Orso E., Klucken J., Langmann T., Boettcher A.,  
 RA Diedrich W., Drobnik W., Barlage S., Buechler C.,  
 RA Porsch-Ozcurumen M., Kaminski J.W.E., Hahnemann H.W., Oette K.,  
 RA Rothe G., Aslanidis C., Lackner K.J., Schmitz G.;  
 RT "The gene encoding ATP-binding cassette transporter 1 is mutated in  
 Tangier disease.";  
 RL Nat. Genet. 22:347-351(1999).  
 RN [10]  
 RP VARIANTS TD ILE-929; ARG-597 AND ARG-1477, AND VARIANTS FHA LEU-693

DEL; THR-1091; 1893-GLU-ASP-1894 DEL AND LEU-2150.  
 RX MEDLINE=20540002; PubMed=11086027;  
 RA Clee S.M., Kastelein J.J.P., van Dam M., Marcel M., Roomp K.,  
 RA Zwarts K.Y., Collins J.A., Roelants R., Tamawwa N., Stlic T.,  
 RA Suda T., Geska R., Boucher B., Rondeau C., Desouch C.,  
 RA Brooks-Wilson A., Molhuizen H.O.F., Frohlich J., Genest J. Jr.,  
 RA Hayden M.R.;  
 RT "Age and residual cholesterol efflux affect HDL cholesterol levels and  
 coronary artery disease in ABCA1 heterozygotes.";  
 RL J. Clin. Invest. 106:1263-1270(2000).  
 RN [11]  
 RP VARIANTS TD ASN-1289 AND HIS-1800.  
 RX MEDLINE=20171564; PubMed=10706591;  
 RA Brousseau M.E., Schaefer E.J., Dupuis J., Eustace B.,  
 RA Van Berendse P., Goldkamp A.L., Thurston L.M., Fitzgerald M.G.,  
 RA Vasek-McKenna D., O'Neill G., Eberhart G.P., Weiffenbach B.,  
 RA Ordovas J.M., Freeman M.W., Brown R.H. Jr., Gu J.Z.;  
 RT "Novel mutations in the gene encoding ATP-binding cassette 1 in four  
 Tangier disease kindreds.";  
 RL J. Lipid Res. 41:433-441(2000).  
 RN [12]  
 RP VARIANT TD ASP-1046, VARIANT FHA CYS-230, AND VARIANTS LYS-219;  
 RP ILE-825, MET-883 AND LYS-1587.  
 RX MEDLINE=20396633; PubMed=10938021;  
 RA Wang J., Burnett J.R., Near S., Young K., Zimman B., Hanley A.J.G.,  
 RA Connelly P.W., Harris S.B., Hegele R.A.;  
 RT "Common and rare ABCA1 variants affecting plasma HDL cholesterol.";  
 RL Arterioscler. Thromb. Vasc. Biol. 20:1983-1989(2000).  
 RN [13]  
 RP VARIANT TD TRP-587, AND VARIANT LEU-2168.  
 RX MEDLINE=21157002; PubMed=11257260;  
 RA Bertolini S., Pisciotto L., Serl M., Cusano R., Cantafora A.,  
 RA Calabresi L., Franceschini G., Ravazzolo R., Calandra S.;  
 RT "A point mutation in ABC1 gene in a patient with severe premature  
 coronary heart disease and mild clinical phenotype of Tangier  
 disease.";  
 RL Atherosclerosis 154:599-605(2001).  
 RN [14]  
 RP VARIANTS LYS-219; MET-883 AND ASP-1172.  
 RX MEDLINE=21157003; PubMed=11257261;  
 RA Brousseau M.E., Bodzioch M., Schaefer E.J., Goldkamp A.L., Kiejar D.,  
 RA Probst M., Ordovas J.M., Aslanidis C., Lackner K.J.,  
 RA Bloomfield Rubins H., Collins D., Robins S.J., Wilson P.W.F.,  
 RA Schmitz G.;  
 RT "Common variants in the gene encoding ATP-binding cassette transporter  
 1 in men with low HDL cholesterol levels and coronary heart disease.";  
 RL Atherosclerosis 154:607-611(2001).  
 RN [15]  
 RP VARIANT TD LEU-1506.  
 RX MEDLINE=21369429; PubMed=11476961;  
 RA Lapicka-Bodzioch K., Bodzioch M., Kruehl M., Kiejar D., Probst M.,  
 RA Kiec B., Andrikovics H., Boettcher A., Hubacek J., Aslanidis C.,  
 RA Sutrop N., Schmitz G.;  
 RT "Homogeneous assay based on 52 primer sets to scan for mutations of  
 the ABCA1 gene and its application in genetic analysis of a new  
 patient with familial high-density lipoprotein deficiency syndrome.";  
 RL Biochim. Biophys. Acta 1537:42-48(2001).  
 RN [16]  
 RP VARIANTS TD ASN-1289 AND TRP-2081, AND VARIANT LYS-219.  
 RX MEDLINE=21369433; PubMed=11476965;  
 RA Huang W., Moriyama K., Koga T., Hua H., Ageta M., Kawabata S.,  
 RA Mawatari K., Imamura T., Eto T., Kawamura M., Teramoto T., Sasaki J.;  
 RT "Novel mutations in ABCA1 gene in Japanese patients with Tangier  
 disease and familial high density lipoprotein deficiency with  
 coronary heart disease.";  
 RL Biochim. Biophys. Acta 1537:71-78(2001).  
 RN [17]  
 RP VARIANTS LYS-219; ALA-399; MET-771; PRO-774; ASN-776; ILE-825;  
 RP MET-883; ASP-1172; LYS-1587 AND CYS-1731.  
 RX MEDLINE=21198379; PubMed=11238261;  
 RA Clee S.M., Zwinderman A.H., Engert J.C., Zwarts K.Y.,  
 RA Molhuizen H.O.F., Roomp K., Jukema J.W., van Wijkland M., van Dam M.,  
 RA Hudson T.J., Brooks-Wilson A., Genest J. Jr., Kastelein J.J.P.,

RA Hayden M.R.;  
 RT "Common genetic variation in ABCA1 is associated with altered  
 RT lipoprotein levels and a modified risk for coronary artery disease.";  
 RL Circulation 103:1198-1205(2001).  
 RN [18]  
 RP VARIANT TD THR-255, AND VARIANT ATHEROSCLEROSIS ASP-1611.  
 RX MEDLINE-21645894; PubMed-11785958;  
 RA Nishida Y., Hirano K., Tsukamoto K., Nagano M., Ikegami C., Roomp K.,  
 RA Ishihara M., Sakane N., Zhang Z., Tsuji K., Matsuyama A., Ohama T.,  
 RA Matsura F., Ishigami M., Sakai N., Hirooka H., Hattori H.,  
 RA Wellington C., Yoshida Y., Misugi S., Hayden M.R., Egashira T.,  
 RA Yamashita S., Matsuzawa Y.;  
 RT "Expression and functional analyses of novel mutations of ATP-binding  
 RT cassette transporter-1 in Japanese patients with high-density  
 RT lipoprotein deficiency.";  
 RL Biochem. Biophys. Res. Commun. 290:713-721(2002).  
 CC -1- FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION  
 CC TRANSPORTER. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL  
 CC TRANSPORT.  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, BUT MOST ABUNDANT IN  
 CC MACROPHAGES.  
 CC -1- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,  
 CC EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN  
 CC ATP BINDING CASSETTE (ABC) DOMAIN.  
 CC -1- DISEASE: DEFECTS IN ABCA1 ARE A CAUSE OF HIGH DENSITY LIPOPROTEIN  
 CC DEFICIENCY TYPE I (HDL1), ALSO KNOWN AS TANGIER DISEASE (TD). TD  
 CC IS A RECESSIVE DISORDER CHARACTERIZED BY ABSENCE OF HIGH DENSITY  
 CC LIPOPROTEIN (HDL) CHOLESTEROL FROM PLASMA, HEPATOSPLENOMEGALY,  
 CC PERIPHERAL NEUROPATHY, AND FREQUENTLY PREMATURE CORONARY ARTERY  
 CC DISEASE (CAD).  
 CC -1- DISEASE: Defects in ABCA1 are a cause of high density lipoprotein

Query Match 47.0%; Score 47; DB 1; Length 2261;  
 Best Local Similarity 56.2%; Pred. No. 1.9e+02;  
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Oy 3 PGTPAPAAEEMTTPSP 18  
 Db 1425 PDRPQAGEEMTTPAP 1440

RESULT 13  
 REPE\_RHOCA STANDARD; PRT; 228 AA.  
 ID REPE\_RHOCA  
 AC P51012;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ribulose-phosphate 3-epimerase (EC 5.1.3.1) (Pentose-5-phosphate 3-  
 DE epimerase) (PPE) (R3P3E).  
 GN CBBE.  
 OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;  
 OC Rhodobacter.  
 OX NCBI\_TaxID=1061;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 11166;  
 RA Latimer F.W., Lu T.-Y.S., Buley D.M.;  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: D-ribulose 5-phosphate = D-xylulose 5-  
 CC phosphate.  
 CC -1- PATHWAY: CALVIN CYCLE.  
 CC -1- SIMILARITY: BELONGS TO THE RIBULOSE-PHOSPHATE 3-EPIMERASE FAMILY.  
 CC -----  
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DR EMBL: U23145; AAB82049.1; -.  
 DR HSSP; Q43843; IRPX.  
 DR InterPro: IPR000056; Ribul\_P\_3\_epim.  
 DR Pfam: PF00834; Ribul\_P\_3\_epim; 1.  
 DR PROSITE; PS01085; RIBUL\_P\_3\_EPIMER\_1; 1.  
 DR PROSITE; PS01086; RIBUL\_P\_3\_EPIMER\_2; FALSE\_NEG.  
 KW Isomerase; Carbohydrate metabolism; Calvin cycle.  
 SQ SEQUENCE 228 AA; 23878 MW; FCD392695BCD396B CRC64;

Query Match 46.5%; Score 46.5; DB 1; Length 228;  
 Best Local Similarity 40.7%; Pred. No. 21;  
 Matches 11; Conservative 2; Mismatches 5; Indels 9; Gaps 1;

Oy 2 SPGRPAPAAE-----TMTTSPG 19  
 Db 120 NPGTPAAEIEHVLDIADYVCWTVNPG 146

RESULT 14  
 CSA\_DICDI STANDARD; PRT; 514 AA.  
 ID CSA\_DICDI  
 AC P08796; P19408;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Contact site A protein precursor (CSA) (Membrane-associated  
 DE glycoprotein gp80) (Cell adhesion molecule gp80).  
 GN CSA.  
 OS Dictyostelium discoideum (Slime mold).  
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.  
 OX NCBI\_TaxID=44689;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Noegel A., Gerisch G., Stadler J., Westphal M.;  
 RT "Complete sequence and transcript regulation of a cell adhesion  
 RT protein from aggregating Dictyostelium cells.";  
 RL EMBO J. 5:1473-1476(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-69105362; PubMed-3063296;  
 RA Siu C.-H., Wong L.M., Lam T.Y., Kamboj R.K., Choi A., Cho A.;  
 RT "Molecular mechanisms of cell-cell interaction in Dictyostelium  
 RT discoideum.";  
 RL Biochem. Cell Biol. 66:1089-1099(1988).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=AX2;  
 RX MEDLINE-92406924; PubMed-1326559;  
 RA Desbarats L., Lam T.Y., Wong L.M., Siu C.H.;  
 RT "Identification of a unique CAMP-response element in the gene  
 RT encoding the cell adhesion molecule gp80 in Dictyostelium  
 RT discoideum.";  
 RL J. Biol. Chem. 267:19655-19664(1992).  
 RN [4]  
 RP SEQUENCE OF 20-49.  
 RA Wong L.M., Siu C.-H.;  
 RT "Cloning of cDNA for the contact site A glycoprotein of Dictyostelium  
 RT discoideum";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:4248-4252(1986).  
 RN [5]  
 RP CELL-BINDING DOMAIN.  
 RX MEDLINE-69034443; PubMed-3182938;  
 RA Kamboj R.K., Wong L.M., Lam T.Y., Siu C.H.;  
 RT "Mapping of a cell-binding domain in the cell adhesion molecule gp80  
 RT of Dictyostelium discoideum.";  
 RL J. Cell Biol. 107:1835-1843(1988).  
 RN [6]  
 RP GPI-ANCHOR.  
 RX MEDLINE-69251561; PubMed-2721485;  
 RA Stadler J., Keenan T.W., Bauer G., Gerisch G.;  
 RT "The contact site A glycoprotein of Dictyostelium discoideum carries  
 RT a phospholipid anchor of a novel type";

RL EMBL J. 8:371-377(1989).  
CC -1- FUNCTION: THIS CELL-SURFACE GLYCOPROTEIN MEDIATES CELL-CELL  
CC BINDING VIA HOMOPHILIC INTERACTION.  
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR  
CC THAT CONTAINS A PHOSPHOCERAMIDE MOIETY. SUCH ANCHOR MEDIATES A  
CC FAST AND LONG PERSISTENCE CELL ADHESION OF THE PROTEIN.  
CC -1- DEVELOPMENTAL STAGE: RESTRICTED TO THE AGGREGATION STAGE OF  
CC DEVELOPMENT OF D.DISCOIDEUM.  
CC -1- PTM: ACETYLATED, PHOSPHORYLATED ON SERINE AND N-GLYCOSYLATED WITH  
CC TWO TYPES OF OLIGOSACCHARIDE CHAINS.  
CC -1- MISCELLANEOUS: THE EXPRESSION OF THIS STRINGENTLY REGULATED  
CC PROTEIN DURING CELL DEVELOPMENT IS MEDIATED THROUGH CELL-SURFACE  
CC CAMP RECEPTORS.  
CC -1- SIMILARITY: THE C-TERMINAL REGION CONTAINS CLUSTERS OF PROLINE  
CC REGULARLY ALTERNATING WITH A HYDROXYAMINO ACID AND SHOWS  
CC SIMILARITY TO THE HINGE REGION OF IMMUNOGLOBULINS. THIS DOMAIN  
CC MIGHT ACT AS A SPACER TO ELEVATE SITES ACTIVE IN CELL CONTACT  
CC INTO THE EXTRACELLULAR SPACE.  
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CC -----  
DR EMBL: X04004; CAA27634.1; -;  
DR EMBL: M36545; AAA33212.1; -;  
DR EMBL: X66483; CAA47110.1; -;  
DR PIR: A23951; A23951.  
DR PIR: A26310; A26310.  
DR PIR: A31643; A31643.  
DR PIR: S22066; S22066.  
DR PIR: A44100; A44100.  
DR Dictydb: DD02005; csaa.  
DR InterPro: IPR002909; IPT\_TIG.  
DR Pfam: PF01833; TIG. 3.  
KW Cell adhesion; Glycoprotein; Membrane; Phosphorylation; Repeat;  
KW GPI-anchor; Lipoprotein; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 492  
FT PROPEP 493 514  
FT DOMAIN 20 453  
FT DOMAIN 454 485  
FT DOMAIN 462 479  
FT REPEAT 462 469  
FT REPEAT 472 479  
FT CARBOHYD 128 128  
FT CARBOHYD 137 137  
FT CARBOHYD 207 207  
FT CARBOHYD 294 294  
FT CARBOHYD 399 399  
FT LIPID 492 492  
FT CONFLICT 216 216  
SQ SEQUENCE 514 AA; 53696 MW; 96A1C7CF42FEC096 CRC64;  
  
Query Match 46.0%; Score 46; DB 1; Length 514;  
Best Local Similarity 50.0%; Pred. No. 55;  
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 TSPGTPAPAAETMTTSP 18  
| | | | | | | | | |  
Db 460 TDTATPSPPTPETATPSP 477  
  
RESULT 15  
ID 2151\_CHICK STANDARD; PRT; 706 AA.  
AC 090625;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Zinc finger protein 151 (Zinc finger protein 213) (Fragment).  
OS Gallus gallus (Chicken).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
CC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=96003919; PubMed=7575457;  
RA Schulz T.C., Hopwood B., Rathjen P.D., Wells J.R.E.;  
RT "An unusual arrangement of 13 zinc fingers in the vertebrate gene  
RT Z13."  
RL Biochem. J. 311:219-224(1995).  
CC -1- SUBCELLULAR LOCATION: Nuclear (potential).  
CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-  
CC FINGER PROTEINS.  
CC -1- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: U14555; AAA21556.1; -;  
DR HSSP: P08047; ISP2.  
DR InterPro: IPR000210; BTB\_POZ.  
DR InterPro: IPR000822; Znf-C2H2.  
DR Pfam: PF00096; Zf-C2H2. 13.  
DR SMART: SM00355; Znf\_C2H2. 13.  
DR PROSITE: PS50097; BTB, PARTIAL.  
DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; 12.  
DR PROSITE: PS50157; ZINC\_FINGER\_C2H2\_2; 13.  
KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;  
KW Nuclear protein; Repeat.  
FT NON\_TER 1 1  
FT DOMAIN <1 12  
FT DOMAIN 205 640  
FT ZN\_FING 205 227  
FT ZN\_FING 233 255  
FT ZN\_FING 261 283  
FT ZN\_FING 289 311  
FT ZN\_FING 317 339  
FT ZN\_FING 345 367  
FT ZN\_FING 373 395  
FT ZN\_FING 401 423  
FT ZN\_FING 427 450  
FT ZN\_FING 457 479  
FT ZN\_FING 485 507  
FT ZN\_FING 513 536  
FT ZN\_FING 618 640  
SQ SEQUENCE 706 AA; 76820 MW; 4BDAC68808F1136 CRC64;  
  
Query Match 46.0%; Score 46; DB 1; Length 706;  
Best Local Similarity 50.0%; Pred. No. 76;  
Matches 9; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
  
QY 2 SPGTPAPAAETMTTSPG 19  
| | | | | | | | | |  
Db 99 SPSRPGPAESEVGNSSPG 116  
  
Search completed: August 13, 2002, 08:36:17  
Job time: 366 sec

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GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: August 13, 2002, 08:37:06 ; Search time 43.32 seconds  
(without alignments)  
75.875 Million cell updates/sec

Title: US-09-826-212-2\_COPY\_215\_233  
Perfect score: 100  
Sequence: 1 TSPGPAPAEETMTSPG 19

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeophages:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	55	55.0	956	10	Q9LJ64	Q9LJ64 arabidopsis
2	53	53.0	536	12	Q9WR75	Q9WR75 macaca mulatta
3	53	53.0	536	12	Q9J2L9	Q9J2L9 macaca mulatta
4	52	52.0	801	5	Q23635	Q23635 caenorhabditis
5	52	52.0	874	2	Q9K4C4	Q9K4C4 streptomyces
6	52	52.0	878	5	P91859	P91859 caenorhabditis
7	51	51.0	379	11	O88852	O88852 mus musculus
8	51	51.0	989	5	O9GY99	O9GY99 leishmania
9	51	51.0	2066	2	Q9LAX1	Q9LAX1 streptomyces
10	51	51.0	2938	11	Q61769	Q61769 mus musculus
11	49.5	49.5	500	12	O68979	O68979 human herpes
12	49.5	49.5	626	12	O68978	O68978 human herpes
13	49.5	49.5	626	12	O9QNF5	O9QNF5 human herpes
14	49.5	49.5	626	12	O9QNF4	O9QNF4 human herpes
15	49	49.0	139	2	Q9AKS1	Q9AKS1 pseudomonas
16	49	49.0	282	13	Q9DF19	Q9DF19 gallus gallus

17	49.0	575	11	O88339	O88339 rattus norvegicus
18	48.0	132	4	P78429	P78429 homo sapiens
19	48.0	253	12	Q99C08	Q99C08 bovine herpes
20	48.0	424	11	Q99N63	Q99N63 mesocricetus
21	48.0	427	16	O83835	O83835 leoponema p
22	48.0	490	3	Q96V97	Q96V97 oriplomycetes
23	48.0	497	4	Q9H6L5	Q9H6L5 homo sapiens
24	48.0	595	11	O922L3	O922L3 mus musculus
25	48.0	606	4	Q9Y2D9	Q9Y2D9 mus musculus
26	48.0	650	5	O17866	O17866 caenorhabditis
27	48.0	778	5	Q9U9K6	Q9U9K6 caenorhabditis
28	48.0	846	5	O01699	O01699 caenorhabditis
29	48.0	862	11	O9JIK1	O9JIK1 rattus norvegicus
30	48.0	864	5	Q93336	Q93336 caenorhabditis
31	48.0	1117	5	Q9U9K7	Q9U9K7 caenorhabditis
32	48.0	1272	4	Q9UGH1	Q9UGH1 homo sapiens
33	48.0	1300	4	Q9BXA9	Q9BXA9 homo sapiens
34	48.0	1323	11	O62255	O62255 mus musculus
35	48.0	3940	3	Q9HE19	Q9HE19 neurospora
36	47.5	2635	12	P88955	P88955 kaposi's sarcoma
37	47.5	2635	12	O40942	O40942 kaposi's sarcoma
38	47.0	191	5	O9VEC7	O9VEC7 drosophila
39	47.0	275	10	O9LIX7	O9LIX7 oryza sativa
40	47.0	375	16	Q9RW21	Q9RW21 delnococtus
41	47.0	405	4	Q9BU21	Q9BU21 homo sapiens
42	47.0	408	2	Q9Z4V4	Q9Z4V4 streptomyces
43	47.0	539	4	Q9NM45	Q9NM45 homo sapiens
44	47.0	551	4	Q9F613	Q9F613 homo sapiens
45	47.0	576	4	Q9HA18	Q9HA18 homo sapiens

## ALIGNMENTS

RESULT 1  
Q9LJ64 PRELIMINARY; PRT; 956 AA.  
ID Q9LJ64  
AC Q9LJ64;  
DT 01-OCR-2000 (TREMREL. 15, Created)  
DT 01-OCR-2000 (TREMREL. 15, Last sequence update)  
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)  
DE EXTENSIN PROTEIN-LIKE.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-COLUMBIA;  
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-COLUMBIA;  
RX MEDLINE=20363099; PubMed=10907853;  
RA Nakamura Y.;  
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,751,695 bp covered by ninety P1, TAC and BAC clones."  
RT DNA Res. 7:217-221(2000).  
DR EMBL: AP000735; BAB01698.1; -;  
DR InterPro: IPR001226; Flavodoxin.  
DR InterPro: IPR003592; LRR\_out.  
DR InterPro: IPR003882; Pistil\_extensin.  
DR InterPro: IPR002965; P-rich\_extensin.  
DR PRINTS: PR01217; PRICHEXTENSIN.  
DR PRINTS: PR01218; PSTLEXTENSIN.  
DR SMART: SM00370; LRR\_5.  
DR PROSITE: PS00201; FLAVODOXIN; UNKNOWN\_1.  
SQ SEQUENCE 956 AA; 102822 MW; E34E1B5E6BBA7C3 CRC64;

Query Match	Score 55;	DB 10;	Length 956;
Best Local Similarity	62.5%;	Pred. No. 15;	
Matches	10;	Conservative	2;
		Mismatches	4;
		Indels	0;
		Gaps	0;
QY	3	PETPAPAAEETWTSP	18
		: : :	
Db	624	POPPSPSTEETKTSP	639

RESULT	2		
Q9WRT5			
ID	Q9WRT5	PRELIMINARY;	PRT; 536 AA.
AC	Q9WRT5;		
DT	01-NOV-1999	(TREMblrel. 12, Created)	
DT	01-NOV-1999	(TREMblrel. 12, Last sequence update)	
DT	01-DEC-2001	(TREMblrel. 19, Last annotation update)	
DE	CARSDI PROTEIN.		
OS	Macaca mulatta	rhadinovirus 17577.	
OC	viruses; dsDNA viruses, no RNA stage; Herpesviridae		
CC	Gammaherpesvirinae; Rhadinovirus.		
OX	NCBI_TaxID=83534;		

RP SEQUENCE FROM N.A.  
 RX MEDLINE=99174001; PubMed=10074154;  
 RA Searle's R.P., Berguam E.P., Axthelm M.K., Wong S.W.;  
 RT "Sequence and genomic analysis of a rhesus macaque rhadinovirus with  
 RT similarity to Kapost's sarcoma-associated Herpesvirus/Human  
 RT herpesvirus 8."  
 RJ J. Virol. 73:3040-3053(1999).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP Searle's R.P., Berguam E.P., Axthelm M.K., Wong S.W.;  
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBD databases.  
 DR EMBL: AF083501; AAD21343.1; -  
 DR HSSP: P16753; IWPO.  
 DR MEROPS: S21.006; -  
 DR InterPro: IPR001847; Assemblin.  
 DR InterPro: IPR001064; Crystallin.  
 DR Pfam: PF00716; Peptidase\_S21; 1.  
 DR PRINTS: PRO0236; HSVCAPIPE40.  
 DR PROSITE: PS00225; CRYSTALLIN.BETACAMMA; UNKNOWN\_1.  
 SO SEQUENCE 536 AA; 58315 MW; E9C3DADB9AD043C0 CRC64;

Query Match	53.0%	Score 53;	DB 12;	Length 536;
Best Local Similarity	52.9%;	Pred. No. 16;		
Matches 9;	Conservative	5;	Mismatches	3;
			Indels	0;
			Gaps	0;
0y	1 TSPGTPAPAAEETMTTS	17		
		::		
Db	470 TOPATPAPAAOESVMSN	486		

```

RESULT 3
09J2L9
ID 09J2L9 PRELIMINARY; PRT; 536 AA.
AC 09J2L9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CAPSID PROTEIN.
OS Macaca mulatta rhadinovirus 26-95.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OC NCBI_TaxID=119193;
RN [1]
RP SEQUENCE FROM N.A.
RP ST6AIN-MACACA MULATTA RHADINOVIRUS ISOLATE 26-95;
RX MEDLINE=20173730; PubMed=10708456;
RA Alexander L., Denekamp L., Knapp A., Auerbach M.R., Damania B.,
RA Desrochers R.C.;
RT "The primary sequence of rhesus monkey rhadinovirus isolate 26-95:
RT sequence similarities to Kaposi's sarcoma-associated herpesvirus and

```

RT rhesus monkey rhadinovirus isolate 17577.",  
 RL J. Virol. 74:3388-3398(2000).  
 DR EMBL: AF210726: AAF5995.1; -.  
 DR HSSP: P16753: IWPO.  
 DR MEROPS: S21.006: -.  
 DR InterPro: IPR001847: Assemblin.  
 DR InterPro: IPR001064: Crystallin.  
 DR Pfam: PF00716: Peptidase\_S21; 1.  
 DR PRINTS: PR00236: HSYCAPSIDP40.  
 DR PROSITE: PS00225: CRYSTALLIN\_BETAGAMMA; UNKNOWN\_1.  
 SQ SEQUENCE 536 AA: 58367 MW: 03432943779669A2 CRC64;

Query Match	53.0%	Score 53	DB 12	Length 536
Best Local Similarity	52.9%	Pred No 16		
Matches 9	Conservative 5	Mismatches 3	Indels 0	Gaps 0
QY	1 TSPGTPAPAAEETMTTS	17		
		::		
DB	470 TGPATPAPAAQESVMSN	486		

RESULT	4	
Q23635		
ID	Q23635	PRELIMINARY; PRT; 801 AA.
AC	Q23635;	
DT	01-NOV-1996 (TrEMBLrel. 01, Created)	
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)	
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
DE	ZK84.1 PROTEIN.	
GN	ZK84.1.	
OS	Caenorhabditis elegans.	
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea	
OC	Rhabditidae; Pelodierinae; Caenorhabditis.	
OX	NCBI_TaxID=6239;	

RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RX MEDLINE=94150718; PubMed=7906398;  
RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,  
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,  
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
RA Parsons J., Percy C., Riken L., Koopa A., Saunders D., Showkneen R.,  
RA Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,  
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;  
RT 2.2 Mb of contiguous nucleotide sequence from chromosome III of *C.  
RT elegans* \*;  
RL Nature 366:32-38(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA Kirsten J.;  
RT "The sequence of *C. elegans* cosmid zK84.";  
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
DS EMBL; U23181; AAC45204.1; -;  
SO SEQUENCE 801 AA; 77123 MW; 070D8F085471EF28 CRC64;

Query Match	52.08;	Score 52;	DB 5;	Length 801;
Best Local Similarity	76.98;	Pred. No. 33;		
Matches 10; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;

QY 6 PAPAEEETMTSP 18  
| | | | | | | | : |  
Db 585 PAPAEEETPATAP 597

RESULT  
Q9K4C4







Query Match 49.5%; Score 49.5; DB 12; Length 500;  
Best Local Similarity 64.7%; Pred. No. 46;  
Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

OY 2 SPGPAPAERTMTTSP 18  
DB 478 SPG-PGPAAETTTSSP 493

## RESULT 12

ID 068978 PRELIMINARY; PRT; 626 AA.  
AC 068978;  
DT 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE ALKALINE EXONUCLEASE.  
GN AE.  
OS human herpesvirus 1.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Simplexvirus.  
OX NCBI\_TaxID=10298;

RN [1]  
RP SEQUENCE OF 1-189 FROM N.A.  
RX MEDLINE=84036396; PubMed=6313961;  
RA Costa R.H., Draper K.G., Banks L., Powell K.L., Cohen G.,  
RA Eisenberg R., Wagner E.K.;  
RT "High-resolution characterization of herpes simplex virus type 1  
transcripts encoding alkaline exonuclease and a 50,000-dalton protein  
tentatively identified as a capsid protein."  
RL J. Virol. 48:591-603(1983).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86144016; PubMed=3005609;  
RA Draper K.G., Devi-Rao G., Costa R.H., Blair E.D., Thompson R.L.,  
RA Wagner E.K.;  
RT "Characterization of the genes encoding herpes simplex virus type 1  
RT and type 2 alkaline exonucleases and overlapping proteins."  
RL J. Virol. 57:1023-1036(1986).  
DE EMBL\_K02022; AAA45771.1; -;  
DR InterPro: IPR001616; Herpes\_alk\_exo.  
DR Pfam: PF01771; Herpes\_alk\_exo; 1.  
DR PRINTS: PR00924; ALKEXNUCLASE.  
KM Exonuclease.  
SQ SEQUENCE 626 AA; 67469 MW; A651D03A29C70260 CRC64;

Query Match 49.5%; Score 49.5; DB 12; Length 626;  
Best Local Similarity 64.7%; Pred. No. 58;  
Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

OY 2 SPGPAPAERTMTTSP 18  
DB 604 SPG-PGPAAETTTSSP 619

## RESULT 13

ID 090NF5 PRELIMINARY; PRT; 626 AA.  
AC 090NF5;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE ALKALINE DEOXYRIBONUCLEASE.  
GN U112.  
OS human herpesvirus 1.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Simplexvirus.  
OX NCBI\_TaxID=10298;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WT51;

RX MEDLINE=99286799; PubMed=10358747;  
RA Chiba A., Suzutani T., Saijo M., Koyano S., Azuma M.;  
RT "Analysis of nucleotide sequence variations in herpes simplex virus  
RT types 1 and 2, and varicella-zoster virus."  
RL Acta Virol. 42:401-407(1998).  
DR EMBL; AB009265; BAA84004.2; -;  
DR InterPro: IPR001616; Herpes\_alk\_exo.  
DR Pfam: PF01771; Herpes\_alk\_exo; 1.  
DR PRINTS: PR00924; ALKEXNUCLASE.  
SQ SEQUENCE 626 AA; 67492 MW; F5F92710E50A54A2 CRC64;

Query Match 49.5%; Score 49.5; DB 12; Length 626;  
Best Local Similarity 64.7%; Pred. No. 58;  
Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

OY 2 SPGPAPAERTMTTSP 18  
DB 604 SPG-PGPAAETTTSSP 619

## RESULT 14

ID 090NF4 PRELIMINARY; PRT; 626 AA.  
AC 090NF4;  
DT 01-MAY-2000 (TReMBLrel. 13, Created)  
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE ALKALINE DEOXYRIBONUCLEASE.  
GN U112.  
OS human herpesvirus 1.  
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Simplexvirus.  
OX NCBI\_TaxID=10298;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KH169;  
RX MEDLINE=99286799; PubMed=10358747;  
RA Chiba A., Suzutani T., Saijo M., Koyano S., Azuma M.;  
RT "Analysis of nucleotide sequence variations in herpes simplex virus  
RT types 1 and 2, and varicella-zoster virus."  
RL Acta Virol. 42:401-407(1998).  
DR EMBL; AB009266; BAA84005.2; -;  
DR InterPro: IPR001616; Herpes\_alk\_exo.  
DR Pfam: PF01771; Herpes\_alk\_exo; 1.  
DR PRINTS: PR00924; ALKEXNUCLASE.  
SQ SEQUENCE 626 AA; 67484 MW; 88183DEAB9B0DA71 CRC64;

Query Match 49.5%; Score 49.5; DB 12; Length 626;  
Best Local Similarity 64.7%; Pred. No. 58;  
Matches 11; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

OY 2 SPGPAPAERTMTTSP 18  
DB 604 SPG-PGPAAETTTSSP 619

## RESULT 15

ID 09AKS1 PRELIMINARY; PRT; 139 AA.  
AC 09AKS1;  
DT 01-JUN-2001 (TReMBLrel. 17, Created)  
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)  
DE TATB PROTEIN.  
GN TATB.  
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Pseudomonas.  
OX NCBI\_TaxID=316;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN-ZOBELL ATCC14405;  
RX MEDLINE=21101859; PubMed=11160097;  
RA Heikilla M.P.; Honisch U.; Wunsch P.; Zumft W.G.;  
RT "Role of the Tat transport system in nitrous oxide reductase  
translocation and cytochrome cdi biosynthesis in Pseudomonas  
stutzeri.";  
RL J. Bacteriol. 183:1663-1671(2001).  
DR EMBL: AJ299712; CAC29148.1; -;  
DR InterPro: IPR003998; TatB.  
DR PRINTS: PR01506; TATBPROTEIN.  
SO SEQUENCE 139 AA; 14772 MW; 5F82C4A9F09195AF CRC64;

Query Match 49.0%; Score 49; DB 2; Length 139;  
Best Local Similarity 58.8%; Pred. No. 15;  
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 SPCTPAPAETMTSP 18  
|| ||||| |  
Db 117 SPAVPAPAEPPTPRP 133

Search completed: August 13, 2002, 08:37:08  
Job time: 392 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 13, 2002, 08:30:31 : Search time 20.64 Seconds  
(Without alignments)  
22.485 Million cell updates/sec

Title: US-09-826-212-2\_COPY\_215\_233  
Perfect score: 100  
Sequence: 1 TSPGTPAPAAETMTTSPG 19

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued\_Patents\_AA:\*  
2: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	100	100.0	259	4	US-09-006-353A-2
2	100	100.0	299	4	US-09-153-927-3
3	54	54.0	440	3	US-08-883-036A-2
4	48	48.0	1057	3	US-08-931-820-4
5	48	48.0	1078	3	US-08-963-825-21
6	48	48.0	1078	4	US-09-570-573-21
7	48	48.0	1078	4	US-09-548-608-21
8	47	47.0	284	4	US-08-793-701-39
9	47	47.0	284	4	US-08-793-701-41
10	47	47.0	284	4	US-08-793-701-57
11	45	45.0	348	3	US-08-415-655-5
12	45	45.0	348	3	US-08-415-655-13
13	45	45.0	348	3	US-08-415-655-15
14	45	45.0	454	3	US-08-348-518C-4
15	45	45.0	454	3	US-08-476-509B-4
16	44	44.0	402	2	US-08-477-254A-2
17	44	44.0	402	2	US-08-477-254A-2
18	44	44.0	402	2	US-08-428-734B-2
19	44	44.0	402	3	US-09-063-237-1
20	44	44.0	402	4	US-08-713-356F-2
21	44	44.0	412	2	US-08-477-254A-4
22	44	44.0	412	2	US-08-477-254B-4
23	44	44.0	412	2	US-08-428-734B-4
24	44	44.0	412	4	US-08-713-356F-4
25	44	44.0	610	1	US-07-821-717B-6
26	44	44.0	610	1	US-08-119-262B-6
27	44	44.0	610	1	US-08-135-929A-11

28	44	44.0	610	1	US-08-234-265A-11	Sequence 11, Appl
29	43	43.0	471	2	US-08-399-889-24	Sequence 24, Appl
30	43	43.0	471	3	US-09-167-364-24	Sequence 24, Appl
31	43	43.0	471	4	US-09-439-897-2	Sequence 2, Appl
32	43	43.0	557	4	US-08-979-608A-5	Sequence 5, Appl
33	43	43.0	659	4	US-09-189-462-4	Sequence 4, Appl
34	43	43.0	4472	2	US-08-804-227C-2	Sequence 2, Appl
35	42	42.0	207	2	US-08-609-443B-15	Sequence 15, Appl
36	42	42.0	207	2	US-08-569-063C-15	Sequence 15, Appl
37	42	42.0	247	3	US-09-129-888-2	Sequence 2, Appl
38	42	42.0	386	4	US-09-086-483A-2	Sequence 2, Appl
39	42	42.0	786	4	US-09-103-429A-3	Sequence 3, Appl
40	42	42.0	805	4	US-09-103-429A-4	Sequence 4, Appl
41	42	42.0	880	2	US-08-916-917-12	Sequence 12, Appl
42	42	42.0	880	3	US-09-225-170-12	Sequence 12, Appl
43	42	42.0	880	4	US-09-378-255-6	Sequence 6, Appl
44	42	42.0	880	4	US-09-141-212-2	Sequence 2, Appl
45	42	42.0	880	4	US-09-141-212-4	Sequence 4, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-006-353A-2
: Sequence 2, Application US/0906353A
: Patent No. 6261801
:
GENERAL INFORMATION:
: APPLICANT: WEI, YING-FEI
: APPLICANT: YU, GUO-LING
: APPLICANT: GENTZ, REINER
: APPLICANT: RUBEN, STEVEN
: TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESS: HUMAN GENOME SCIENCES, INC.
: STREET: 9410 KEY WEST AVENUE
: CITY: ROCKVILLE
: STATE: MD
: COUNTRY: US
: ZIP: 20850
:
COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/006,353A
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: BROOKS, ANDERS A
: REFERENCE/DOCKET NUMBER: PR341
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8512
: TELEFAX: (301) 309-8512
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 259 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
US-09-006-353A-2

Query Match 100.0%; Score 100; DB 4; Length 259;
Best Local Similarity 100.0%; Pred. No. 8.4e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TSPGTPAPAAETMTTSPG 19
Db 185 TSPGTPAPAAETMTTSPG 203
```

RESULT 2  
US-09-153-927-3  
Sequence 3, Application US/09153927A  
Patent No. 6297022  
GENERAL INFORMATION:  
APPLICANT: McDONNELL, Peter C.  
APPLICANT: Young, Peter R.  
APPLICANT: Zou, Jun  
TITLE OF INVENTION: A Method of Identifying Agonists and  
TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3  
TITLE OF INVENTION: and TR5  
FILE REFERENCE: GH50031  
CURRENT APPLICATION NUMBER: US/09/153,927A  
CURRENT FILING DATE: 1998-09-16  
EARLIER APPLICATION NUMBER: 60/061,334  
EARLIER FILING DATE: 1997-10-08  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 299  
TYPE: PRT  
ORGANISM: Human  
US-09-153-927-3

Query Match 100.0%; Score 100; DB 4; Length 299;  
Best Local Similarity 100.0%; Pred. No. 9,8e-06;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSPGTPAPAAEETMTTSPG 19  
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Db 225 TSPGTPAPAAEETMTTSPG 243

RESULT 3  
US-08-883-036A-2  
Sequence 2, Application US/08883036A  
Patent No. 6072047  
GENERAL INFORMATION:  
APPLICANT: Rauch, Charles  
APPLICANT: Walczak, Hennig  
TITLE OF INVENTION: Receptor That Binds TRAIL  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESS: Kathryn A. Anderson, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle,  
STATE: WA  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Macintosh 7.6  
SOFTWARE: Microsoft Word, Version 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/883,036A  
FILING DATE: 26-JUN-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US --to be assigned--  
FILING DATE: 04-JUN-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/829,536  
FILING DATE: 28-MAR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/815,255  
FILING DATE: 12-MAR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/799,861  
FILING DATE: 13-FEB-1997

ATTORNEY/AGENT INFORMATION:  
NAME: Anderson, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2625-D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 440 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-883-036A-2

Query Match 54.0%; Score 54; DB 3; Length 440;  
Best Local Similarity 76.9%; Pred. No. 9.6;  
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 7 APAEETMTTSPG 19  
||| ||| : |||  
Db 191 APAEETMTTSPG 203

RESULT 4  
US-08-931-820-4  
Sequence 4, Application US/08931820  
Patent No. 6010863  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Assay for collagen degradation  
NUMBER OF SEQUENCES: 4  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/931,820  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 96202596.1  
FILING DATE:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1057 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
TISSUE TYPE: Collagen type III  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1055  
OTHER INFORMATION: /label=Modified  
OTHER INFORMATION: /note="Ala may be Pro"  
US-08-931-820-4

Query Match 48.0%; Score 48; DB 3; Length 1057;  
Best Local Similarity 44.4%; Pred. No. 1.4e+02;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 2 SPGTPAPAAEETMTTSPG 19  
: || : || : ||  
Db 969 AFGSPGAGGGAIGSPG 986

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RESULT 5
US-08-963-825-21
; Sequence 21, Application US/08963825
; Patent No. 6110689
; GENERAL INFORMATION:
; APPLICANT: Qvist, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/963,825
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/187,319
; FILING DATE: 21-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Gogoris, Adda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/08701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1078 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: COLLAGEN ALPHA 1 (III)
; US-08-963-825-21

Query Match 48.0%; Score 48; DB 3; Length 1078;
Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 SPCGPAPAEFTMTSPG 19
Db 970 APGSPGAGGGAIGSPG 987

RESULT 6
US-09-570-573-21
; Sequence 21, Application US/09570573
; Patent No. 6342361
; GENERAL INFORMATION:
; APPLICANT: Qvist, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
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NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/570,573
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
US-09-570-573-21

Query Match 48.0%; Score 48; DB 4; Length 1078;
Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 SPCGPAPAEFTMTSPG 19
Db 970 APGSPGAGGGAIGSPG 987

RESULT 7
US-09-548-608-21
; Sequence 21, Application US/09548608
; Patent No. 6353442
; GENERAL INFORMATION:
; APPLICANT: Qvist, Per
; APPLICANT: Bonde, Martin
; TITLE OF INVENTION: A Method for Assaying Collagen Fragments
; TITLE OF INVENTION: In Body Fluids, A Test Kit and Means for Carrying Out the
; TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of
; TITLE OF INVENTION: Disorders Associated with the Metabolism of
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.05  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/548,608  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/187,319  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Gogoris, Adda C  
REGISTRATION NUMBER: 29,714  
REFERENCE/DOCKET NUMBER: 4305/08701  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1078 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
IMMEDIATE SOURCE:  
CLONE: COLLAGEN ALPHA 1 (III)  
US-09-548-608-21

Query Match 48.0%; Score 48; DB 4; Length 1078;  
Best Local Similarity 44.4%; Pred. No. 1.4e+02;  
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SPCTPAPAEETMTSPG 19  
:||:||||:  
Db 970 APGSPRAGCGGATGSPG 987

RESULT 8  
US-08-793-701-39  
Sequence 39, Application US/08793701  
Patent No. 6248581  
GENERAL INFORMATION:  
APPLICANT: GICQUEL, Brigitte  
APPLICANT: LIM, Eng Mong  
APPLICANT: PORTNOI, Denis  
APPLICANT: BERTHER, Francois-Xavier  
APPLICANT: TIMM, Juliano  
TITLE OF INVENTION: MYCOBACTERIA FUNCTIONAL SCREENING AND/OR  
TITLE OF INVENTION: EXPRESSION VECTORS  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: C/O FINNEGAN, HENDERSON, FARRABOW, GARRETT &  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,701  
FILING DATE: 09-JUN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR9501133  
FILING DATE: 30-AUG-1995  
PRIOR APPLICATION DATA: FR 94/10585  
APPLICATION NUMBER: FR 94/10585

FILING DATE: 02-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: McDonnell, Leslie A.  
REGISTRATION NUMBER: 34,872  
REFERENCE/DOCKET NUMBER: 02356.0075  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4132  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 284 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-793-701-39

Query Match 47.0%; Score 47; DB 4; Length 284;  
Best Local Similarity 47.4%; Pred. No. 47;  
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 1 TSPCTPAPAEETMTSPG 19  
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Db 100 TSPGLTSPGLTDPALISPG 118

RESULT 9  
US-08-793-701-41  
Sequence 41, Application US/08793701  
Patent No. 6248581  
GENERAL INFORMATION:  
APPLICANT: GICQUEL, Brigitte  
APPLICANT: LIM, Eng Mong  
APPLICANT: PORTNOI, Denis  
APPLICANT: BERTHER, Francois-Xavier  
APPLICANT: TIMM, Juliano  
TITLE OF INVENTION: MYCOBACTERIA FUNCTIONAL SCREENING AND/OR  
TITLE OF INVENTION: EXPRESSION VECTORS  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: C/O FINNEGAN, HENDERSON, FARRABOW, GARRETT &  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,701  
FILING DATE: 09-JUN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR9501133  
FILING DATE: 30-AUG-1995  
PRIOR APPLICATION DATA: FR 94/10585  
APPLICATION NUMBER: FR 94/10585  
FILING DATE: 02-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: McDonnell, Leslie A.  
REGISTRATION NUMBER: 34,872  
REFERENCE/DOCKET NUMBER: 02356.0075  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4132  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 284 amino acids  
TYPE: amino acid



TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-793-701-41

Query Match 47.0%; Score 47; DB 4; Length 284;  
Best Local Similarity 47.4%; Pred. No. 47;  
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

OY 1 TSPGTPAPAAETMTSPG 19  
||||| : : : |||||  
Db 100 TSPGLTSPGLTPALTSFG 118

RESULT 10  
US-08-793-701-57  
Sequence 57, Application US/08793701  
Patent No. 6248581  
GENERAL INFORMATION:  
APPLICANT: GICQUEL, Brigitte  
APPLICANT: LIM, Eng Mong  
APPLICANT: BERTHET, Denis  
APPLICANT: BERTHET, Francois-Xavier  
APPLICANT: TIMM, Giuliano  
TITLE OF INVENTION: MYCOBACTERIA FUNCTIONAL SCREENING AND/OR  
EXPRESSION VECTORS  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: C/O FINNEGAN, HENDERSON, FARRABOW, GARRETT &  
ADDRESSEE: DUNNER, L.L.P.  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/793,701  
FILING DATE: 09-JUN-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR9501133  
FILING DATE: 30-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 94/10585  
FILING DATE: 02-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: McDonnell, Leslie A.  
REGISTRATION NUMBER: 34,872  
REFERENCE/DOCKET NUMBER: 02356, 0075  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 408-4132  
TELEFAX: (202) 408-4400  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 284 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-793-701-57

Query Match 47.0%; Score 47; DB 4; Length 284;  
Best Local Similarity 47.4%; Pred. No. 47;  
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
OY 1 TSPGTPAPAAETMTSPG 19  
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Db 100 TSPGLTSPGLTPALTSFG 118

RESULT 11  
US-08-415-655-5  
Sequence 5, Application US/08415655  
Patent No. 6025480  
GENERAL INFORMATION:  
APPLICANT: Massague, Joan  
APPLICANT: Lee, Mong-hong  
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING  
TITLE OF INVENTION: p75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF  
TITLE OF INVENTION: SAME  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/415,655  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/47418  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 348 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-415-655-5

Query Match 45.0%; Score 45; DB 3; Length 348;  
Best Local Similarity 50.0%; Pred. No. 1e+02;  
Matches 9; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

OY 1 TSPGTPAPAAETMTSP 18  
||||| : : : |||||  
Db 152 TSPATPAPASD-LTSDP 167

RESULT 12  
US-08-415-655-13  
Sequence 13, Application US/08415655  
Patent No. 6025480  
GENERAL INFORMATION:  
APPLICANT: Massague, Joan  
APPLICANT: Lee, Mong-hong  
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING  
TITLE OF INVENTION: p75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF  
TITLE OF INVENTION: SAME  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 1185 Avenue of the Americas  
CITY: New York

STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/415,655  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/47418  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 348 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-415-655-13

Query Match 45.0%; Score 45; DB 3; Length 348;  
Best Local Similarity 50.0%; Pred. No. 1e+02;  
Matches 9; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

QY 1 TSPGTPAPAAEETMTSP 18  
| | | | | : : : : :  
Db 152 TTPATPAPASD--LTS DP 167

RESULT 13  
US-08-415-655-15  
Sequence 15, Application US/08415655  
Patent No. 6025480  
GENERAL INFORMATION:  
APPLICANT: Massague, Joan  
APPLICANT: Lee, Mong-hong  
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING  
TITLE OF INVENTION: P75KIP2, A CYCLIN-DEPENDENT KINASE INHIBITOR AND USES OF  
TITLE OF INVENTION: SAME  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/415,655  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 1747/47418  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 348 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-415-655-15

Query Match 45.0%; Score 45; DB 3; Length 348;  
Best Local Similarity 50.0%; Pred. No. 1e+02;  
Matches 9; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

QY 1 TSPGTPAPAAEETMTSP 18  
| | | | | : : : : :  
Db 152 TTPATPAPASD--LTS DP 167

RESULT 14  
US-08-348-518C-4  
Sequence 4, Application US/08348518C  
Patent No. 6022740  
GENERAL INFORMATION:  
APPLICANT: SUDOL, MARIUS  
APPLICANT: PEER, BORK  
APPLICANT: HENRY, CHEN  
TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A  
TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE  
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTIC USES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/348,518C  
FILING DATE: 01-DEC-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 454 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-348-518C-4

Query Match 45.0%; Score 45; DB 3; Length 454;  
Best Local Similarity 44.4%; Pred. No. 1.4e+02;  
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 TSPGTPAPAAEETMTSP 18  
| | | | | : : : : :  
Db 31 SGPQAPAPATOAPOAP 48

RESULT 15

US-08-476-509B-4

; Sequence 4, Application US/08476509B

; Patent No. 6034212

; GENERAL INFORMATION:

; APPLICANT: SUDOL, MARIUS

; APPLICANT: PEER, BORK

; APPLICANT: HENRY, CHEN

; TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A

; TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE

; TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTICS

; TITLE OF INVENTION: THEREOF

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber &amp; Jackson

; STREET: 411 Hackensack Avenue

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/476,509B

; FILING DATE: 01-DEC-1994

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 600-1-101 CIP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201 343-1684

; TELEFAX: 201 343-1684

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 454 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-476-509B-4

; Query Match 45.0%; Score 45; DB 3; Length 454;

; Best Local Similarity 44.4%; Pred. No. 1.4e+02;

; Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

; DB 31 SGGGPAPAPATQAAPAP 48

Search completed: August 13, 2002, 08:30:32  
Job time: 66 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 13, 2002, 08:31:31 ; Search time 29.73 Seconds  
(without alignments)  
870,508 Million cell updates/sec

Title: US-09-826-212-2\_COPY\_27\_259  
Perfect score: 233  
Sequence: 1 TTARQEEYPOQTVAPOOORH.....YLSCTIVGIVLIVLIVFV 233

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 5

Total number of hits satisfying chosen parameters: 10957

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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22: /SIDSI/gcgdata/hold-geneseq/geneeqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	233	100.0	259	19	AAW64668 Human TRIP protein
2	233	100.0	259	20	AAW88408 Human Apo-2Dcr pro
3	233	100.0	259	22	AAU12321 Human PRO366 poly
4	233	100.0	259	22	AAW20111 Human immunostimul
5	233	100.0	259	22	AAW36696 Human tumour necro
6	233	100.0	259	22	AAW53091 Human anglogenesis
7	233	100.0	268	19	AAW62181 FLAG-TRID clone w1
8	233	100.0	299	19	AAW76331 Human tumour necro
9	233	100.0	299	20	AAW29864 Human secreted pro
10	233	100.0	299	20	AAW05744 Tumour necrosis fa
11	233	100.0	299	20	AAW0933 Human TRAIL-R3 pro

12	233	100.0	299	20	AAW94671 Human TNF-related
13	233	100.0	299	20	AAW88409 Human Apo-2Dcr pro
14	233	100.0	299	21	AAW01343 Death receptor. H
15	214	91.8	249	22	AAW82182 FLAG-TRID clone w1
16	185	79.4	259	20	AAW93578 Human hsp90 protei
17	140	60.1	259	20	AAW05726 Tumour necrosis fa
18	48	20.6	48	20	AAW88450 Human Apo-2Dcr pep
19	14	6.0	386	20	AAW98200 RTD, inhibitor of
20	14	6.0	386	20	AAW04144 Human TANGO-74 pro
21	14	6.0	386	20	AAW99018 Human TRAIL recept
22	14	6.0	386	20	AAW99019 Human TRAIL recept
23	14	6.0	386	20	AAW92792 Human TNF receptor
24	14	6.0	386	21	AAW01341 TNF-related apopt
25	14	6.0	386	21	AAW69991 Human receptor-ass
26	14	6.0	386	22	AAU12341 Human PRO366 poly
27	14	6.0	386	22	AAW31187 Antio acid sequenc
28	14	6.0	386	22	AAW50892 Human TR10 recepto
29	14	3.4	109	22	AAW68231 Drosophila melanog
30	8	3.4	217	22	AAW93909 Human protein sequ
31	8	3.4	272	22	AAW41810 Human polypeptide
32	8	3.4	272	22	AAW41811 Human TR6 partial
33	8	3.4	303	19	AAW76828 Human Apo-2 poly
34	8	3.4	303	22	AAW48349 Partial amino acid
35	8	3.4	350	20	AAW0934 Human DR5 protein
36	8	3.4	411	19	AAW79261 Tumour necrosis fa
37	8	3.4	411	19	AAW76827 Human TR6 protein.
38	8	3.4	411	19	AAW79083 Human death domain
39	8	3.4	411	20	AAW93608 Human killer adria
40	8	3.4	411	20	AAW93576 Human hsp90 protei
41	8	3.4	411	20	AAW09332 Human DR5 protein
42	8	3.4	411	20	AAW88410 Human Apo-2 ligand
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46	8	3.4	411	22	AAW04038 Human Apoptotic pr
47	8	3.4	411	22	AAW73442 Human Apo-2 recept
48	8	3.4	411	22	AAW73443 Human Apo-2 recept
49	8	3.4	411	22	AAW48348 Human tumour necro
50	8	3.4	424	22	AAW48352 TR6-Ig fusion prot
51	8	3.4	440	19	AAW99284 Human TRAIL recept
52	8	3.4	440	19	AAW79260 Tumour necrosis fa
53	8	3.4	440	20	AAW05725 Tumour necrosis fa
54	8	3.4	440	21	AAW01340 TNF-related apopot
55	8	3.4	444	20	AAW35231 Protein involved i
56	8	3.0	24	18	AAW33935 Beta1-adrenergic r
57	7	3.0	29	18	AAW10929 Polyclonal anti-fe
58	7	3.0	54	21	AAW52674 Arabidopsis thalia
59	7	3.0	61	20	AAW30434 Mature nematode ex
60	7	3.0	61	21	AAW15319 N. american nemat
61	7	3.0	71	21	AAW10929 Arabidopsis thalia
62	7	3.0	74	21	AAW10928 Arabidopsis thalia
63	7	3.0	75	21	AAW10927 Arabidopsis thalia
64	7	3.0	76	22	AAW75966 Human colon cancer
65	7	3.0	79	17	AAW91704 Namfap. Necator a
66	7	3.0	79	20	AAW30412 Nematode extracte
67	7	3.0	85	21	AAW52673 Arabidopsis thalia
68	7	3.0	93	15	AAW50794 G-protein coupled
69	7	3.0	93	17	AAW02986 Arabidopsis thalia
70	7	3.0	98	21	AAW52672 Arabidopsis thalia
71	7	3.0	100	22	AAW67913 Drosophila melanog
72	7	3.0	112	22	AAW38574 Arabidopsis thalia
73	7	3.0	122	21	AAW09814 Arabidopsis thalia
74	7	3.0	124	21	AAW09813 Arabidopsis thalia
75	7	3.0	136	21	AAW32125 Arabidopsis thalia
76	7	3.0	166	21	AAW47702 Arabidopsis thalia
77	7	3.0	138	21	AAW32124 Arabidopsis thalia
78	7	3.0	138	21	AAW47701 Arabidopsis thalia
79	7	3.0	153	21	AAW38573 Arabidopsis thalia
80	7	3.0	155	21	AAW38572 Arabidopsis thalia
81	7	3.0	215	22	ABG10788 Novel human diagno
82	7	3.0	235	22	ABG17696 Novel human diagno
83	7	3.0	235	22	ABG18326 Novel human diagno
84	7	3.0	240	19	AAW85914 S. pneumoniae deri

85	7	3.0	244	21	AG09812	Arabidopsis thalia	158	6	2.6	44	22	ABB32242	Peptide #4893 enco
86	7	3.0	256	22	ABB60500	Drosophila melanog	159	6	2.6	44	22	ABB37490	Peptide #4996 enco
87	7	3.0	258	21	AG47700	Arabidopsis thalia	160	6	2.6	44	22	ABB22791	Protein #4790 enco
88	7	3.0	262	21	AG32123	Arabidopsis thalia	161	6	2.6	44	22	AAW70610	Human bone marrow
89	7	3.0	262	19	AAW81726	M. tuberculosis im	162	6	2.6	44	22	AAW18450	Peptide #4884 enco
90	7	3.0	267	19	AAW64359	Mycobacterium tube	163	6	2.6	44	22	AAW30925	Peptide #4962 enco
91	7	3.0	267	20	AAW39156	M. tuberculosis an	164	6	2.6	44	22	AAW06046	Peptide #4728 enco
92	7	3.0	289	22	ABG17560	Novel human diagno	165	6	2.6	48	20	AAW77494	Human colon cancer
93	7	3.0	292	18	AAW18809	Dihydrofolinic a	166	6	2.6	49	22	AAW60201	Human endometrium
94	7	3.0	325	22	ABW93734	Human protein sequ	167	6	2.6	50	22	AAW9498	Human reproductive
95	7	3.0	330	22	AAW94001	Human stomach can	168	6	2.6	51	22	AAW62748	Proteinibacterium
96	7	3.0	330	22	AAW94271	Human protein sequ	169	6	2.6	52	21	AAW34661	Arabidopsis thalia
97	7	3.0	332	21	AAW41611	Human ORFX ORP1375	170	6	2.6	52	21	AAW34661	Human secreted pro
98	7	3.0	332	21	AAW40024	Human polypeptide	171	6	2.6	54	21	AAW19541	Arabidopsis thalia
99	7	3.0	345	19	AAW80643	S. pneumoniae prot	172	6	2.6	54	22	AAW11444	Human polypeptide
100	7	3.0	360	22	AAW40025	Human polypeptide	173	6	2.6	57	22	AAW05225	Human polypeptide
101	7	3.0	365	20	AAW13737	Murine beta-1 adre	174	6	2.6	58	22	AAW45956	Proteinibacterium
102	7	3.0	377	15	AAW48653	G-protein coupled	175	6	2.6	58	22	AAW65301	Proteinibacterium
103	7	3.0	377	15	AAW02665	Drosophila melanog	176	6	2.6	62	22	AAW44360	Proteinibacterium
104	7	3.0	390	22	ABW65316	Proteinibacterium	177	6	2.6	63	22	AAW55914	Proteinibacterium
105	7	3.0	397	22	AAW46161	Onchocerca volvulu	178	6	2.6	63	22	AAW86245	Human immune/haema
106	7	3.0	401	18	AAW11802	Onchocerca volvulu	179	6	2.6	64	21	AAW76162	Human secreted pro
107	7	3.0	407	18	AAW11800	Human APORP protei	180	6	2.6	64	21	AAW80687	PTDOL APB-encode
108	7	3.0	410	20	AAW93577	Human DR4. Homo s	181	6	2.6	68	21	AAW21112	Arabidopsis thalia
109	7	3.0	466	13	AAW26505	Human DR4. Homo s	182	6	2.6	68	21	AAW28554	Arabidopsis thalia
110	7	3.0	467	22	AAW50896	Human DR4. Homo s	183	6	2.6	68	21	AAW34705	Arabidopsis thalia
111	7	3.0	468	19	AAW64483	Human DR4 protein.	184	6	2.6	68	21	AAW47081	Arabidopsis thalia
112	7	3.0	468	20	AAW93609	Human DR4 protein.	185	6	2.6	68	21	AAW52668	Arabidopsis thalia
113	7	3.0	468	20	AAW93609	Human DR4 protein.	186	6	2.6	69	21	AAW41928	Arabidopsis thalia
114	7	3.0	468	21	AAW72022	Human Death Domain	187	6	2.6	70	22	AAW44399	Proteinibacterium
115	7	3.0	468	21	AAW72023	Human Death Domain	188	6	2.6	70	22	AAW06357	Human foetal prote
116	7	3.0	468	21	AAW808546	Amino acid sequenc	189	6	2.6	71	21	AAW74316	Neisseria meningit
117	7	3.0	468	21	AAW801339	TNF-related apopto	190	6	2.6	74	21	AAW74316	Arabidopsis thalia
118	7	3.0	468	22	AAW49241	Human DR4 protein.	191	6	2.6	74	21	AAW34066	Arabidopsis thalia
119	7	3.0	477	22	AAW70765	Human beta1-adreno	192	6	2.6	74	21	AAW35084	Arabidopsis thalia
120	7	3.0	477	22	AAW58143	Proteinibacterium	193	6	2.6	74	21	AAW60607	Novel human diagno
121	7	3.0	482	22	AAW52714	Arabidopsis thalia	194	6	2.6	75	22	AAW604503	Novel human diagno
122	7	3.0	482	21	AAW52713	Arabidopsis thalia	195	6	2.6	75	22	AAW614408	Novel human diagno
123	7	3.0	513	21	AAW52713	Arabidopsis thalia	196	6	2.6	75	22	AAW614661	Novel human diagno
124	7	3.0	521	21	AAW52712	Arabidopsis thalia	197	6	2.6	75	22	AAW616989	Novel human diagno
125	7	3.0	537	21	AAW84870	Amino acid sequenc	198	6	2.6	75	22	AAW617397	Novel human diagno
126	7	3.0	551	21	AAW42049	Human ORFX ORF1813	199	6	2.6	75	22	AAW89055	Human immune/haema
127	7	3.0	576	21	AAW24234	Human vesicle asso	200	6	2.6	77	22	AAW42286	Proteinibacterium
128	7	3.0	576	22	AAW95100	Human protein sequ	201	6	2.6	79	22	AAW00856	Human bone marrow
129	7	3.0	677	22	ABW61957	Drosophila melanog	202	6	2.6	80	22	AAW50707	Proteinibacterium
130	7	3.0	1247	22	ABW61174	Rat brain alpha-ii	203	6	2.6	83	21	AAW34660	Arabidopsis thalia
131	7	3.0	1792	22	ABW66477	Rat T-type voltage	204	6	2.6	84	21	AAW74315	Neisseria meningit
132	7	3.0	1835	20	AAW14597	Amino acid sequenc	205	6	2.6	84	22	AAW22575	Novel human colon
133	7	3.0	3739	21	AAW18658	S. venezuelae macr	206	6	2.6	84	22	AAW92538	Human digestive sy
134	7	3.0	3739	21	AAW77193	S. venezuelae pik	207	6	2.6	85	22	AAW19540	Proteinibacterium
135	7	3.0	3739	21	AAW77201	Narboxonolide synth	208	6	2.6	86	22	AAW48698	Novel human diagno
136	7	3.0	3739	21	AAW67202	S. venezuelae pik	209	6	2.6	86	22	AAW26420	Homologous sequenc
137	7	3.0	12199	21	AAW77180	peptry motif conta	210	6	2.6	87	17	AAW92991	H. pylori cytoplas
138	6	2.6	13	18	AAW38117	SH3-binding peptid	211	6	2.6	88	18	AAW20911	Proteinibacterium
139	6	2.6	14	17	AAW05449	peptry motif conta	212	6	2.6	88	22	AAW45191	Enterococcus faeca
140	6	2.6	14	18	AAW37657	Human DNA/RNA bind	213	6	2.6	91	20	AAW00202	Human protein SEQ
141	6	2.6	14	22	AAW00224	Plasmiid PSY617 en	214	6	2.6	93	22	AAW80048	Human high mobil
142	6	2.6	16	21	AAW27953	PTDOLA 103L-enco	215	6	2.6	93	22	AAW80048	Arabidopsis thalia
143	6	2.6	23	22	AAW60685	Ramyla signal pept	216	6	2.6	95	19	AAW21419	Human HVS VH regio
144	6	2.6	25	19	AAW59638	Plasmiid TTOLA 103L	217	6	2.6	97	17	AAW92078	Peptide #3932 enco
145	6	2.6	33	22	AAW60686	peptide #4591 enco	218	6	2.6	97	22	AAW05174	Peptide #3856 enco
146	6	2.6	33	22	AAW60686	peptide #4598 enco	219	6	2.6	98	21	AAW16621	Bacteriophage 192
147	6	2.6	37	22	AAW64183	Human bone marrow	220	6	2.6	98	21	AAW44934	Zea mays protein f
148	6	2.6	37	22	AAW64183	Human secreted pro	221	6	2.6	99	21	AAW21111	Arabidopsis thalia
149	6	2.6	34	22	AAW37085	Peptide #1155 enco	222	6	2.6	99	21	AAW21111	Arabidopsis thalia
150	6	2.6	34	22	AAW30561	Plasmiid RBD1-enco	223	6	2.6	99	21	AAW21111	Arabidopsis thalia
151	6	2.6	37	22	AAW63233	Human immune/haema	224	6	2.6	99	21	AAW21111	Arabidopsis thalia
152	6	2.6	37	22	AAW63233	Human immune/haema	225	6	2.6	99	21	AAW21111	Arabidopsis thalia
153	6	2.6	37	22	AAW64183	Human immune/haema	226	6	2.6	99	21	AAW21111	Arabidopsis thalia
154	6	2.6	37	22	AAW64183	Human immune/haema	227	6	2.6	99	21	AAW21111	Arabidopsis thalia
155	6	2.6	40	22	AAW37118	Human immune/haema	228	6	2.6	99	21	AAW21111	Arabidopsis thalia
156	6	2.6	41	22	AAW60689	Human immune/haema	229	6	2.6	99	21	AAW21111	Arabidopsis thalia
157	6	2.6	41	22	AAW85060	Human immune/haema	230	6	2.6	99	21	AAW21111	Arabidopsis thalia

231	6	2.6	99	21	AA652667	Arabidopsis thalia	304	6	2.6	131	22	ABR23066	Protein #5065 enco
232	6	2.6	99	21	AA652671	Arabidopsis thalia	305	6	2.6	131	22	AAW58399	Human brain expres
233	6	2.6	99	21	AA600044	Human secreted pro	306	6	2.6	131	22	AAW70885	Human bone marrow
234	6	2.6	100	18	AAW13527	Anti-melanoma anti	307	6	2.6	131	22	AAW18715	Peptide #5149 enco
235	6	2.6	100	21	AA641927	Arabidopsis thalia	308	6	2.6	131	22	AAW18715	Peptide #5214 enco
236	6	2.6	101	20	AAW29245	Amino acid sequenc	309	6	2.6	131	22	AAW31177	S. epidermidis ope
237	6	2.6	105	21	AA644933	Zea mays protein f	310	6	2.6	133	22	ABR68834	Drosophila melanog
238	6	2.6	105	22	ABR65119	Drosophila melanog	311	6	2.6	133	22	ABR62686	Murine OR-1 like pol
239	6	2.6	105	22	ABR65122	Drosophila melanog	312	6	2.6	134	21	AA624064	Arabidopsis thalia
240	6	2.6	105	22	ABR67261	Drosophila melanog	313	6	2.6	134	21	AA644247	Arabidopsis thalia
241	6	2.6	105	22	AAW31125	Peptide #5162 enco	314	6	2.6	135	21	AAW80291	Humanised anti-Fas
242	6	2.6	106	22	AA682034	S. epidermidis ope	315	6	2.6	135	21	AAW80292	Humanised anti-Fas
243	6	2.6	107	22	AA654125	Propionibacterium	316	6	2.6	135	22	AAW44502	Propionibacterium
244	6	2.6	109	21	AA634350	Zea mays protein f	317	6	2.6	136	15	AAW57481	Humanised 1308F VH
245	6	2.6	110	17	AAW88692	Allergen Alt a 12	318	6	2.6	136	17	AAW92084	Humanised antibody
246	6	2.6	111	19	AAW83192	Wheat 4-alpha-gluc	319	6	2.6	136	22	ABG17564	Novel human diagno
247	6	2.6	111	21	AA612573	Zea mays protein f	320	6	2.6	138	22	AAW62797	Propionibacterium
248	6	2.6	111	21	ABR38499	Peptide #6005 enco	321	6	2.6	138	22	AAW66337	Novel human diagno
249	6	2.6	111	22	ABR23651	Protein #5650 enco	322	6	2.6	138	22	ABG01165	Novel human diagno
250	6	2.6	111	22	AAW59115	Human brain expres	323	6	2.6	138	22	ABG26296	Novel human diagno
251	6	2.6	111	22	AAW71650	Human bone marrow	324	6	2.6	138	22	ABG28151	Novel human diagno
252	6	2.6	111	22	AAW19253	Peptide #5687 enco	325	6	2.6	139	21	AAW75079	Neisseria gonorrhoe
253	6	2.6	111	22	AAW31944	Peptide #5981 enco	326	6	2.6	139	21	AAW75080	Neisseria meningit
254	6	2.6	112	20	AAW18127	Clone 1 of A. thal	327	6	2.6	139	21	AAW75081	Neisseria meningit
255	6	2.6	112	21	AA621110	Arabidopsis thalia	328	6	2.6	139	21	AAW75081	S. epidermidis ope
256	6	2.6	112	21	AA628552	Arabidopsis thalia	329	6	2.6	140	22	ABG26320	Novel human diagno
257	6	2.6	112	21	AA634703	Arabidopsis thalia	330	6	2.6	142	21	AAW47049	Arabidopsis thalia
258	6	2.6	112	21	AA652666	Arabidopsis thalia	331	6	2.6	142	21	AAW47064	Arabidopsis thalia
259	6	2.6	112	21	AA652670	Arabidopsis thalia	332	6	2.6	142	21	AAW57167	Arabidopsis thalia
260	6	2.6	113	21	AA604869	Arabidopsis thalia	333	6	2.6	142	22	AAW41513	Propionibacterium
261	6	2.6	113	21	AA641926	Arabidopsis thalia	334	6	2.6	144	22	ABG13852	Novel human diagno
262	6	2.6	113	21	AA647050	Arabidopsis thalia	335	6	2.6	145	19	AAW60119	Mycobacterium vacc
263	6	2.6	113	21	AA647065	Arabidopsis thalia	336	6	2.6	145	20	AAW14865	Novel human diagno
264	6	2.6	113	21	AA647080	Arabidopsis thalia	337	6	2.6	145	22	ABG16992	Novel human diagno
265	6	2.6	113	22	ABR39444	Peptide #6950 enco	338	6	2.6	146	18	AAW22841	Human anti-tumour
266	6	2.6	113	22	ABR24209	Protein #6208 enco	339	6	2.6	146	21	AAW46658	Arabidopsis thalia
267	6	2.6	113	22	AAW60131	Human brain expres	340	6	2.6	148	22	AAW10299	Human polypeptide
268	6	2.6	113	22	AAW72745	Human bone marrow	341	6	2.6	149	22	ABR59178	Drosophila melanog
269	6	2.6	113	22	AAW32973	Peptide #7010 enco	342	6	2.6	151	21	AAW44246	Arabidopsis thalia
270	6	2.6	114	22	AAW44336	Propionibacterium	343	6	2.6	151	22	AAW03604	Human polypeptide
271	6	2.6	114	22	AAW11521	Human polypeptide	344	6	2.6	151	21	AAW00836	Human secreted pro
272	6	2.6	116	22	ABG25103	Novel human diagno	345	6	2.6	153	21	AAW33173	Eucalyptus grandis
273	6	2.6	117	15	AAW57476	CDR-grafted anti-R	346	6	2.6	155	21	AAW17607	Arabidopsis thalia
274	6	2.6	117	16	AAW66296	Human immunoglobul	347	6	2.6	155	21	AAW56304	Propionibacterium
275	6	2.6	117	16	AAW66334	Human immunoglobul	348	6	2.6	155	22	AAW13344	Novel human secret
276	6	2.6	117	17	AAW92079	Murine 1308F VH CD	349	6	2.6	157	21	AAW17606	Arabidopsis thalia
277	6	2.6	119	18	AAW13526	Anti-melanoma anti	350	6	2.6	158	22	AAW39656	Propionibacterium
278	6	2.6	119	22	ABR40557	Peptide #8063 enco	351	6	2.6	158	22	AAW16464	Human novel secret
279	6	2.6	119	22	ABR24855	Protein #6854 enco	352	6	2.6	158	22	AAW98515	Gorilla olfactory
280	6	2.6	119	22	AAW61415	Human bone expres	353	6	2.6	160	22	ABG26487	Novel human diagno
281	6	2.6	119	22	AAW614205	Human bone marrow	354	6	2.6	161	22	ABG29965	Novel human diagno
282	6	2.6	119	22	AAW43319	Peptide #8356 enco	355	6	2.6	165	22	AAW05113	Human polypeptide
283	6	2.6	120	15	AAW47491	Humanised anti-CD1	356	6	2.6	166	22	AAW07352	Interleukin-X (IL-
284	6	2.6	120	18	AAW27551	Human Ab heavy cha	357	6	2.6	168	21	AAW04868	Arabidopsis thalia
285	6	2.6	120	22	AAW07768	Human polypeptide	358	6	2.6	168	21	AAW54695	Arabidopsis thalia
286	6	2.6	120	22	AAW02535	Anti-radiopocyte mon	359	6	2.6	172	21	AAW47063	Arabidopsis thalia
287	6	2.6	123	19	AAW79228	Heavy chain variab	360	6	2.6	172	22	ABG07576	Novel human diagno
288	6	2.6	123	20	AAW19814	B. burgdorferi ant	361	6	2.6	172	22	ABG14155	Novel human diagno
289	6	2.6	123	22	ABG16390	Novel human diagno	362	6	2.6	172	22	ABG14414	Novel human diagno
290	6	2.6	123	22	ABG26294	Novel human diagno	363	6	2.6	172	22	AAW32808	Novel human secret
291	6	2.6	125	20	AAW13036	Human secreted pro	364	6	2.6	175	22	ABR62382	Drosophila melanog
292	6	2.6	125	21	AAW47079	Arabidopsis thalia	365	6	2.6	176	22	AAW55201	Propionibacterium
293	6	2.6	126	15	AAW45609	Monoclonal antibod	366	6	2.6	178	22	ABG14807	Novel human diagno
294	6	2.6	126	21	AAW00026	Human secreted pro	367	6	2.6	180	22	AAW66383	Human partial olfa
295	6	2.6	126	22	AAW92417	C glutamicum prote	368	6	2.6	182	21	AAW82504	Human adenovirus t
296	6	2.6	129	21	AAW46659	Arabidopsis thalia	369	6	2.6	184	21	AAW42698	Propionibacterium
297	6	2.6	129	21	AAW52669	Arabidopsis thalia	370	6	2.6	184	22	ABG06690	Novel human diagno
298	6	2.6	129	21	AAW64703	Human 5' EST relat	371	6	2.6	184	22	ABG14160	Novel human diagno
299	6	2.6	129	21	AAW1859	Human cardiovascu	372	6	2.6	184	22	ABG19507	Novel human diagno
300	6	2.6	130	21	AAW57218	Human prostate can	373	6	2.6	185	19	AAW98230	H. pylori GHPO 234
301	6	2.6	130	22	ABR63591	Drosophila melanog	374	6	2.6	187	22	ABG16394	Novel human diagno
302	6	2.6	130	22	AAW64604	Propionibacterium	375	6	2.6	189	22	AAW42341	Propionibacterium
303	6	2.6	131	22	ABR37784	Peptide #5290 enco	376	6	2.6	191	21	AAW39548	Arabidopsis thalia

377	6	2.6	192	16	AAR69640	Hepatitis C virus	450	6	2.6	249	16	AAR77611	Humanised 5G1.1 VH
378	6	2.6	192	16	AAR69658	Hepatitis C virus	451	6	2.6	249	18	AAW24061	Human ORFX receptor
379	6	2.6	192	16	AAR69656	Hepatitis C virus	452	6	2.6	250	21	AAAB42957	Human ORFX ORF2721
380	6	2.6	192	16	AAR69644	Hepatitis C virus	453	6	2.6	250	22	ABG07012	Novel human diagno
381	6	2.6	192	17	AAR89527	Hepatitis C virus	454	6	2.6	250	22	AAW78506	Human protein sequ
382	6	2.6	192	17	AAR89529	Hepatitis C virus	455	6	2.6	250	22	AAAB93330	Human protein sequ
383	6	2.6	192	17	AAR89511	Hepatitis C virus	456	6	2.6	253	22	ABG22238	Novel human diagno
384	6	2.6	192	17	AAR89515	Hepatitis C virus	457	6	2.6	252	22	ABAB11941	Human CGI-97 prote
385	6	2.6	192	19	AAW41596	Hepatitis C virus	458	6	2.6	253	22	AAW79490	Human protein sequ
386	6	2.6	192	22	ABG15682	Novel human diagno	459	6	2.6	254	21	AAV53010	Human secreted pro
387	6	2.6	194	21	AAAG10530	Arabidopsis thalia	460	6	2.6	254	22	AAW78341	Human protein sequ
388	6	2.6	194	21	AAAG24413	Arabidopsis thalia	461	6	2.6	256	22	ABG14800	Novel human diagno
389	6	2.6	194	21	AAU31017	Novel human secret	462	6	2.6	256	22	AAAG92545	C glutaminicum prote
390	6	2.6	195	21	AAAB40635	Human ORFX ORF399	463	6	2.6	256	22	AAAG2681	Murine OR-1like pol
391	6	2.6	196	22	AAAG08071	Lipid biosynthesis	464	6	2.6	257	21	AAAG07568	Arabidopsis thalia
392	6	2.6	196	22	AAAG83319	P patens lipid met	465	6	2.6	257	21	AAAG17567	Arabidopsis thalia
393	6	2.6	201	21	AAAG47048	Arabidopsis thalia	466	6	2.6	262	21	AAAB42488	Human ORFX ORF2262
394	6	2.6	201	22	ABAB68183	Drosophila melanog	467	6	2.6	263	22	ABG06689	Novel human diagno
395	6	2.6	202	17	AAR89497	Penicillin acylase	468	6	2.6	263	22	ABG16991	Novel human diagno
396	6	2.6	202	17	AAR89495	Penicillin acylase	469	6	2.6	264	22	ABG14668	Novel human diagno
397	6	2.6	202	17	AAR89496	Penicillin acylase	470	6	2.6	264	22	ABG16528	Novel human diagno
398	6	2.6	202	22	AAAG72674	Murine OR-1like pol	471	6	2.6	265	22	AAU48363	Proprionibacterium
399	6	2.6	204	22	AAE10920	Human gene 12 enco	472	6	2.6	268	21	AAAG11289	Arabidopsis thalia
400	6	2.6	205	22	AAAB66985	Ox40 protein. Uni	473	6	2.6	268	21	AAAG49632	Arabidopsis thalia
401	6	2.6	208	22	AAAB5399	Human protein sequ	474	6	2.6	269	22	ABG16993	Novel human diagno
402	6	2.6	210	20	AAU07103	Colon cancer assoc	475	6	2.6	271	22	AAU53107	Proprionibacterium
403	6	2.6	210	21	AAAG39547	Arabidopsis thalia	476	6	2.6	271	22	ABG15685	Novel human diagno
404	6	2.6	211	18	AAW14495	Urease accessory m	477	6	2.6	272	21	ABG19951	Novel human diagno
405	6	2.6	211	18	AAW14495	Peptide #3832 enco	478	6	2.6	272	21	AAV70732	Klebsiella oxytoca
406	6	2.6	211	22	ABAB36378	Peptide #3884 enco	479	6	2.6	272	22	ABAB11203	Drosophila melanog
407	6	2.6	211	22	ABAB21732	Protein #3751 enco	480	6	2.6	272	22	AAW40815	Human polypeptide
408	6	2.6	211	22	AAW57143	Human brain expres	481	6	2.6	272	22	AAU19621	Human diagnostic a
409	6	2.6	211	22	AAW69536	Human bone marrow	482	6	2.6	273	19	AAW60128	M. vaccae antigen
410	6	2.6	211	22	AAW17366	Peptide #3800 enco	483	6	2.6	273	20	AAW14874	Partial amino acid
411	6	2.6	211	22	AAW29876	Peptide #3913 enco	484	6	2.6	274	22	ABAB58196	Drosophila melanog
412	6	2.6	211	22	AAW05055	Peptide #3737 enco	485	6	2.6	274	22	ABG20434	Novel human diagno
413	6	2.6	212	22	ABAB71999	Drosophila melanog	486	6	2.6	275	14	AAAR43390	Sequence specific
414	6	2.6	213	22	AAAB60357	Chicken atonal hom	487	6	2.6	275	17	AAAR8993	Neisseria gonorrhoe
415	6	2.6	218	14	AAAR33259	Sj23-1-like protein.	488	6	2.6	275	21	AAV67400	N. gonorrhoeae spec
416	6	2.6	218	22	ABAB60938	Drosophila melanog	489	6	2.6	278	22	ABG07552	Novel human diagno
417	6	2.6	219	21	AAV96302	Human IGFAM-14 imm	490	6	2.6	279	21	AAAG20607	Arabidopsis thalia
418	6	2.6	220	22	ABAB58448	Drosophila melanog	491	6	2.6	284	22	AAU59854	Proprionibacterium
419	6	2.6	220	22	AAAB94801	Human protein sequ	492	6	2.6	284	22	ABG07559	Novel human diagno
420	6	2.6	221	22	AAU57429	Proprionibacterium	493	6	2.6	286	22	ABAB62405	Drosophila melanog
421	6	2.6	222	21	AAAG10529	Arabidopsis thalia	494	6	2.6	287	22	ABG14156	Novel human diagno
422	6	2.6	222	21	AAAG24412	Arabidopsis thalia	495	6	2.6	289	22	AAU16031	Human novel secret
423	6	2.6	222	22	ABAB58672	Drosophila melanog	496	6	2.6	291	22	ABG07730	Novel human diagno
424	6	2.6	222	22	ABAB38154	Novel human diagno	497	6	2.6	292	22	ABG24161	Novel human diagno
425	6	2.6	224	19	AAW98587	H. pylori GHPO 85	498	6	2.6	294	22	ABAB60740	Novel human diagno
426	6	2.6	226	21	AAAG07569	Arabidopsis thalia	499	6	2.6	294	22	AAAB52463	Mycobacterium tube
427	6	2.6	226	21	AAAG11062	Arabidopsis thalia	500	6	2.6	295	21	AAV68463	Mouse testis speci
428	6	2.6	226	21	AAAG17568	Arabidopsis thalia	501	6	2.6	295	22	ABG03705	Novel human diagno
429	6	2.6	228	22	AAU35239	Enterococcus faeca	502	6	2.6	297	22	AAAB78949	C. glutamicum SRT
430	6	2.6	228	22	AAU05775	Rice invertase inh	503	6	2.6	298	22	AAAG72929	Human olfactory re
431	6	2.6	230	21	AAAG46657	Arabidopsis thalia	504	6	2.6	298	22	AAAG72930	Human olfactory re
432	6	2.6	231	22	ABG05553	Novel human diagno	505	6	2.6	298	22	AAAG72935	Human olfactory re
433	6	2.6	232	22	ABAB60555	Drosophila melanog	506	6	2.6	299	22	AAAG72931	Human olfactory re
434	6	2.6	232	22	ABAG07577	Novel human diagno	507	6	2.6	299	22	AAAG72936	Human olfactory re
435	6	2.6	235	21	AAAG44245	Arabidopsis thalia	508	6	2.6	299	22	AAAG72937	Human olfactory re
436	6	2.6	235	22	AAU61793	Proprionibacterium	509	6	2.6	300	22	ABG14415	Novel human diagno
437	6	2.6	236	22	ABG33665	Novel human diagno	510	6	2.6	300	22	AAAG72932	Human olfactory re
438	6	2.6	237	22	AAW79065	Human protein sequ	511	6	2.6	300	22	AAAG72933	Human olfactory re
439	6	2.6	238	21	AAAG34396	Arabidopsis thalia	512	6	2.6	300	22	AAAG72934	Human olfactory re
440	6	2.6	239	22	AAW79064	Human protein sequ	513	6	2.6	301	22	AAAG72927	Human olfactory re
441	6	2.6	241	22	ABG04939	Novel human diagno	514	6	2.6	302	19	AAW98243	H. pylori GHPO 852
442	6	2.6	242	21	AAU33231	Novel human secret	515	6	2.6	305	22	AAAG66367	Human partial olfa
443	6	2.6	242	21	AAV15137	Anti-murine CTLA-4	516	6	2.6	305	22	AAAG66389	Human partial olfa
444	6	2.6	245	22	AAAB67619	Human leukocyte an	517	6	2.6	306	21	AAV51614	S. avermitilis HRP
445	6	2.6	247	18	AAW20248	H. pylori cytoplas	518	6	2.6	311	22	ABG19950	Novel human diagno
446	6	2.6	247	18	ABG29563	Novel human diagno	519	6	2.6	312	22	AAAG66377	Human partial olfa
447	6	2.6	248	16	AAAR77616	Humanised CDR-graf	520	6	2.6	313	19	AAW53955	Bacillus subtilis
448	6	2.6	248	16	AAAR77607	Humanised CDR-graf	521	6	2.6	314	22	AAU24694	Human olfactory re
449	6	2.6	249	16	AAAR77615	Humanised 5G1.1 VH	522	6	2.6	314	22	AAU24763	Human olfactory re



523	6	2.6	314	22	AA672151	Human olfactory re	596	6	2.6	362	19	AAW69717	Herpesviral VP22 p
524	6	2.6	315	22	AA673015	Olfactory receptor	597	6	2.6	362	21	AAW82497	Human adenovirus t
525	6	2.6	316	22	AAU16014	Human novel secret	598	6	2.6	362	22	AA625272	Follicular conjunc
526	6	2.6	317	22	AAE10692	G-protein coupled	599	6	2.6	366	18	AAW40348	B. cereus LeuDH pr
527	6	2.6	317	22	AAE11901	Human G-protein co	600	6	2.6	366	21	AA636484	Arabidopsis thalia
528	6	2.6	317	22	AA671408	Human olfactory re	601	6	2.6	366	22	AAW78703	Human protein seg
529	6	2.6	317	22	AA671703	Human olfactory re	602	6	2.6	367	21	AA613801	Arabidopsis thalia
530	6	2.6	317	22	AA672330	Human OR-like poly	603	6	2.6	367	21	AA640335	Arabidopsis thalia
531	6	2.6	317	22	AA672925	Human olfactory re	604	6	2.6	368	22	AA620307	Novel human diagno
532	6	2.6	317	22	AA672977	Olfactory receptor	605	6	2.6	369	22	ABG16527	Novel human diagno
533	6	2.6	318	22	AAU58952	Propionibacterium	606	6	2.6	370	20	AA114924	Amino acid sequenc
534	6	2.6	320	21	AA634713	Arabidopsis thalia	607	6	2.6	372	19	AAW72164	HSV-2 strain SB5 C
535	6	2.6	320	21	AA195055	Canida albicans p	608	6	2.6	372	19	AA623647	Arabidopsis thalia
536	6	2.6	321	22	AB803778	Human musculoskele	609	6	2.6	375	19	AAW41441	Thermotable alkyl
537	6	2.6	321	22	AAU23231	Novel human enzyme	610	6	2.6	376	22	AB860164	Drosophila melanog
538	6	2.6	321	22	AAU23757	Novel human enzyme	611	6	2.6	377	21	AA688643	Amino acid sequenc
539	6	2.6	322	21	AA634712	Arabidopsis thalia	612	6	2.6	377	22	AA631728	Amino acid sequenc
540	6	2.6	323	21	AA640336	Arabidopsis thalia	613	6	2.6	377	22	AA671711	Mastadenovirus 9 f
541	6	2.6	324	22	AA693112	C glutamicum prote	614	6	2.6	378	21	AA646131	Arabidopsis thalia
542	6	2.6	324	22	AA679609	Arabidopsis thalia	615	6	2.6	378	22	AA688081	Amino acid sequenc
543	6	2.6	325	21	AA632391	Drosophila thalia	616	6	2.6	382	22	AAU48462	Propionibacterium
544	6	2.6	326	22	AB863538	Drosophila melanog	617	6	2.6	383	22	AB865888	Drosophila melanog
545	6	2.6	326	22	AA672717	Murine OR-like pol	618	6	2.6	384	22	AB860223	Drosophila melanog
546	6	2.6	327	22	ABG15678	Novel human diagno	619	6	2.6	388	18	AAW47066	Human brain p2x-1
547	6	2.6	327	22	ABG17556	Novel human diagno	620	6	2.6	388	18	AAW55035	HPuRR amino acid s
548	6	2.6	328	22	AB858351	Drosophila melanog	621	6	2.6	388	22	AA884382	Amino acid sequenc
549	6	2.6	329	22	AB826298	Novel human diagno	622	6	2.6	388	22	AA868075	Amino acid sequenc
550	6	2.6	330	22	AAU38133	Salmonella typhi c	623	6	2.6	389	21	AA646130	Arabidopsis thalia
551	6	2.6	331	21	AA195072	Novel human diagno	624	6	2.6	391	21	AA636483	Arabidopsis thalia
552	6	2.6	331	22	ABG16651	Novel human diagno	625	6	2.6	391	21	AA646129	Arabidopsis thalia
553	6	2.6	333	21	AA650874	Arabidopsis thalia	626	6	2.6	391	22	AB856335	Non-endogenous hum
554	6	2.6	333	22	AA671843	Human olfactory re	627	6	2.6	392	20	AAV00139	Enterococcus faeca
555	6	2.6	334	22	AA672928	Human olfactory re	628	6	2.6	392	22	AA896350	Putative P. abyssi
556	6	2.6	335	22	AAU37137	Staphylococcus aur	629	6	2.6	392	22	AA868079	Amino acid sequenc
557	6	2.6	336	20	AA137733	Protein involved i	630	6	2.6	393	22	ABG20187	Novel human diagno
558	6	2.6	344	19	AA69762	Acetobacter xylinu	631	6	2.6	394	22	AAU32882	Novel human secret
559	6	2.6	344	22	AA684959	Human secreted pro	632	6	2.6	395	22	ABG03788	Novel human diagno
560	6	2.6	347	20	AAV08214	Rat glucuronyltran	633	6	2.6	395	22	ABG14173	Novel human diagno
561	6	2.6	347	20	AAW90057	Rat GlCAT-P protei	634	6	2.6	398	22	AA868073	Amino acid sequenc
562	6	2.6	348	21	AA636485	Arabidopsis thalia	635	6	2.6	399	22	AB860049	Drosophila melanog
563	6	2.6	350	18	AAW09968	HSV-1 (F) protease	636	6	2.6	401	22	ABG17572	Novel human diagno
564	6	2.6	350	18	AAW09978	HSV-1 (F) protease	637	6	2.6	402	22	AB860625	Drosophila melanog
565	6	2.6	350	18	AAW09977	HSV-1 (F) protease	638	6	2.6	404	21	AAW47067	Human brain p2x-2
566	6	2.6	350	18	AAW09976	HSV-1 (F) protease	639	6	2.6	405	21	AA845447	Human secreted pro
567	6	2.6	350	18	AAW09975	HSV-1 (F) protease	640	6	2.6	405	22	ABG10424	Novel human diagno
568	6	2.6	350	18	AAW09974	HSV-1 (F) protease	641	6	2.6	407	18	AAW08384	Novel human CAP
569	6	2.6	350	18	AAW09973	HSV-1 (F) protease	642	6	2.6	408	22	AAE12887	Human chordin-like
570	6	2.6	350	18	AAW09972	HSV-1 (F) protease	643	6	2.6	409	22	AAU38241	Salmonella typhi c
571	6	2.6	350	18	AAW09971	HSV-1 (F) protease	644	6	2.6	410	19	AAW60054	Brain-associated l
572	6	2.6	350	18	AAW09970	HSV-1 (F) protease	645	6	2.6	410	20	AAV31663	Mouse neuroserpin.
573	6	2.6	350	18	AAW09969	HSV-1 (F) protease	646	6	2.6	410	20	AAV31664	Human brain-associ
574	6	2.6	350	18	AAW09967	HSV-1 (F) protease	647	6	2.6	410	21	AA819550	Human neuroserpin.
575	6	2.6	350	18	AAW09965	HSV-1 (F) protease	648	6	2.6	410	21	AAV58172	Murine neuroserpin
576	6	2.6	350	18	AAW09964	HSV-1 (F) protease	649	6	2.6	410	21	AAV58173	Human neuroserpin
577	6	2.6	350	18	AAW09963	HSV-1 (F) protease	650	6	2.6	410	21	AAV67239	Brain-Associated I
578	6	2.6	350	18	AAW09962	HSV-1 (F) protease	651	6	2.6	410	22	AAU00537	Human BA1F polypep
579	6	2.6	350	18	AAW09961	HSV-1 (F) protease	652	6	2.6	413	21	AA845448	Human secreted pro
580	6	2.6	350	18	AAW09960	HSV-1 (F) protease	653	6	2.6	413	21	AB868607	Drosophila melanog
581	6	2.6	350	18	AAW09959	HSV-1 (F) protease	654	6	2.6	414	22	AA893964	Human polypeptide,
582	6	2.6	350	18	AAW09958	HSV-1 (F) protease	655	6	2.6	415	13	AA828638	UL26 protease dele
583	6	2.6	350	18	AAW09957	HSV-1 (F) protease	656	6	2.6	415	12	ABG14164	Novel human diagno
584	6	2.6	350	18	AAW09956	HSV-1 (F) protease	657	6	2.6	416	22	ABG04597	Novel human diagno
585	6	2.6	350	18	AAW09955	HSV-1 (F) protease	658	6	2.6	417	22	ABG07733	Novel human diagno
586	6	2.6	350	18	AAW10155	HSV-1 (F) protease	659	6	2.6	417	22	ABG12837	Novel human diagno
587	6	2.6	353	22	AB862613	Drosophila melanog	660	6	2.6	417	22	AA680962	Human gpCR58 #1.
588	6	2.6	353	22	ABG05551	Novel human diagno	661	6	2.6	419	22	AAU36502	Pseudomonas aerugi
589	6	2.6	353	22	ABG06757	Novel human diagno	662	6	2.6	419	22	AA680975	Human gpCR58 #3.
590	6	2.6	353	22	AA896441	Putative P. abyssi	663	6	2.6	420	22	AAU35408	Haemophilus influe
591	6	2.6	355	22	AA893925	Human protein sequ	664	6	2.6	420	22	AAU35837	Helicobacter pylor
592	6	2.6	356	22	AA868082	Amino acid sequenc	665	6	2.6	420	22	AAU35992	Helicobacter pylor
593	6	2.6	357	22	AAU32816	Novel human secret	666	6	2.6	422	22	AA874772	Human secreted pro
594	6	2.6	359	21	AA193397	Amino acid sequenc	667	6	2.6	423	22	ABG03642	Novel human diagno
595	6	2.6	361	22	AA623563	Follicular conjunc	668	6	2.6	423	22	AAE04796	Human aspartyl pro

669	6	2.6	423	22	AAB88479	Human membrane or	742	6	2.6	476	19	AAW72024	HSV-2 strain SB5 C
670	6	2.6	425	21	AAG23387	Arabidopsis thalia	743	6	2.6	478	22	ABG15687	Novel human diagno
671	6	2.6	425	22	AAB92792	Human protein sequ	744	6	2.6	481	22	AAG75592	Human colon cancer
672	6	2.6	427	22	ABR71359	Drosophila melanog	745	6	2.6	482	22	AAU38270	Salmonella typhi C
673	6	2.6	428	20	AAV05332	Inflammatory cytoK	746	6	2.6	487	18	AAW15471	Hantaan virus poly
674	6	2.6	428	21	AAI12798	Rice alpha-Amy7-C	747	6	2.6	489	22	ABG14285	Novel human diagno
675	6	2.6	428	22	AAW50251	Rice alpha-amyase	748	6	2.6	494	21	AAAG48093	Arabidopsis thalia
676	6	2.6	428	22	AAAB7245	Alpha-amyase rela	749	6	2.6	496	22	ABAB69420	Drosophila melanog
677	6	2.6	429	16	AAAR76520	Alpha-amyase-7-C	750	6	2.6	498	21	AAAB10038	LCMV coat glycopro
678	6	2.6	429	18	AAAW22727	Membrane protein M	751	6	2.6	499	22	AAAG82195	S. epidermidis ope
679	6	2.6	429	22	AAE12886	Human choridin-like	752	6	2.6	500	19	AAW56791	L. lactis RI portl
680	6	2.6	429	22	AAAG1874	C glutamicum prote	753	6	2.6	502	22	AAU04832	E. coli cellular p
681	6	2.6	429	22	AAU02750	Novel Human Protei	754	6	2.6	503	20	AAV02867	Thermotoga neopoli
682	6	2.6	429	22	AAAB76819	Corynebacterium q1	755	6	2.6	503	22	ABAB62834	Drosophila melanog
683	6	2.6	432	22	ABAB64855	Drosophila melanog	756	6	2.6	503	22	AAU35487	Haemophilus influe
684	6	2.6	433	15	AAAR55130	Rice alpha-amyase	757	6	2.6	505	22	AAU36334	Pseudomonas aerugi
685	6	2.6	433	19	AAW72144	HSV-2 strain SB5 C	758	6	2.6	505	22	AAAG80974	Human nPCR58 #2.
686	6	2.6	433	19	AAW72012	HSV-2 strain SB5 C	759	6	2.6	506	22	ABAB61810	Drosophila melanog
687	6	2.6	433	22	AAU19572	Human diagnostic a	760	6	2.6	507	21	AAV82488	Human L-type amino
688	6	2.6	434	14	AAAR32987	Rice alpha-amyase	761	6	2.6	507	22	ABG11780	Novel human diagno
689	6	2.6	434	18	AAW10469	Rice alpha-amyase	762	6	2.6	507	22	ABG14659	Novel human diagno
690	6	2.6	434	18	AAW11871	Rice alpha-amyase	763	6	2.6	513	22	ABG06546	Novel human diagno
691	6	2.6	434	20	AAV01375	O. sativa alpha-am	764	6	2.6	514	13	AAAR28643	UL26 protease dele
692	6	2.6	434	20	AAW84383	Rice alpha-amyase	765	6	2.6	517	22	ABG16617	Novel human diagno
693	6	2.6	434	21	AAV87792	Rice alpha-amyase	766	6	2.6	518	19	AAW61362	Aspartic proteinas
694	6	2.6	435	22	ABAG29570	Novel human diagno	767	6	2.6	518	20	AAV41714	Human PPO852 prote
695	6	2.6	436	22	ABG16422	Novel human diagno	768	6	2.6	518	20	AAV22239	Human CSP56, aspar
696	6	2.6	439	22	AAU34200	Staphylococcus aur	769	6	2.6	518	20	AAV13799	Human aspartyl pro
697	6	2.6	439	22	AAAB80076	Amino acid sequenc	770	6	2.6	518	21	AAAB44270	Human PPO852 (UNQ4
698	6	2.6	443	22	AAAB68080	Amino acid sequenc	771	6	2.6	518	21	AAV88424	Human aspartyl pro
699	6	2.6	444	22	AAU30756	Novel human secret	772	6	2.6	518	21	AAV51063	S. tendae nicomycl
700	6	2.6	445	22	ABG05552	Novel human secret	773	6	2.6	518	21	AAV50817	Streptomyces tende
701	6	2.6	446	21	AAAB25414	Pinus radiata cell	774	6	2.6	518	22	AAE10628	Human aspartyl pro
702	6	2.6	447	22	AAU36154	Klebsiella pneumon	775	6	2.6	518	22	AAE10656	Human Asp 1 protel
703	6	2.6	448	22	AAAG1349	C glutamicum prote	776	6	2.6	518	22	AAU29059	Human PRO polypept
704	6	2.6	449	22	AAAB75201	Drosophila gustato	777	6	2.6	518	22	AAE06858	Human aspartyl pro
705	6	2.6	451	21	AAV93382	Human PPO157 (UNQ	778	6	2.6	518	22	AAU06602	Human aspartyl pro
706	6	2.6	451	22	AAU029164	Human PRO polypept	779	6	2.6	518	22	AAU07201	Human aspartyl pro
707	6	2.6	451	22	AAU02749	Novel Human Protei	780	6	2.6	518	22	AAE02580	Human aspartyl pro
708	6	2.6	451	22	AAAB87566	Human PPO1557. Ho	781	6	2.6	518	22	AAE02608	Human Aspartyl pro
709	6	2.6	451	22	AAAB66131	Protein of the inv	782	6	2.6	524	22	AAE05440	Novel human diagno
710	6	2.6	451	22	AAAB48069	Human extracellular	783	6	2.6	525	22	ABAB71642	Drosophila melanog
711	6	2.6	452	21	AAAG13800	Arabidopsis thalia	784	6	2.6	526	10	AAAP90587	Polyepitide with m
712	6	2.6	453	21	AAAG40334	Arabidopsis thalia	785	6	2.6	527	22	ABG15862	Novel human diagno
713	6	2.6	453	22	ABG14171	Novel human diagno	786	6	2.6	528	22	ABG13737	Novel human diagno
714	6	2.6	455	22	ABG12029	Novel human diagno	787	6	2.6	529	19	AAW73045	Ply virus G glyco
715	6	2.6	457	22	ABAB12464	Human bone marrow	788	6	2.6	529	19	AAW73046	Chandipura virus G
716	6	2.6	458	18	AAAO9030	Neutonal nicotinic	789	6	2.6	529	21	AAV99528	Ply virus membran
717	6	2.6	458	22	ABAG16999	Novel human diagno	790	6	2.6	529	21	AAV99529	Chandipura virus m
718	6	2.6	458	22	ABAB11778	Human FGF receptor	791	6	2.6	530	22	ABAG16998	Novel human diagno
719	6	2.6	458	22	AAE12775	Human cholinergic	792	6	2.6	534	22	ABG04517	Novel human diagno
720	6	2.6	458	22	AAAW79325	Human protein sequ	793	6	2.6	536	21	AAAB53136	Macaca mulatta rha
721	6	2.6	458	22	AAAW5740	Human protein sequ	794	6	2.6	537	22	ABAB1550	Drosophila melanog
722	6	2.6	458	22	AAAG89932	C glutamicum prote	795	6	2.6	537	22	ABAB67157	Drosophila melanog
723	6	2.6	459	21	AAAG13799	Arabidopsis thalia	796	6	2.6	539	22	AAAB68074	Amino acid sequenc
724	6	2.6	461	18	AAW14006	Caenorhabditis ele	797	6	2.6	541	22	ABG17001	Novel human diagno
725	6	2.6	461	19	AAW14007	Pyridine nucleotid	798	6	2.6	542	22	AAAB66342	Castor bean calnex
726	6	2.6	462	18	AAW69359	Arabidopsis thalia	799	6	2.6	545	22	ABAB68867	Drosophila melanog
727	6	2.6	463	21	AAAG07155	Arabidopsis thalia	800	6	2.6	545	22	AAU38979	Drosophila melanog
728	6	2.6	463	21	AAAG48101	Novel human diagno	801	6	2.6	546	22	AAU04063	Mouse interleukin-
729	6	2.6	466	22	ABAG17916	Novel human diagno	802	6	2.6	546	22	AAAB85275	Mouse IL-20 recept
730	6	2.6	467	19	AAW72177	HSV-2 strain SB5 C	803	6	2.6	547	17	AAW06135	Choline oxidase us
731	6	2.6	468	21	AAV71295	Human orphan G pro	804	6	2.6	547	18	AAW22053	Choline oxidase us
732	6	2.6	468	21	AAAB02829	Human G protein co	805	6	2.6	547	22	AAE07054	Human gene 4 encod
733	6	2.6	468	22	AAAG91023	C glutamicum prote	806	6	2.6	549	22	AAAB68077	Amino acid sequenc
734	6	2.6	468	22	AAAB76815	Corynebacterium g1	807	6	2.6	549	22	AAAB68078	Amino acid sequenc
735	6	2.6	470	21	AAV94267	Human G-protein co	808	6	2.6	550	21	AAAG46256	Arabidopsis thalia
736	6	2.6	470	21	AAV94268	Human G-protein co	809	6	2.6	551	11	AAAR07282	Maltoetraose. Ps
737	6	2.6	470	22	AAE10175	Human lipoxin A4 r	810	6	2.6	554	21	AAAG46255	C glutamicum thalia
738	6	2.6	470	22	AAE04567	Human G-protein co	811	6	2.6	554	22	AAAG92535	C glutamicum prote
739	6	2.6	470	22	AAAB46838	Human G-protein co	812	6	2.6	554	22	AAAB79255	Corynebacterium gl
740	6	2.6	475	22	ABG14170	Novel human diagno	813	6	2.6	555	22	ABG06700	Novel human diagno
741	6	2.6	476	19	AAW72127	HSV-2 strain SB5 C	814	6	2.6	555	22	ABG12798	Novel human diagno

815	6	2.6	557	21	AA808112	A polypheanol oxida	888	6	2.6	705	22	AAU29322	Human PRO polypept
816	6	2.6	561	18	AAW14440	Protein involved i	889	6	2.6	705	22	AAU04956	Human Interleukin
817	6	2.6	564	22	AB558411	Drosophila melanog	890	6	2.6	705	22	AA887606	Human PRO20040. H
818	6	2.6	565	22	ABG08794	Novel human diagno	891	6	2.6	705	22	AA861884	Chimeric zcytor14
819	6	2.6	567	21	AA818197	Plasmodium falcipa	892	6	2.6	706	22	AB866693	Drosophila melanog
820	6	2.6	569	16	AA849293	Splachn 2-oxogluta	893	6	2.6	707	20	AAW83395	Rabbit protein-con
821	6	2.6	569	22	AAU34910	Enterococcus faeca	894	6	2.6	707	22	ABG24674	Novel human diagno
822	6	2.6	571	22	AAU16075	Human novel secret	895	6	2.6	708	20	AAW74088	Human hPEP1 prote
823	6	2.6	575	22	AAU34647	E. coli cellular p	896	6	2.6	708	20	AAW74087	Gastro-intestinal
824	6	2.6	575	22	AA861881	Human variant zcyt	897	6	2.6	708	20	AAW83394	Human protein-comp
825	6	2.6	585	20	AAU08485	Y. lipolytica. Paec	898	6	2.6	717	10	AA891933	BI antigen. Toxop
826	6	2.6	588	22	AB869947	Drosophila melanog	899	6	2.6	717	21	AA829900	Arabidopsis thalia
827	6	2.6	588	22	AA883117	S. epidermidis ope	900	6	2.6	717	22	ABG17438	Novel human diagno
828	6	2.6	592	9	AA860477	Pyruvate oxidase.	901	6	2.6	722	22	AAW39029	Human polypeptide
829	6	2.6	601	21	AA808123	A polypheanol oxida	902	6	2.6	730	22	ABG17032	Novel human diagno
830	6	2.6	603	13	AA828641	UL26 protease dele	903	6	2.6	735	21	AA827789	Arabidopsis thalia
831	6	2.6	608	21	AA829904	Arabidopsis thalia	904	6	2.6	735	21	AAU32806	Novel human secret
832	6	2.6	609	20	AAU14957	Amino acid sequenc	905	6	2.6	745	21	AA827788	Arabidopsis thalia
833	6	2.6	609	22	ABG07734	Novel human diagno	906	6	2.6	758	22	AB864656	Drosophila melanog
834	6	2.6	609	22	ABG14417	Novel human diagno	907	6	2.6	764	12	AA812504	Canine thyroid sti
835	6	2.6	609	22	AA883257	Murine FAMP3 parti	908	6	2.6	764	15	AA860568	Down-regulated in
836	6	2.6	610	20	AA821628	Ligand binding dom	909	6	2.6	775	22	ABG17219	Novel human diagno
837	6	2.6	612	17	AA891947	Brevibacterium fla	910	6	2.6	783	11	AA805804	C-terminal of natl
838	6	2.6	613	20	AAU14933	Amino acid sequenc	911	6	2.6	794	22	ABG08768	Novel human diagno
839	6	2.6	613	22	AB860220	Drosophila melanog	912	6	2.6	814	21	AA830844	Arabidopsis thalia
840	6	2.6	613	22	AAU34632	E. coli cellular p	913	6	2.6	815	22	ABG10390	Novel human diagno
841	6	2.6	613	22	AA883223	Murine FAMP3 SEQ I	914	6	2.6	816	12	AA814444	A. faecalis penticil
842	6	2.6	614	17	AA883271	Murine FAMP3 SEQ I	915	6	2.6	824	22	ABG25104	Novel human diagno
843	6	2.6	614	17	AAW07908	Pemphigus vulgaris	916	6	2.6	827	11	AA805049	Human villin. Hom
844	6	2.6	614	21	AA829903	Arabidopsis thalia	917	6	2.6	837	22	AB863623	Drosophila melanog
845	6	2.6	615	13	AA828642	UL26 protease dele	918	6	2.6	865	21	AA826153	Neospora NC-p65 ve
846	6	2.6	619	22	AB870767	Drosophila melanog	919	6	2.6	872	22	AB869476	Drosophila melanog
847	6	2.6	626	13	AA828640	UL26 protease dele	920	6	2.6	885	17	AA892747	SAB virus gB glyco
848	6	2.6	627	22	ABG14169	Novel human diagno	921	6	2.6	903	20	AAU37116	Protein involved i
849	6	2.6	635	13	AA828634	UL26 protease. He	922	6	2.6	930	22	ABG04240	Novel human diagno
850	6	2.6	635	13	AA828650	UL26 protease subs	923	6	2.6	930	22	ABG17993	Novel human diagno
851	6	2.6	635	13	AA828649	UL26 protease subs	924	6	2.6	939	14	AA830742	Human pemphigus vu
852	6	2.6	635	13	AA828651	UL26 protease subs	925	6	2.6	999	22	AA859815	Tutd protein #6.
853	6	2.6	635	13	AA828652	UL26 protease subs	926	6	2.6	1014	22	ABG12435	Novel human diagno
854	6	2.6	635	13	AA828646	UL26 protease subs	927	6	2.6	1018	22	AB861379	Drosophila melanog
855	6	2.6	635	13	AA828646	UL26 protease subs	928	6	2.6	1059	22	ABG07732	Novel human diagno
856	6	2.6	635	16	AA871031	HSV-1 UL26 gene pr	929	6	2.6	1059	22	AAU32823	Novel human secret
857	6	2.6	635	22	AB862805	UL26 protease inseq	930	6	2.6	1060	22	ABG20068	Novel human diagno
858	6	2.6	636	13	AA828635	UL26 protease inseq	931	6	2.6	1062	22	ABG14418	Novel human diagno
859	6	2.6	636	13	AA828636	UL26 protease inseq	932	6	2.6	1087	22	AA878992	Human cancer-inhib
860	6	2.6	636	13	AA828637	UL26 protease inseq	933	6	2.6	1088	21	AAU06527	Human WART2, ortho
861	6	2.6	637	22	AAU32818	Novel human secret	934	6	2.6	1088	21	AA807663	Amino acid sequenc
862	6	2.6	643	22	AA859119	Human polypeptide	935	6	2.6	1088	21	AA807664	Amino acid sequenc
863	6	2.6	643	22	AA870155	DNA encoding human	936	6	2.6	1088	22	AA862429	Human kidney ankyr
864	6	2.6	647	22	AAW40905	Kidney injury asso	937	6	2.6	1097	12	ABG21941	Novel human diagno
865	6	2.6	651	20	AAW86313	Drosophila melanog	938	6	2.6	1099	17	AAW05177	Lats large tumour
866	6	2.6	652	22	AB864920	Drosophila melanog	939	6	2.6	1099	21	AAU70393	Drosophila melanog
867	6	2.6	654	22	AA894772	Human protein sequ	940	6	2.6	1101	22	AA882299	Wheat starch branc
868	6	2.6	655	22	AA894770	Human protein sequ	941	6	2.6	1105	22	AB858401	Drosophila melanog
869	6	2.6	658	22	ABG03643	Novel human diagno	942	6	2.6	1121	22	AA879244	Amino acid sequenc
870	6	2.6	663	21	AA830846	Arabidopsis thalia	943	6	2.6	1135	15	AA850037	Hantaan virus G1/
871	6	2.6	664	16	AA875190	Osteoinductive ret	944	6	2.6	1135	21	AA868784	Amino acid sequenc
872	6	2.6	669	20	AAU00141	Enterococcus faeca	945	6	2.6	1141	14	AA831961	Human cardiac CGT
873	6	2.6	671	15	AA861135	Delta-pyrrolone-5-	946	6	2.6	1165	21	AA843016	Human OREF OREF2780
874	6	2.6	671	18	AAW24386	Delta1-pyrrolone-5	947	6	2.6	1165	22	ABG17468	Novel human diagno
875	6	2.6	672	21	AA830845	Arabidopsis thalia	948	6	2.6	1175	22	ABG17468	Novel human diagno
876	6	2.6	675	22	AA861885	Chimeric zcytor14	949	6	2.6	1191	22	ABG12436	Novel human diagno
877	6	2.6	683	22	AA829231	C glutamicum prote	950	6	2.6	1212	22	AA804368	Human kinase (PKIN
878	6	2.6	686	22	AB857992	Drosophila melanog	951	6	2.6	1216	18	AAW14487	Urease protein. M
879	6	2.6	687	22	AA894945	Canine retrovirus	952	6	2.6	1219	22	ABG17469	Novel human diagno
880	6	2.6	688	22	AA861883	Chimeric zcytor14	953	6	2.6	1233	20	AAU55954	Mouse STE20-relate
881	6	2.6	688	22	AA861880	Human cytokine rec	954	6	2.6	1236	20	AB865297	Drosophila melanog
882	6	2.6	692	22	AA830113	C glutamicum prote	955	6	2.6	1239	20	AAU55931	Human zcl protein.
883	6	2.6	697	21	AA827790	Arabidopsis thalia	956	6	2.6	1257	22	AB867273	Drosophila melanog
884	6	2.6	697	21	AA816532	Novel human diagno	957	6	2.6	1268	22	ABG29502	Novel human diagno
885	6	2.6	699	22	AB859209	Drosophila melanog	958	6	2.6	1272	22	AA884881	Murine protein, SE
886	6	2.6	700	21	AA846254	Arabidopsis thalia	959	6	2.6	1272	22	AA884883	Murine protein, SE
887	6	2.6	703	19	AAW47389	Rice delta-1-pyrro	960	6	2.6	1291	22	ABG28604	Novel human diagno

961	6	2.6	1307	22	ABBS9336	Drosophila melanog
962	6	2.6	1311	22	ABBS0748	Drosophila melanog
963	6	2.6	1329	22	AAU34519	E. coli cellular p
964	6	2.6	1372	22	ABG24404	Novel human diagno
965	6	2.6	1428	21	AAV97033	Caspase 8-Interact
966	6	2.6	1477	16	AAK67691	S. cerevisiae scau
967	6	2.6	1477	18	AAW10424	Saccharomyces cere
968	6	2.6	1477	20	AAV06819	Fumonisin-resistan
969	6	2.6	1480	22	ABBS9227	Drosophila melanog
970	6	2.6	1583	22	ABBS9828	Protein #5 encoded
971	6	2.6	1596	22	ABBS9845	Drosophila melanog
972	6	2.6	1638	20	AAV00138	Enterococcus faeca
973	6	2.6	1638	20	AAV00140	Enterococcus faeca
974	6	2.6	1638	20	AAV00142	Enterococcus faeca
975	6	2.6	1655	22	ABG17466	Novel human diagno
976	6	2.6	1730	22	ABBS2049	Corn earworm Bt to
977	6	2.6	1742	22	ABBS9031	Drosophila melanog
978	6	2.6	1959	12	AAK10562	Mutant protease (d
979	6	2.6	1962	12	AAK10560	Mutant protease (K
980	6	2.6	1962	12	AAK10561	Mutant protease (K
981	6	2.6	1962	12	AAK10557	Mutant protease (A
982	6	2.6	1962	12	AAK10558	Mutant protease (N
983	6	2.6	1962	12	AAK10559	Mutant protease (A
984	6	2.6	1962	12	AAK10563	Mutant protease (K
985	6	2.6	1968	12	AAK10941	Mutant protease (d
986	6	2.6	1974	12	AAK10940	Mutant protease (d
987	6	2.6	2037	22	ABBS9099	Drosophila melanog
988	6	2.6	2225	22	ABBS1877	Drosophila melanog
989	6	2.6	2243	22	ABBS8484	Murine protein, SE
990	6	2.6	2724	22	ABBS0119	Novel human diagno
991	6	2.6	2737	22	ABBS8288	Novel human diagno
992	6	2.6	2771	22	ABBS3880	Drosophila melanog
993	6	2.6	2778	22	ABBS8683	Drosophila melanog
994	6	2.6	2819	22	ABBS5408	Human 07CG27 gene
995	6	2.6	3076	22	ABG07038	Novel human diagno
996	6	2.6	3256	21	AAV50976	Human cell cycle p
997	6	2.6	3313	22	AAU30134	Novel human secret
998	6	2.6	3389	22	AAE07984	Dengue virus (DEN)
999	6	2.6	3391	12	AAK13166	Proteins encoded b
1000	6	2.6	3391	18	AAW06591	Polypeptide of atc

## ALIGNMENTS

RESULT 1	
AAW64668	standard; Protein: 259 AA.
XX	
AC	AAW64668;
XX	
DT	23-OCT-1998 (first entry)
XX	
DE	Human TRID protein.
XX	
KW	TRAIL receptor without intracellular domain; TRID; TNFR-5; human;
KW	tumour necrosis factor receptor-5; TNF-related apoptosis-inducing ligand;
KW	hematopoietic tissue; immune system; ligand; apoptosis; treatment.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Peptide
FT	1..27
FT	/label= signal
FT	27..259
FT	/label= TRID
FT	Region
FT	42..52
FT	/label= epitope
FT	58..66
FT	Region
FT	/label= epitope
FT	68..76
FT	Region
FT	/label= epitope
FT	79..85
FT	Region

FT	/label= epitope
FT	91..102
FT	/label= epitope
FT	Region
FT	110..122
FT	/label= epitope
FT	Region
FT	126..136
FT	/label= epitope
FT	Region
FT	142..148
FT	/label= epitope
XX	
PN	WO9830693-A2.
XX	
PD	16-JUL-1998.
XX	
PF	13-JAN-1998; 98WO-US00152.
XX	
PR	07-AUG-1997; 97US-0054885.
XX	
PR	14-JAN-1997; 97US-0035496.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Ehner R, Feng P, Gentz RL, Ni J, Ruben SM, Wei Y;
XX	
PI	Yu G;
XX	
PI	WPI: 1998-399141/34.
XX	
DR	N-PSDB; AAV51348.
XX	
PT	Human TRAIL receptor without an intracellular domain polypeptide -
XX	
PT	used in the diagnosis of immune system-related disorder(s)
XX	
PS	Claim 1b: Fig 1; 90pp; English.
XX	
CC	This sequence represents a human TRID (TRAIL (TNF-related
CC	apoptosis-inducing ligand) receptor without an intracellular domain).
CC	TRID is a member of the tumour necrosis factor receptor (TNFR) family
CC	also known as TNFR-5. TRID is expressed in haematopoietic tissues and
CC	other normal human tissues. For a number of immune system-related
CC	disorders, substantially altered (whether increased or decreased) levels
CC	of TRID gene expression can be detected, therefore the TRID polypeptides,
CC	nucleic acids and antibodies are useful in the diagnosis of such immune
CC	system related disorders. Mutations of the TRID gene can also be
CC	detected. TRID can also be used to identify ligands which may be useful
CC	in the treatment of apoptosis related disorders. TRID is administered to
CC	humans at a parenteral dose of 0.01 to 1 mg/kg/day.
XX	
SQ	Sequence 259 AA;

Query Match 100.0%; Score 233; DB 19; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 2,4e-233;  
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TTARQEEVPOQTAPVAPQOQRHSFKGEECPAGSHRSFHTGACNCPFGVDYTNASNNPSCF	60
DB	27	ltarqeevpgqtvpqqrhrshfkgeecpagshrshcgtacnccpctegvdytnasnnpscfc	86
QY	61	PCYVCKSDQKHKSCTMTRTDYVCOCKEGTFRNENSPENCRCRCSRCPGSEVOVSNCTSMWD	120
DB	87	pctvcksdqkhkssctmtrdtyvcckegtfrenenspencrcrcsrgpsegevyvsnctswd	146
QY	121	IQCVBEFGANATVETPAAEETMTNTPSGTPAPAAETMTNTPSGTPAPAAETMTNTPSGTPA	180
DB	147	iqcveefganatvetpaaeeetmntpsgtppaaeeetmntpsgtppaaeeetmntpsgtppa	206
QY	181	PAAEETMTNTPSGTPAPAAETMTNTPSGTPASSHYSCTIVGIIIVLIVFV	233
DB	207	paaeetmtntpsgtppaaeeetmntpsgtppasshylsctivgiiivliviivf	259

RESULT 2	
AAW88408	
XX	AAW88408 standard; Protein: 259 AA.
XX	

Query Match	100.0%	Score 233:	DB 20:	Length 259:	
Best Local Similarity	100.0%	Pred. No. 2,4e-233:			
Matches 233:	Conservative	0:	Mismatches 0:	Indels 0:	Gaps 0:
QY 1	TTAROEVPQQTVAAPQOQRHSPKSGECPAGSHRSHTGACNPFCEGVDTYNASNNPSCF	60			
DB 27	ttargeevpqgtvapgqqrhstfxgcecpagshrshtgacnptcgvdyvtasnnepscf	86			
QY 61	PCTVCKSDOKHKSSCTMTRDYVQCKEGTFERNENSPDMCRKCSRCPSEGVQVSNCTSWDD	120			
DB 87	pctvcksdokhkssctmtrdyvcckegtferrnenspdmcrkcsrpsgevgvsnctswdd	146			
QY 121	ICQVEBFGANATVPEPAAEETMNTSPGAPAPAAEETMTSPCTPAPAAEETMTTSPGTPA	180			
DB 147	iqcveefganatvelpeaaeetmtspgtpapaaeetmtspgtpapaaeetmtspgtpa	206			
QY 181	PAAEETMTTSPCTPAPAAEETMTTSPGTPASSHYISCTIVGIIIVLIVLIVFV	233			
DB 207	paaeetmttspgtpapaaeetmttspgtpasshyisctivgiiivlilivlvf	259			
RESULT 3					
AAU12321					
ID AAU12321	standard; Protein; 259 AA.				
XX AC	AAU12321;				
XX DT	24-OCT-2001 (first entry)				
XX DE	Human PRO366 polypeptide sequence.				
XX KW	Human secretory and transmembrane; PRO; mammalian; cancer; lung;				
XX KW	breast; prostate; cervical; tumour necrosis factor- $\alpha$ 1pha; TNF- $\alpha$ 1pha;				
XX KW	carilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;				
XX KM	adipocyte; A-peptide; factor VIIA; gene therapy.				
OS	Homo sapiens.				
PN	WO200140466-A2.				
PD	07-JUN-2001.				
PF	01-DEC-2000; 2000WO-US32678.				
PR	01-DEC-1999; 99WO-US28301.				
PR	01-DEC-1999; 99WO-US28634.				
PR	02-DEC-1999; 99WO-US28551.				
PR	02-DEC-1999; 99WO-US28564.				
PR	02-DEC-1999; 99WO-US28565.				
PR	09-DEC-1999; 99US-0170262.				
PR	16-DEC-1999; 99WO-US30095.				
PR	20-DEC-1999; 99WO-US30911.				
PR	20-DEC-1999; 99WO-US30999.				

PR 30-DEC-1999; 99WO-US31243.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US04914.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 21-MAR-2000; 2000WO-US07532.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 10-NOV-2000; 2000WO-US30873.

(GETH ) GENENTECH INC.

XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

DR WPI: 2001-408281/43.  
 DR N-PSDB: AAS21393.

XX Isolated, secretory and transmembrane PRO polypeptide used to detect  
 XX other PRO polypeptides, link bioactive molecules to cells expressing  
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 PT lung, breast, prostate, cervical

XX Claim 12; Fig 300; 813pp: English.

XX AAU12172-AAU12446 represent novel human secretory and transmembrane  
 CC PRO polypeptides. The PRO polypeptides are useful to detect other  
 CC PRO polypeptides, to link bioactive molecules to cells expressing  
 CC PRO polypeptides, to modulate biological activities of cells expressing  
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample.  
 CC Some of the 275 sequences are also useful to stimulate the release of  
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
 CC proliferation or differentiation of chondrocytes, the proliferation or  
 CC gene expression in pericyte cells, the release of proteoglycans from  
 CC cartilage, the proliferation of inner ear utricular supporting cells or  
 CC of T-lymphocytes, the release of a cytokine from peripheral blood  
 CC monocytes (PMNCs), or the proliferation of endothelial cells. Some of  
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by  
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
 CC to factor VIIa. The PRO polypeptides can be used in assays to identify  
 CC molecules involved in binding interactions. The polynucleotides encoding  
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy.

XX Sequence 259 AA:

Query Match 100.0%; Score 233; DB 22; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-233;  
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAROEYVPOOTVAPQOQRHSEKGECPAGSHRSHTGACNCTEGVDYTNASNNPSCF 60  
 |||||||  
 Db 27 ttarqeevpgqtlvapqqrshsfkgeecpagsrshsehtjaacnptcgvdvtmasnepsf 86  
 QY 61 PCTVCKSDQKHKRSCTMTRDVYCQCKEKTFRNENSPKCRKSCRPSEVQVSNCTSWMD 120  
 |||||||  
 Db 87 pctvcksdqkhkrsctmtrdvtcvcqckegtfrenspemckrcscpsgevgvsnctswd 146  
 QY 121 IQCVEEFGANATVETPAPAEETMTSPGTPAPAEETMTSPGTPAPAEETMTSPGTPA 180  
 |||||||

Db 147 iqcvEEfganAtVeTpAaeEtmtSPgTpAaeEtmtSPgTpAaeEtmtSPgTpA 206  
 QY 181 PAAETMTTSPGTPAPAEETMTSPGTPASSHYLSCTIVGIIYLVLLIVFY 233  
 |||||||  
 Db 207 paaEetmttSPgTpAaeEtmttSPgTpAsshyLSctIvGIiYlVllIvfy 259

RESULT 4  
 AAB20111  
 ID AAB20111 standard; Protein; 259 AA.

XX AAB20111;

DT 30-APR-2001 (first entry)

DE Human immunostimulant PRO366 (Apo-2DCR).

XX PRO366; UNQ321; human; immune disease; autoimmune disease;  
 KW antirheumatic; antiarthritic; antiinflammatory; antiinfective;  
 KW immunosuppressive; antidiabetic; antidiabetic; neuroprotective;  
 KW hepatotropic; virucide; dermatological; antipsoriatic;  
 KW antiasthmatic; antiallergic; immunostimulant; Apo-2DCR;  
 KW tumour necrosis factor receptor; apoptosis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..29

FT Protein /label= Signal\_peptide

FT Domain /label= Mature\_protein

FT Region /note= "transmembrane domain"

FT Modified-site 85..92

FT Modified-site 126..130

FT Modified-site /note= "TNFR/NGFR family cysteine-rich region"

FT Modified-site /note= "cAMP- and cGMP-dependent protein kinase phosphorylation site"

FT Modified-site 56..62

FT Modified-site /note= "N-myristoylation site"

FT Modified-site 72..78

FT Modified-site /note= "N-myristoylation site"

FT Modified-site 114..120

FT Modified-site /note= "N-myristoylation site"

FT Modified-site 154..160

FT Modified-site /note= "N-myristoylation site"

FT Modified-site 233..239

FT Modified-site /note= "N-myristoylation site"

FT Modified-site 72..78

FT Modified-site /note= "N-myristoylation site"

FT Modified-site 114..120

FT Modified-site /note= "N-myristoylation site"

FT Modified-site 154..160

FT Modified-site /note= "N-myristoylation site"

FT Modified-site 233..239

FT Modified-site /note= "N-myristoylation site"

WO200105972-A1.

25-JAN-2001.

15-MAR-2000; 2000WO-US06884.

20-JUL-1999; 99US-0144758.

(GETH ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ, Gurney AL;  
 PI Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D, Watanabe CK;  
 PI Wood WI;

DR WPI: 2001-103149/11.  
 DR N-PSDB: AAF30053.

XX New PRO polypeptides, nucleic acids and (ant)agonists, useful for  
 PT diagnosing and treating immune-related disorders, such as multiple  
 PT sclerosis, rheumatoid arthritis and diabetes -  
 PS Claim 20; Fig 8; 127pp; English.

CC The present sequence is that of PRO366 (UNQ321), also designated

CC Apo-2DcR, a novel human immunomodulator (27 kDa, pI 4.84), as  
CC deduced from a human breast carcinoma cDNA clone (see AAF30053).  
CC Apo-2DcR shows homology to apoptosis-linked receptors of the tumour  
CC necrosis factor receptor family, such as DR4 and Apo-2. The invention  
CC provides polynucleotides (see AAF30050-62) encoding novel human PRO  
CC proteins (see AAB20108-20) including PRO366. Claimed compositions  
CC comprising these proteins or their agonists are useful for increasing  
CC infiltration of inflammatory cells into a tissue of a mammal,  
CC stimulating or enhancing an immune response, or increasing the  
CC proliferation of T-lymphocytes in a mammal in response to an antigen.  
CC Claimed compositions comprising a PRO polypeptide or its antagonist  
CC have the opposite effect. A claimed method for treating an immune  
CC related disorder, such as a T cell disorder, involves administering  
CC a PRO polypeptide, an agonist antibody or an antagonist antibody.  
CC The disorder is selected from systemic lupus erythematosus,  
CC rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis,  
CC spondyloarthropathy, systemic sclerosis, idiopathic inflammatory  
CC myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis,  
CC autoimmune haemolytic anaemia, autoimmune thrombocytopenia,  
CC thyroiditis, diabetes mellitus, immune-mediated renal disease,  
CC demyelinated diseases (such as multiple sclerosis), autoimmune  
CC chronic active hepatitis, primary biliary cirrhosis, granulomatous  
CC hepatitis, sclerosing cholangitis, inflammatory bowel disease  
CC (ulcerative colitis and Crohn's disease), gluten-sensitive  
CC enteropathy, Whipple's disease, (auto)immune-mediated skin diseases  
CC (such as bullous skin disease, erythema multiforme and psoriasis),  
CC allergic diseases (such as asthma, allergic rhinitis, atopic  
CC dermatitis, food hypersensitivity and urticaria), immunologic  
CC diseases of the lung and transplantation associated diseases (such  
CC as graft rejection and graft-versus-host disease) (all claimed).  
CC Claimed methods of diagnosing these disorders comprise detecting  
CC the level of expression of the PRO gene. Also claimed are a method  
CC of identifying a compound capable of inhibiting the expression or  
CC activity of the PRO polypeptide, vectors, host cells, antibodies,  
CC and a method of stimulating an immune response in a mammal using  
CC PRO366.

XX Sequence 259 AA:

Query Match 100.0%; Score 233; DB 22; Length 259;  
Best Local Similarity 100.0%; Pred. No. 2.4e-233;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAQEEVPOOTVAPQOORHSFKGEECPAGSHRSEHTGACNPTCEGVDTYTNASNNPSCF 60  
DB 27 ttarqeevpqgtlvapqgrhsfkgeecpagshrehtgacncptcegvdytnasnnpscf 86  
QY 61 PCTVCKSDQKHRSCTMTRTDTCCKCKGTFFNENSPENCRCRCSRCPGSEVOVSNCTSWD 120  
DB 87 pctvcksdqkhksctmttrdtvcckckgtffnenspencrcrcsrgpsgegvsnctswd 146  
QY 121 IQCVEEFGANATVETPAAEETMTNTSPGTAPAAEETMTNTSGTAPAAEETMTTSPGTAPA 180  
DB 147 iqveefganatvetpaaeetmtntspgtapaaeetmtntsgtapaeeetmttspgtapa 206  
QY 181 PAAEETMTTSPGTAPAAEETMTTSPGTAPASHTLCTIVGIIYVLIYLVFV 233  
DB 207 paaeetmttspgtapaaeetmttspgtapashlylctivgiiyvlivlvfv 259

RESULT 5

AAB36696 ID AAB36696 standard; Protein; 259 AA.

XX AAB36696;

XX 15-MAR-2001 (first entry)

DE Human tumour necrosis factor receptor 5 (TRID) protein SEQ ID NO:2.

XX Human: tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; noctropic;

KW TRAIL receptor without intracellular domain; diagnosis; cytosolic;

KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;  
KW immunosuppressive; neuroprotective; antiviral; anti-inflammatory;  
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;  
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;  
KW cardioprotic cell death related disease; autoimmune disorder;  
KW cardiovascular disorder; viral infection.

XX Homo sapiens.

XX WO200071150-A1.

XX 30-NOV-2000.

XX 18-MAY-2000; 2000MO-US13515.

XX 20-MAY-1999; 99US-0135164.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Wei Y, Ruben SM, Gentz RL, NI J;

XX WPI: 2001-041051/05.

XX N-PSDB; AAC90774.

PT Nucleic acid encoding a TRID polypeptide, also referred to as tumor  
PT necrosis factor receptor 5, useful in the diagnosis, treatment or  
PT prevention of cancer, autoimmune disorders and viral infection -

PS Claim 15; Fig 1; 285pp: English.

XX The present sequence represents the human TRID protein (tumour necrosis  
XX factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without  
XX intracellular domain, also referred to as tumour necrosis factor  
XX receptor 5 (TNFR-5 or TR5). TRID has cytostatic, immunosuppressive,  
XX neurotropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant,  
XX antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotrophic  
XX activities; and can be used in gene therapy. The TRID polynucleotides  
XX are useful for detecting complementary polynucleotides. TRID proteins and  
XX polynucleotides are useful in the treatment of tumours, resistance to  
XX parasite, bacteria and viruses, restenosis and graft versus host disease.  
XX They are also useful for inducing proliferation of T-cells, endothelial  
XX cells and certain haematopoietic cells, to regulate antiviral responses  
XX and to prevent certain autoimmune diseases after stimulation of TRID by  
XX an agonist or TRAIL binding facilitator. The antibodies which bind TRID  
XX polypeptides are useful for treating and/or preventing diseases  
XX associated with increased or decreased apoptotic cell death. The TRID  
XX polynucleotides, proteins, antibodies, agonists and antagonists are  
XX useful in the diagnosis, treatment or prevention of: (a) cancer;  
XX (b) autoimmune disorders; (c) diseases associated with increased  
XX apoptosis; (d) cardiovascular disorders; and (e) viral infection.

XX Sequence 259 AA:

Query Match 100.0%; Score 233; DB 22; Length 259;  
Best Local Similarity 100.0%; Pred. No. 2.4e-233;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAQEEVPOOTVAPQOORHSFKGEECPAGSHRSEHTGACNPTCEGVDTYTNASNNPSCF 60  
DB 27 ttarqeevpqgtlvapqgrhsfkgeecpagshrehtgacncptcegvdytnasnnpscf 86  
QY 61 PCTVCKSDQKHRSCTMTRTDTCCKCKGTFFNENSPENCRCRCSRCPGSEVOVSNCTSWD 120  
DB 87 pctvcksdqkhksctmttrdtvcckckgtffnenspencrcrcsrgpsgegvsnctswd 146  
QY 121 IQCVEEFGANATVETPAAEETMTNTSPGTAPAAEETMTNTSGTAPAAEETMTTSPGTAPA 180  
DB 147 iqveefganatvetpaaeetmtntspgtapaaeetmtntsgtapaeeetmttspgtapa 206  
QY 181 PAAEETMTTSPGTAPAAEETMTTSPGTAPASHTLCTIVGIIYVLIYLVFV 233  
DB 207 paaeetmttspgtapaaeetmttspgtapashlylctivgiiyvlivlvfv 259

RESULT 6  
AAB53091  
ID AAB53091 standard; Protein: 259 AA.  
XX  
AC AAB53091;  
XX  
DT 28-FEB-2001 (first entry)  
XX  
DE Human angiogenesis-associated protein PRO366, SEQ ID NO:152.  
XX  
KW Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
KW gene therapy; transgenic animal.  
XX  
OS Homo sapiens.  
XX  
PN MO200053753-A2.  
PD 14-SEP-2000.  
XX  
PF 05-JAN-2000; 2000MO-US00219.  
XX  
PR 08-MAR-1999; 99MO-US05028.  
PR 12-MAR-1999; 99US-0123957.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99MO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99MO-US45698.  
PR 01-SEP-1999; 99MO-US20111.  
PR 08-SEP-1999; 99MO-US20594.  
PR 15-SEP-1999; 99MO-US21090.  
PR 15-SEP-1999; 99MO-US21547.  
PR 05-OCT-1999; 99MO-US23089.  
PR 30-NOV-1999; 99MO-US28313.  
PR 30-NOV-1999; 99MO-US28409.  
PR 02-DEC-1999; 99MO-US28564.  
PR 02-DEC-1999; 99MO-US28565.  
XX  
PA (GENTECH ) GENENTECH INC.  
XX  
PI Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
PI Pooni NF, Plett RM, Watanabe CK, Williams PM, Wood WI;  
XX  
DR WPI: 2001-090793/10.  
DR N-PSDB; AAC97488.  
XX  
XX  
PT New isolated nucleic acid for producing a PRO polypeptide, analyzing  
PT genetic disorders and treating cardiovascular, endothelial or  
PT angiogenic disorders, such as atherosclerosis, wounds or cancer -  
XX  
PS Claim 69; Fig 56; 293pp; English.  
XX  
XX  
CC The invention relates to novel human angiogenesis-associated proteins  
CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
CC PRO proteins. The invention also relates to vectors and host cells  
CC comprising a PRO nucleic acid, the recombinant production of a PRO  
CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
CC compounds which inhibit the expression of a PRO gene. The invention  
CC additionally encompasses methods of identifying modulators of PRO  
CC expression or activity; diagnosing a cardiovascular, endothelial or  
CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
CC mutations in a PRO gene, or the expression level of a PRO gene within a  
CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
CC disorder via the administration of a PRO protein, PRO nucleic acid, or

CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
CC administration of a PRO protein, or an agonist or antagonist thereof.  
CC PRO nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
CC agonists and PRO antagonists may be used as therapeutic agents to treat  
CC cardiovascular, endothelial or angiogenic disorders, such as  
CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
CC endometriosis, ulcers, cancer, Alzheimer's disease, Huntington's  
CC disease, or stroke. PRO nucleic acids are additionally useful in the  
CC recombinant production of PRO proteins, as hybridisation probes to  
CC screen libraries to isolate cDNAs with sequence identity to PRO proteins,  
CC to map genes encoding PRO proteins, to analyse genetic disorders, and in  
CC gene therapy. PRO nucleic acids can also be used to produce transgenic  
CC animals useful for the development and screening of potential  
CC therapeutic agents. The present sequence represents a PRO protein of the  
CC invention.  
XX  
SQ Sequence 259 AA;

Query Match 100.0%; Score 233; DB 22; Length 259;  
Best Local Similarity 100.0%; Pred. No. 2,4e-233;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TTARQEEVPOQTVAPOQORHSFKGECPPAGSHRSHTGACNCPBQVYTNASNNPSCF 60  
DB 27 ttaqgeevpqqvapqqrhshfkgeecppagshrshtgacnbpctevytnasnnpscf 86  
OY 61 PCTVCKSDQKHKRSCTMTRTDYCOCKEGTFRNENSPENCKRCRCSPGSEVOVSNCTSMDD 120  
DB 87 pctvcksdqkhkrsctmtrtdycockegtfrenenspencrcrcspgsevoysnctswdd 146  
OY 121 IQCVSEFGANATVERPAAEETMTNTSPGTPAPAAEETMTNTSGTPAPAAEETMTNTSPGTPA 180  
DB 147 iqcvsefganatlvetrpaaeetmtntspgtpapaaetmtntspgtpapaaetmtntspgtpa 206  
OY 181 PAAEETMTNTSPGTPAPAAEETMTNTSPGTPASSHYSCITVIGIVLVLLIVFV 233  
DB 207 paaeeetmtntspgtpapaaetmtntspgtpasshyiscitvlgivlvllivfv 259

RESULT 7  
AAB82181  
ID AAB82181 standard; Protein: 268 AA.  
XX  
AC AAB82181;  
XX  
DT 23-JUL-2001 (first entry)  
XX  
DE FLAG-TRID clone with a transmembrane domain.  
XX  
KW FLAG-epitope tag; transmembrane domain; death domain; apoptosis;  
KW cell suicide; tissue homeostasis; cell proliferation;  
KW cell-cell signalling; Trail Receptor without Intracellular Domain; TRID.  
XX  
OS Synthetic.  
XX  
FH key Location/Qualifiers  
FT Peptide 1..23  
FT /label= signal\_peptide  
FT Protein 24..268  
FT /label= FLAG\_TRID-protein  
FT Peptide 27..34  
FT /label= FLAG-epitope\_TAG  
FT Region 250..268  
FT /label= Transmembrane\_region  
PN MO200114542-A1.  
PD 01-MAR-2001.  
XX



PF 23-AUG-2000; 2000MO-US23112.  
XX  
XX 25-AUG-1999; 99US-0150747.  
XX  
XX (GENO-) GENOME THERAPEUTICS CORP.  
XX  
XX Denome SA, Swain PM, Tzellas N;  
XX  
XX WPI: 2001-374162/39.  
DR N-PSDB; AAH19325.  
XX  
XX  
PT Identifying a transmembrane domain of a membrane-spanning protein  
PT useful in defining processes in cell suicide and tissue homeostasis,  
PT comprises modifying the nucleic acid encoding a death domain-lacking  
PT membrane spanning protein -  
XX  
XX  
PS Disclosure; Fig 1; 38bp; English.  
XX  
XX The present invention relates to methods for identifying a transmembrane  
CC domain (TM) of a membrane-spanning protein. The method comprises  
CC modifying a nucleic acid encoding a death domain (DD)-lacking membrane  
CC spanning protein (e.g. Trail Receptor without Intracellular Domain; TRID)  
CC by replacing the nucleic acid encoding the TM of the DD-lacking  
CC membrane-spanning protein with a candidate nucleic acid sequence to  
CC produce a nucleic acid encoding a modified DD-lacking membrane spanning  
CC protein. The modified nucleic acid is then transfected into a host cell,  
CC which expresses a DD-containing receptor. The absence of apoptosis of the  
CC host cell is determined following exposure of the transfected cell to an  
CC apoptosis-inducing ligand. Candidate nucleic acids encoding TM prevent  
CC apoptosis of the host cell. The modified nucleic acid encoding the  
CC modified death domain-lacking membrane-spanning protein can also include  
CC a nucleic acid sequence encoding an epitope tag. The present sequence is  
CC a FLAG-TRID clone, which was used in the method of the present invention.  
CC This sequence comprises human TRID protein and the FLAG-epitope tag. The  
CC FLAG-epitope is a useful marker to purify proteins encoded by the  
CC modified DD-lacking membrane-spanning protein. The identified TM and  
CC membrane-spanning proteins may be used in defining processes involved in  
CC cell suicide and tissue homeostasis, and to evaluate, interfere and treat  
CC events, such as cell proliferation and cell-cell signalling pathways.  
XX  
XX  
SQ Sequence 268 AA:  
  
Query Match 100.0%; Score 233; DB 22; Length 268;  
Best Local Similarity 100.0%; Pred. No. 2.5e-233;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TTRQGEVPOQYIAVPOQQRHSFKGEECPAGSHSEHTGACNPCTEGVDYTNASNNEPSCF 60  
DB |||||||  
DB 36 tIarqeevppqvtvbpqqrhnsfkgeecpagshrsehtgacnptcegydytnasnepsc 95  
QY 61 PCVVCSDOKHKSSCTMRTRTVCOCKRGRNENSPCKRCSCRGEGVOVNSCTSWMD 120  
DB |||||||  
DB 96 pCvvcSdGhKssctmrtldtvcqckegltrenspemckrcscrgegvqvsncstswd 155  
QY 121 IQCVERGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPA 180  
DB |||||||  
DB 156 iQvveefganatvetpaaetmtltpptpaaetmtltpptpaaetmtltpptpaaetmtltp 215  
QY 181 PAAEETMTSPGTPAPAAEETMNTSPGTPASSHYLCTIGIIVLIVLVFV 233  
DB |||||||  
DB 216 paaeeImtspgtpapaaetmtltpasshylsctIvgIvllvIvfv 268  
  
RESULT 8  
AAW76331  
ID AAW76331 standard; Protein; 299 AA.  
XX  
AC AAW76331;  
XX  
XX  
DT 11-JAN-1999 (first entry)  
XX  
DE Human tumour necrosis related receptor TR5.

XX  
XX Tumour necrosis related receptor; TR5; human; inflammation;  
KW arthritis; septicemia; transplant rejection; autoimmune disease;  
KW inflammatory bowel disease; graft versus host disease; infection;  
KW stroke; ischemia; acute respiratory disease syndrome; psoriasis;  
KW restenosis; brain injury; AIDS; bone disease; cancer;  
KW atherosclerosis; Alzheimer's disease; therapy; diagnosis.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..165  
FT /label= sig\_peptide  
FT Protein 66..299  
FT /label= Mat\_protein  
XX  
XX EP867509-A2.  
XX  
XX  
PD 30-SEP-1998.  
XX  
XX  
PF 04-FEB-1998; 98EP-0300827.  
XX  
XX 28-JUL-1997; 97US-0901469.  
PR 05-FEB-1997; 97US-0795910.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
XX  
PI Lyn SDP, Tan KB, Truneh A, Young PR;  
XX  
XX WPI: 1998-497862/43.  
DR N-PSDB; AAV56990.  
XX  
XX  
PT New polynucleotide encoding TR5 polypeptide - used to diagnose,  
PT prevent and treat e.g. inflammation, arthritis, septicemia,  
PT autoimmune diseases, infections, stroke, ischemia, ARDS, psoriasis,  
PT restenosis, brain injury, AIDS and bone diseases  
XX  
XX  
PS Claim 5; Fig 1; 22pp; English.  
XX  
XX This is the amino acid sequence of human tumour necrosis related  
CC receptor TR5, as deduced from the sequence of an isolated cDNA  
CC clone (see AAV56990). The protein is characterised as a GPI-linked  
CC protein that has a membrane proximal O-glycosylation region. The  
CC invention provides methods for the recombinant production of TR5  
CC and its use in diagnostic and therapeutic methods. Treatment of a  
CC subject in need of enhanced TR5 activity comprises administering an  
CC agonist to the polypeptide and/or providing TR5 polynucleotide in a  
CC form so as to effect production of the polypeptide activity in vivo.  
CC Treatment of a subject with the need to inhibit TR5 polypeptide  
CC activity comprises administering an antagonist to the polypeptide,  
CC administering a nucleic acid that inhibits the expression of the  
CC nucleotide sequence encoding the polypeptide and/or administering a  
CC polypeptide that competes with the polypeptide for its ligand,  
CC substrate or receptor. Diagnosing a disease or a susceptibility  
CC to a disease related to expression or activity of TR5 polypeptide,  
CC comprises determining the presence or absence of mutation in the  
CC nucleotide sequence encoding the TR5 polypeptide in the genome of  
CC the subject and/or analysing for the presence or amount of TR5  
CC polypeptide expression in a sample. Identification of compounds  
CC which bind to TR5 comprises contacting host cells with a candidate  
CC compound and assessing the ability of it to bind to the cells. The  
CC active agents can be used for the treatment of chronic and acute  
CC inflammation, arthritis, septicemia, autoimmune diseases (e.g.  
CC inflammatory bowel disease, psoriasis), transplant rejection,  
CC graft vs host disease, infection, stroke, ischemia, acute  
CC respiratory disease syndrome, restenosis, brain injury, AIDS, bone  
CC diseases, cancer (e.g. lymphoproliferative disorders),  
CC atherosclerosis and Alzheimer's disease.  
XX  
XX  
SQ Sequence 299 AA:  
  
Query Match 100.0%; Score 233; DB 19; Length 299;

Best Local Similarity 100.0%; Pred. No. 2.8e-233;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 TTAEOEEVPOOTVAPQOORHSFKGECPAGSHRSRHTACNPGCEGVDTNANSNNEPSCF 60
    |||||||
Db 67 tlargeevpqglvppqgrhshfkgeecpagsrhshgacnpgcegvdytnasnepscfcf 126
QY 61 PCTVCKSDQKHKSCTMTTRDTVCOCKEGTFRNENSPEMCRKCSRCPSGEVOVSNCTSWMD 120
    |||||||
Db 127 pctrcksdqkhksctmttrdtvcqckegtfrenspemcrkcsrpsgegvsnctswdd 186
QY 121 IQCYEEGAMNTVETPPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPA 180
    |||||||
Db 187 iqcyeeifganaiveltpaaeelmtspgtpapaaeelmtspgtpapaaeelmtspgtpa 246
QY 181 PAAEETMTSPGTPAPAAEETMTSPGTPASSHYLSCTIVGIVLVLIYV 233
    |||||||
Db 247 paaeelmtspgtpapaaeelmtspgtpashylsctivgivilvliyvfv 299
```

## RESULT 9

AAV29864  
ID AAV29864 standard; Protein: 299 AA.

AC AAV29864;  
XX  
DT 17-NOV-1999 (first entry)  
XX

Human secreted protein clone i1442\_1.

XX Human; secreted protein; biological activity; nutritional; cytokine;  
KW cell proliferation; differentiation; immune stimulating; vaccine;  
KW haematopoiesis regulation; tissue growth; haemostatic; thrombolytic;  
KW anti-inflammatory; tumour inhibition.  
XX

OS Homo sapiens.

XX  
PN W09946287-A1.

XX  
PD 16-SEP-1999.

XX  
PE 11-MAR-1999; 99MO-US05243.

XX  
PR 11-MAR-1998; 98US-0077521.

XX  
PR 14-MAY-1998; 98US-0079124.

XX  
PR 10-MAR-1999; 99US-0266105.

XX  
PA (GEMV ) GENETICS INST INC.

XX  
PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;  
PI Werberg D, Treacy M, Agostino MJ, Steininger RJ;

XX  
DR WPI; 1999-551362/46.

XX  
DR N-PSDB; AA221096.

XX  
PT Polynucleotides encoding secreted human proteins, derived from human  
PT fetal brain, human adult blood, human adult bladder, or human adult  
PT neural tissue CDNA libraries. -

XX  
PS Claim 17; Page 104; 118pp; English.

XX  
AA221093 to AA221102 encode new human secreted proteins and AAV29861 to

XX  
AAV29873 represent the secreted proteins encoded by the polynucleotide

XX  
sequences. AA221103 to AA221112 represent probes for the secreted

XX  
proteins. The polynucleotides and proteins are predicted to have

XX  
biological activities which would make them suitable for treating,

XX  
preventing or ameliorating medical conditions in humans and animals,

XX  
although no supporting data is given. Suggested activities include  
XX nutritional activity, cytokine and cell proliferation/differentiation  
XX activity, immune stimulating (e.g. as vaccines) or suppressing activity,  
XX haematopoiesis regulating activity, tissue growth activity,  
XX activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
XX and thrombolytic activity, receptor/ligand activity, anti-inflammatory

CC activity, cadherin/tumour invasion suppressor activity, and tumour  
CC inhibition activity. The polynucleotides and proteins can also be used  
CC as nutritional sources or supplements. Such uses include use as a protein  
CC or amino acid supplement, use as a carbon source, use as a nitrogen  
CC source and use as a source of carbohydrate. They may also have utility  
CC in compositions used for bone, cartilage, tendon, ligament, and/or nerve  
CC tissue growth or regeneration, as well as for wound healing and tissue  
CC repair and replacement, and in the treatment of burns, incisions and  
CC ulcers. The proteins which induce cartilage and/or bone growth in  
CC circumstances where bone is not normally formed, have application in  
CC the healing of bone fractures and cartilage damage or defects in humans  
CC and other animals.  
SQ Sequence 299 AA;

Query Match 100.0%; Score 233; DB 20; Length 299;  
Best Local Similarity 100.0%; Pred. No. 2.8e-233;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 TTAEOEEVPOOTVAPQOORHSFKGECPAGSHRSRHTACNPGCEGVDTNANSNNEPSCF 60
    |||||||
Db 67 tlargeevpqglvppqgrhshfkgeecpagsrhshgacnpgcegvdytnasnepscfcf 126
QY 61 PCTVCKSDQKHKSCTMTTRDTVCOCKEGTFRNENSPEMCRKCSRCPSGEVOVSNCTSWMD 120
    |||||||
Db 127 pctrcksdqkhksctmttrdtvcqckegtfrenspemcrkcsrpsgegvsnctswdd 186
QY 121 IQCYEEGAMNTVETPPAAEETMTSPGTPAPAAEETMTSPGTPAPAAEETMTSPGTPA 180
    |||||||
Db 187 iqcyeeifganaiveltpaaeelmtspgtpapaaeelmtspgtpapaaeelmtspgtpa 246
QY 181 PAAEETMTSPGTPAPAAEETMTSPGTPASSHYLSCTIVGIVLVLIYV 233
    |||||||
Db 247 paaeelmtspgtpapaaeelmtspgtpashylsctivgivilvliyvfv 299
```

## RESULT 10

AAV05744  
ID AAV05744 standard; Protein: 299 AA.

XX  
AC AAV05744;

XX  
DT 19-JUL-1999 (first entry)  
XX

XX  
DE Tumour necrosis factor receptor TR5.

XX  
KW Tumour necrosis factor receptor; TR5; TR1D; DCRL; agonist;

XX  
KW antagonist; screening; human; cancer; AIDS; Alzheimer's disease;

XX  
KW inflammation; arthritis; septicemia; autoimmune disease;

XX  
KW psoriasis; inflammatory bowel disease; transplant rejection;

XX  
KW graft versus host disease; infection; stroke; ischaemia;

XX  
KW acute respiratory disease syndrome; restenosis; brain injury;

XX  
KW bone disease; atherosclerosis; therapy.

XX  
OS Homo sapiens.

XX  
PN EP911633-A1.

XX  
PD 28-APR-1999.

XX  
PE 02-OCT-1998; 98EP-0203332.

XX  
PR 08-OCT-1997; 97US-0061334.

XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX  
PI McDonnell PC, Young PR, Zou J;

XX  
DR WPI; 1999-246560/21.

XX  
PT Identifying agonists and antagonists of tumor necrosis factor  
PT related receptors TR1, TR3 and TR5, and of ligand TR3, useful for

PT treatment of cancer, AIDS, Alzheimer's disease, bone disease etc  
XX Disclosure; Page 13-14; 23pp; English.  
XX  
CC The present sequence represents tumour necrosis factor receptor  
CC (TNFR) TR5, also known as TR1D or DR1. The invention relates  
CC to TNFR related polypeptides TR1, TR3 and TR5 (see AAY05742-44) and  
CC their ligand TR3 (see AAY05745). TR1, TR3, TR5 and TR3 are used in  
CC claimed methods of identifying agonists and antagonists, i.e.  
CC compounds that bind to the receptors or ligand, and which activate  
CC (agonist) or inhibit activation of (antagonists) TR1, TR3, TR5 or  
CC TR3. A screening kit for identifying agonists, antagonists,  
CC ligands, receptors, substrates, enzymes etc. for TR1, TR3, TR5 or  
CC TR3 polypeptides is provided. The agonists and antagonists are  
CC useful for treatment of chronic and acute inflammation, arthritis,  
CC septicemia, autoimmune disease e.g. inflammatory bowel disease,  
CC psoriasis, transplant rejection, graft versus host disease,  
CC infection, stroke, ischaemia, acute respiratory disease syndrome,  
CC restenosis, brain injury, AIDS, bone diseases, cancer (e.g.  
CC lymphoproliferative disorders), atherosclerosis and Alzheimer's  
CC disease, etc., caused by imbalance of TR1, TR3, TR5 or TR3.  
XX  
SQ Sequence 299 AA;  
  
Query Match 100.0%; Score 233; DB 20; Length 299;  
Best Local Similarity 100.0%; Pred. No. 2.8e-233;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TTAAROEVPQOTVAPQOORHSFKGECPCAGSHREHTGACNPCTEGVDYTNASNNPSCF 60  
Db 67 ttargeevpqgtvapgqgrhsfkgeecpagsrhshgacnpctegvdytnasnnpscf 126  
QY 61 PCTVCKSDQKHKSCTMTROTVCCKEGTFRNENSPKCRKSCPSGEVYVSNCTSDMD 120  
Db 127 pcvcksdqkhksctmtrdvcckegtfrenenspckrcscpsgevyvsnctswdd 186  
QY 121 IQCVEEFGANATVETPAAEETMNTSPGTPAPAEETMNTSPGTPAPAEETMNTSPGTPA 180  
Db 187 iqveefganatvetpaaeetmntspgtpapaeetmntspgtpapaeetmntspgtpa 246  
QY 181 PAAEETMTSPGTPAPAPAEETMTSPGTPASSHLSCTIVGIIYVLLIVFV 233  
Db 247 paaeetmtspgtpapapaeetmtspgtpasshlylsctivgiiyvllylvfv 299  
  
RESULT 11  
ID AAY00933 standard; Protein; 299 AA.  
XX  
AC AAY00933;  
XX  
DT 02-JUN-1999 (first entry)  
XX  
DE Human TRAIL-R3 protein sequence.  
XX  
KW Human; DR5; TRAIL-R3; apoptosis related condition; cancer; therapy;  
KW autoimmune disease; viral infection; degenerative disorder;  
KW amyotrophic lateral sclerosis; retinitis pigmentosa; ischaemic injury;  
KW cerebellar degeneration; myelodysplastic syndrome.  
XX  
OS Homo sapiens.  
XX  
PN MO9909165-A1.  
XX  
PD 25-FEB-1999.  
XX  
PE 14-AUG-1998; 98WO-051694.5.  
XX  
PR 15-AUG-1997; 97US-0055906.  
XX  
PA (IDUN-) IDUN PHARM INC.

PI Alnemri ES;  
XX  
XX WPI; 1999-181035/15.  
DR N-PSDB; AAX27280.  
XX  
PT Newly isolated polynucleotide encoding a mammalian TRAIL receptor  
PT protein - useful in for screening for (ant)agonists that modulate  
PT the apoptotic activity mediated by DR5 or TRAIL-R3 proteins  
XX  
PS Claim 16; Page 62-63; 71pp; English.  
XX  
CC This sequence is the human TRAIL receptor TRAIL-R3 of the invention. An  
CC antibody against the TRAIL receptors is useful for detecting mammalian  
CC DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in  
CC bioassays for screening for (ant)agonists of DR5 or TRAIL-R3 proteins.  
CC (Ant)agonists identified by the assay are useful for modulating the  
CC apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis  
CC related conditions which are treated in this way, include cancer  
CC (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus  
CC erythematosus and immune-mediated glomerulonephritis), viral infections  
CC (e.g. herpes virus, poxvirus and adenovirus), degenerative disorders  
CC (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral  
CC sclerosis, retinitis pigmentosa, cerebellar degeneration, myelodysplastic  
CC syndromes (e.g. aplastic anaemia) and ischaemic injury (e.g. myocardial  
CC infarction and stroke). The polynucleotides can also be used to treat  
CC these diseases. Antisense oligonucleotides to the DNA sequences can be  
CC used to form a composition that is useful for inhibiting expression of a  
CC human DR5 or TRAIL-R3 protein.  
XX  
SQ Sequence 299 AA;  
  
Query Match 100.0%; Score 233; DB 20; Length 299;  
Best Local Similarity 100.0%; Pred. No. 2.8e-233;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 TTAAROEVPQOTVAPQOORHSFKGECPCAGSHREHTGACNPCTEGVDYTNASNNPSCF 60  
Db 67 ttargeevpqgtvapgqgrhsfkgeecpagsrhshgacnpctegvdytnasnnpscf 126  
QY 61 PCTVCKSDQKHKSCTMTROTVCCKEGTFRNENSPKCRKSCPSGEVYVSNCTSDMD 120  
Db 127 pcvcksdqkhksctmtrdvcckegtfrenenspckrcscpsgevyvsnctswdd 186  
QY 121 IQCVEEFGANATVETPAAEETMNTSPGTPAPAEETMNTSPGTPAPAEETMNTSPGTPA 180  
Db 187 iqveefganatvetpaaeetmntspgtpapaeetmntspgtpapaeetmntspgtpa 246  
QY 181 PAAEETMTSPGTPAPAPAEETMTSPGTPASSHLSCTIVGIIYVLLIVFV 233  
Db 247 paaeetmtspgtpapapaeetmtspgtpasshlylsctivgiiyvllylvfv 299  
  
RESULT 12  
ID AAW94671 standard; Protein; 299 AA.  
XX  
AC AAW94671;  
XX  
DT 04-MAY-1999 (first entry)  
XX  
DE Human TNF-related apoptosis-inducing ligand binding protein.  
XX  
KW Human; TNF-related apoptosis-inducing ligand binding protein; clotting;  
KW TRAIL-RP; tumour necrosis factor; T cell death; HIV; gene therapy;  
KW thrombotic microangiopathy; thrombotic thrombocytopenic purpura;  
KW haemolytic-uraemic syndrome; systemic lupus erythematosus.  
XX  
OS Homo sapiens.  
XX  
PN WO9900423-A1.  
XX  
PD 07-JAN-1999.

XX 25-JUN-1998; 98WO-US13491.  
 XX 26-JUN-1997; 97US-0883529.  
 XX (IMV ) IMMUNEX CORP.  
 XX Smith CA, Walczak H;  
 XX WPI: 1999-095685/08.  
 DR N-PSDB: AAX16692.  
 XX  
 XX New isolated TRAIL binding protein - which binds to a tumour  
 PT necrosis factor-related apoptosis inducing ligand, used in the  
 PT diagnosis and treatment of TRAIL-mediated disorders  
 PS  
 PS Claim 1; Fig 1; 47pp; English.  
 XX  
 XX The present sequence is human tumour necrosis factor (TNF)-related  
 CC apoptosis-inducing ligand (TRAIL) binding protein (BP). TRAIL-BP can be  
 CC used for inhibiting the biological activities of TRAIL or for purifying  
 CC TRAIL. TRAIL-BP proteins can be used for treating a TRAIL-mediated  
 CC disorder such as T cell death in HIV-infected patients. They can be used  
 CC for treating thrombotic microangiopathies such as thrombotic  
 CC thrombocytopenic purpura, haemolytic-uraemic syndrome, clotting of small  
 CC blood vessels or systemic lupus erythematosus. The TRAIL-BP nucleic  
 CC acids can also be used for gene therapy. They can also be used as  
 CC carriers for delivering attached agents to cells bearing TRAIL.  
 XX  
 XX Sequence 299 AA;

Query Match 100.0%; Score 233; DB 20; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-233;  
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TTAQOEFPQOTVAPQOORHSFKGECPAGSGHRSHTACNPTCEGVYTANSNNEPCF 60  
 Db 67 tlarqeevpgqlvppqqrhshkgeecpagsrhshetlqacnptcegvdytnasnepcsf 126  
 QY 61 PCTWCKSDQKHSCTMTMDTVCCCKEGTFRNENSPKCRKRCRCPGSEGVSNCTSD 120  
 Db 127 pctvcksdqkhsctmtmdtvccckegtlfrnenspmcrtkscrcpsgevgvsnctswdd 186  
 QY 121 IQCVEEFGANATVETPAEETMTNTSPGTAPAEETMTNTSPGTAPAEETMTNTSPGTAP 180  
 Db 187 iqcvelfganatvetpaeetmtntspgtapaeetmtntspgtapaeetmtntspgtapa 246  
 QY 181 PAAEETMTNTSPGTAPAEETMTNTSPGTAPASSHLSCTIVGIIIVLLIVFV 233  
 Db 247 paaeetmtntspgtapaeetmtntspgtapashylsctivgiiivllivfv 299

RESULT 13  
 AAW88409 ID AAW88409 standard; Protein; 299 AA.  
 XX AAW88409;  
 XX 26-APR-1999 (first entry)  
 DE Human Apo-2DcR protein (amino acids -40 to 259).  
 XX  
 KM Apo-2DcR; human; apoptosis; tumour necrosis factor receptor;  
 KM neurodegeneration; autoimmune disease; inflammation; cancer;  
 KM therapy.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH Peptide 1..40  
 FT /note= "-40 to -1 region of Apo-2DcR"  
 FT Peptide 41..69

FT Domain /note= "predicted signal peptide"  
 FT 41..201 /note= "extracellular domain, this domain is specifically claimed in claim 5"  
 FT Domain 108..149 /note= "cysteine-rich domain"  
 FT Domain 150..189 /note= "cysteine-rich domain"  
 FT Peptide 202..216 /note= "tandem repeat peptide"  
 FT Peptide 217..231 /note= "tandem repeat peptide"  
 FT Peptide 232..246 /note= "tandem repeat peptide"  
 FT Peptide 247..261 /note= "tandem repeat peptide"  
 FT Peptide 262..276 /note= "tandem repeat peptide"  
 FT Peptide 277..299 /note= "tandem repeat peptide"  
 FT Region /note= "hydrophobic C-terminal region"  
 FT Modified-site 117 /note= "N-glycosylation"  
 FT Modified-site 180 /note= "N-glycosylation"  
 FT Modified-site 196 /note= "N-glycosylation"  
 FT Modified-site 209 /note= "N-glycosylation"  
 FT Modified-site 224 /note= "N-glycosylation"  
 FT Modified-site 224 /note= "N-glycosylation"

XX WO958062-A1.  
 XX 23-DEC-1998.  
 XX 12-JUN-1998; 98WO-US12456.  
 XX 18-JUN-1997; 97US-0878168.  
 XX (GENTH ) GENENTECH INC.  
 PI Ashtkenazi AJ, Baker KP, Chuntarapai A, Gurney A;  
 PI Kim KJ, Wood WT;  
 DR WPI: 1999-095340/08.  
 DR N-PSDB: AAV84347.  
 XX New Apo-2DcR polypeptide - used for modulation and diagnosis of  
 PT apoptosis, e.g. in neurodegeneration  
 PS Claim 9; Page 53-54; 88pp; English.  
 XX This polypeptide comprises human Apo-2DcR, a novel member of the  
 CC tumour necrosis factor receptor family that binds to Apo-2 ligand.  
 CC Its amino acid sequence was deduced from the nucleotide sequence  
 CC of an isolated cDNA clone (see AAV84347); an alternative translation  
 CC initiation site in this clone will encode a polypeptide (see  
 CC AAW88408) lacking the first 40 amino acid residues of this sequence.  
 CC Apo-2DcR shows more sequence identity to DR4 (60%) and Apo-2 (50%)  
 CC than to other apoptosis-linked receptors. The polypeptide can be  
 CC obtained by expression in host cells using the vector deposited as  
 CC ATCC 209087. The invention provides vectors and host cells for  
 CC recombinant production of Apo-2DcR polypeptides, antibodies, and  
 CC transgenic and knockout animals (useful e.g. for screening and  
 CC developing drugs that protect against excessive apoptosis).  
 CC Apo-2DcR, or chimeras comprising Apo-2DcR or its (claimed)  
 CC extracellular domain fused to a heterologous polypeptide are used  
 CC to modulate apoptosis of mammalian cells (claimed) and/or NF-kappaB  
 CC activation by Apo-2 ligand, and may be expressed in vivo or ex vivo  
 CC for gene therapy. They can be used in methods for the modulation  
 CC and diagnosis of apoptosis e.g. in cases of neurodegeneration,  
 CC autoimmune diseases and inflammation. Most human tumour cells do  
 CC not express Apo-2DcR transcripts, but normal tissues do, suggesting

CC that Apo-2DR may permit selective killing of cancer cells by Apo-2  
CC ligand, possibly by protecting normal, but not cancerous, cells.  
XX  
XX  
SQ Sequence 299 AA;

Query Match 100.0%; Score 233; DB 20; Length 299;  
Best Local Similarity 100.0%; Pred. No. 2.8e-233;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTARQEEVPOQYVAPQOQRHSFKGEECPAGSHRSEHTGACNPGCEGVDYTNASNNESECF 60  
DB 67 tttarqeevppqvtvapgqqrhsfkgeecpagshrsehtgacnpgcegvdytnasnepsc 126  
QY 61 PCYVCKSDOKHKSCTMTPTVCCKEGTRFNENSPMCRCRSCSPGGEVQVSNCTSMDD 120  
DB 127 pcyvcksdqghkssctmtptvcckegtrfnenpamcrkscspggevqvsncstsmdd 186  
QY 121 IOCVEEFGANATVETPAAEETMTNTSPGTPAPAAEETMTNTSPGTPAPAAEETMTNTSPGTPA 180  
DB 187 igcvееfganatvetpaaеetmtntspgtpapaaеetmtntspgtpapaaеetmtntspgtpa 246  
QY 181 PAAEETMTNTSPGTPAPAAEETMTNTSPGTPASSHLSCTIVGIIVLYLVLFV 233  
DB 247 paaеetmtntspgtpapaaеetmtntspgtpasshlylsctivgiivlylvlfv 299

## RESULT 14

AAB01343  
ID AAB01343 standard; Protein: 299 AA.

AC AAB01343;

DT 25-SEP-2000 (first entry)

XX Death receptor.

XX UL144; death receptor; apoptosis; programmed cell death; FAS;

KW TNF- $\alpha$ ; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;

KM human.

XX Homo sapiens.

XX WO200034335-A2.

PN 15-JUN-2000.

PF 03-DEC-1999; 99WO-US26035.

XX 04-DEC-1998; 98US-0205018.

XX (SCHE ) SCHERING CORP.

XX Leong C, Phillips JH;

XX WPI; 2000-423383/36.

XX Purified or recombinant polypeptide for modulating apoptosis comprises

PT a sequence which binds to an antibody specific for UL144 or its

PT fragments

XX

XX

XX

XX

XX

Disclosure; Page 75-76; 76pp; English.

A pure or recombinant polypeptide which binds to a polyclonal antibody  
specific for the mature UL144 is useful for screening molecules which  
block induction of apoptosis or interfere with antiapoptotic activity.

The polypeptide is also useful for modulating apoptosis and useful in

treatment of conditions associated with abnormal physiology or

development, such as cancer or degenerative conditions and for

regulation of viral infection and replication. At least five

different death receptors are known, which include the CD95

(Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated

protein (TRAMP), death receptor-6 (DR-6), and TNF-related

CC apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.  
XX  
XX  
SQ Sequence 299 AA;

Query Match 100.0%; Score 233; DB 21; Length 299;  
Best Local Similarity 100.0%; Pred. No. 2.8e-233;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTARQEEVPOQYVAPQOQRHSFKGEECPAGSHRSEHTGACNPGCEGVDYTNASNNESECF 60  
DB 67 tttarqeevppqvtvapgqqrhsfkgeecpagshrsehtgacnpgcegvdytnasnepsc 126  
QY 61 PCYVCKSDOKHKSCTMTPTVCCKEGTRFNENSPMCRCRSCSPGGEVQVSNCTSMDD 120  
DB 127 pcyvcksdqghkssctmtptvcckegtrfnenpamcrkscspggevqvsncstsmdd 186  
QY 121 IOCVEEFGANATVETPAAEETMTNTSPGTPAPAAEETMTNTSPGTPAPAAEETMTNTSPGTPA 180  
DB 187 igcvееfganatvetpaaеetmtntspgtpapaaеetmtntspgtpapaaеetmtntspgtpa 246  
QY 181 PAAEETMTNTSPGTPAPAAEETMTNTSPGTPASSHLSCTIVGIIVLYLVLFV 233  
DB 247 paaеetmtntspgtpapaaеetmtntspgtpasshlylsctivgiivlylvlfv 299

## RESULT 15

AAB82182  
ID AAB82182 standard; Protein: 249 AA.

AC AAB82182;

DT 23-JUL-2001 (first entry)

XX FLAG-TRID clone without a transmembrane domain.

XX FLAG-epitope tag; transmembrane domain; death domain; apoptosis;

KW cell suicide; tissue homeostasis; cell proliferation;

KM cell-cell signaling; Trail Receptor without Intracellular Domain; TRID.

XX Synthetic.

XX key Location/Qualifiers

XX Peptide 1..23

XX Protein /label= Signal\_peptide

XX Peptide /label= FLAG-TRID

XX MISC-difference 249

XX /note= "Insertion site for candidate sequences"

XX WO200114542-A1.

XX 01-MAR-2001.

XX 23-AUG-2000; 2000WO-US23112.

XX 25-AUG-1999; 99US-0150747.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Denome SA, Swain PM, Tzellas N;

XX WPI; 2001-374162/39.

XX N-PSDB; AAH19326.

XX Identifying a transmembrane domain of a membrane-spanning protein  
useful in defining processes in cell suicide and tissue homeostasis,  
PT comprises modifying the nucleic acid encoding a death domain-lacking  
PT membrane spanning protein -  
XX  
XX  
PS Disclosure; Fig 2; 38pp; English.

XX The present invention relates to methods for identifying a transmembrane  
CC domain (TM) of a membrane-spanning protein. The method comprises  
CC modifying a nucleic acid encoding a death domain (DD)-lacking membrane  
CC spanning protein (e.g., Trail Receptor without Intracellular Domain; TRID)  
CC by replacing the nucleic acid encoding the TM of the DD-lacking  
CC membrane-spanning protein with a candidate nucleic acid sequence to  
CC produce a nucleic acid encoding a modified DD-lacking membrane spanning  
CC protein. The modified nucleic acid is then transfected into a host cell,  
CC which expresses a DD-containing receptor. The absence of apoptosis of the  
CC host cell is determined following exposure of the transfected cell to an  
CC apoptosis-inducing ligand. Candidate nucleic acids encoding TM prevent  
CC apoptosis of the host cell. The modified nucleic acid encoding the  
CC modified death domain-lacking membrane-spanning protein can also include  
CC a nucleic acid sequence encoding an epitope tag. The present sequence is  
CC a FLAG-TRID clone, which was used in the method of the present invention.  
CC This sequence comprises human TRID protein and the FLAG-epitope tag. The  
CC FLAG-epitope is a useful marker to purify proteins encoded by the  
CC modified DD-lacking membrane-spanning protein. The identified TM and  
CC membrane-spanning proteins may be used in defining processes involved in  
CC cell suicide and tissue homeostasis, and to evaluate, interfere and treat  
CC events, such as cell proliferation and cell-cell signalling pathways.

XX Sequence 249 AA:

Query Match 91.8%; Score 214; DB 22; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1.2e-213;  
Matches 214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAROEYVPOQTVAPOOQRHSFKGECPAGSHRSEHTGACNPGTEGVDTNANNEPSCF 60  
DB 36 ttargeevpqgtvapgqrhshfkgecpagshrehtgacnpgtegvdytnasnepscfcf 95  
QY 61 PCTVCKSDQKHKSCTMTFRTDVCOCKEGRFNENSPKCRKCRSPGSEVOVSNCTSMDD 120  
DB 96 pctvcksdqkhksctmtftrdvcqckeglfrenspemcrkscrcpsgsevoysnctswdd 155  
QY 121 IQCYEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPA 180  
DB 156 iqcyeeifganatvetpaaeeumntspgtpapaaeeumntspgtpapaaeeumntspgtpa 215  
QY 181 PAAEETMTSPGTPAPAAEETMTSPGTPASSHY 214  
DB 216 paaeeumntspgtpapaaeeumntspgtpasshy 249

RESULT 16

AAW93578 AAW93578 standard; Protein: 259 AA.

AC AAW93578;

DT 18-JUN-1999 (first entry)

DE Human hAPO9 protein.

XX Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;  
KM developmental abnormality; gestational abnormality; prostate cancer;  
KM APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;  
KM cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;  
KM apoptosis; human.

OS Homo sapiens.

PN W09911791-A2.

PD 11-MAR-1999.

PF 04-SEP-1998; 98WO-US18393.

PR 05-SEP-1997; 97US-0924634.

XX

PA (UNIV ) UNIV WASHINGTON.

XX Chaudhary PM.

XX WPI: 1999-205191/17.

DR N-PSDB: AAX23412.

XX New Tumor Necrosis Factor family receptor polypeptides and ligands -  
PT useful for diagnosis and treatment of prostate cancer and  
PT developmental or gestational abnormalities

XX Claim 24; Fig 6; 156pp; English.

PS This invention describes isolated Tumor Necrosis Factor (TNF) family  
CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active  
CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or  
CC their active fragments. APO4 is useful for diagnosing prostate cancer  
CC by determining levels of APO4 in an individual. Prostate cancer can also  
CC be treated using APO4 selective binding agents linked to a therapeutic  
CC moiety. APO4 polypeptides are also useful for identifying selective  
CC binding agents, useful in diagnosis/treatment of disease by binding of  
CC agents to the polypeptide/active fragment which is extracellular, or  
CC expressed on the cell surface. The binding is preferably performed in  
CC vivo. APO4 polypeptides/active fragments are also useful for screening  
CC for agonists and antagonists by binding and observing the change in APO4  
CC activity. Effective pharmacological agents useful in diagnosis or  
CC treatment of disease are also identified using APO4 polypeptides/active  
CC fragments and APO4 signal transducer molecules that specifically interact  
CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4  
CC activity. The method is performed in vivo or in vitro. APO polypeptides  
CC are all useful as immunogens for preparing antibodies. APO4 is also  
CC useful for diagnosis/treatment of developmental or gestational  
CC abnormalities. APO8 was transfected to human breast carcinoma cell line  
CC MCF-7, and induced apoptosis.

XX Sequence 259 AA:

Query Match 79.4%; Score 185; DB 20; Length 259;  
Best Local Similarity 100.0%; Pred. No. 1.5e-183;  
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAROEYVPOQTVAPOOQRHSFKGECPAGSHRSEHTGACNPGTEGVDTNANNEPSCF 60  
DB 27 ttargeevpqgtvapgqrhshfkgecpagshrehtgacnpgtegvdytnasnepscfcf 86  
QY 61 PCTVCKSDQKHKSCTMTFRTDVCOCKEGRFNENSPKCRKCRSPGSEVOVSNCTSMDD 120  
DB 87 pctvcksdqkhksctmtftrdvcqckeglfrenspemcrkscrcpsgsevoysnctswdd 146  
QY 121 IQCYEEFGANATVETPAAEETMNTSPGTPAPAAEETMNTSPGTPAPAAEETMNTSPGTPA 180  
DB 147 iqcyeeifganatvetpaaeeumntspgtpapaaeeumntspgtpapaaeeumntspgtpa 206  
QY 181 PAEE 185  
DB 207 paaee 211

RESULT 17

AAV05726 AAV05726 standard; Protein: 259 AA.

AC AAV05726;

DT 19-JUL-1999 (first entry)

DE Tumour necrosis factor receptor TRAIL-R3.

XX Tumour necrosis factor receptor; apoptosis; cancer;

XX Mammalia.

OS

```

XX Key Location/Qualifiers
FH Peptide 1..24
FT /note="signal peptide"
FT Protein 25..259
FT /note="mature protein"
FT Region 162..175
FT /note="TAPE repeat"
FT Region 176..191
FT /note="TAPE repeat"
FT Region 192..206
FT /note="TAPE repeat"
FT Region 207..221
FT /note="TAPE repeat"
FT Region 222..236
FT /note="TAPE repeat"
FT Domain 238..259
FT /note="Transmembrane domain"
XX WO912963-A2.
XX 18-MAR-1999.
XX 11-SEP-1998; 98WO-US19029.
XX 06-MAY-1998; 98US-0084422.
XX 12-SEP-1997; 97US-0058631.
XX (BIOJ ) BIOGEN INC.
XX Tschoopp J;
XX WPI; 1999-276942/23.
XX N-PSDB; AAX25349.
XX Novel tumor necrosis factor receptor proteins TRAIL-R2 and TRAIL-R3
XX Disclosure; Page 28; 28pp; English.
XX The present sequence represents TRAIL-R3, a novel mammalian
XX cysteine-rich receptor of the tumor necrosis factor receptor family.
XX The invention is related to novel receptors for TRAIL, i.e. TRAIL-2
XX (see AAY05725) and TRAIL-3. TRAIL-3 is highly glycosylated. It is
XX a putative glycosylphosphatidylinositol-anchored protein, which is
XX either cell-associated or processed and secreted. Secreted
XX TRAIL-R3 competes for the binding of TRAIL to TRAIL-R1 and/or
XX TRAIL-R2, thereby acting as an inhibitor of apoptosis. Expression
XX of TRAIL-R3 is restricted to peripheral blood lymphocytes and
XX skeletal muscle. It is likely that TRAIL-3 acts as an important
XX regulator of TRAIL-R2 and -R3 induced cell death in vivo. A method
XX for preventing or reducing the advancement, severity or effects of
XX an immunological disease involves administering a TRAIL-R2 or
XX TRAIL-R3 blocking agent such as a soluble TRAIL-R (preferably
XX comprising a human immunoglobulin Fc domain) and an antibody. A
XX method of treating cancer involves administration of antibodies
XX against TRAIL-R3 or TRAIL-R2. A method of inducing cell death
XX involves administration of an agent capable of inhibiting the
XX binding of TRAIL-R2 or -R3 to its ligand.
XX Sequence 259 AA:
SO
Query Match 60.1%; Score 140; DB 20; Length 259;
Best Local Similarity 100.0%; Pred. No. 6.8e-137;
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 94 NSPEMCKKCSGPGEGVQVNSCTSWDDIOCYEEFGANAYETPAAEETMTSPTPAPAA 153
DB 120 nspemckkcsrpsgeqvnsctswddiqcyeeefganatvelpaaeeemntspptpaa 179
OY 154 EETNTNTSGPGPAPAAEETMTSPTPAPAAEETMTSPTPAPAAEETMTSPTPAPAA 213
DB 180 eetntntspgtpapaaeetmtspptpapaaeetmtspgtpapaaeetmtspptpash 239

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OY 214 YLSCTGIVLIVLIVFV 233
DB 240 ylsctgivilvllivfv 259
RESULT 18
ID AAW88450
XX AAW88450 standard; Peptide; 48 AA.
AC AAW88450;
DE 26-APR-1999 (first entry)
XX Human Apo-2Dcr peptide.
XX Apo-2Dcr, human; apoptosis; tumor necrosis factor receptor;
XX neurodegeneration; autoimmune disease; inflammation; cancer;
XX therapy.
XX Homo sapiens.
XX OS
XX PN WO9858062-A1.
XX 23-DEC-1998.
XX 12-JUN-1998; 98WO-US12456.
XX 18-JUN-1997; 97US-0878168.
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Chuntarapai A, Gurney A;
XX Kim KJ, Wood WJ;
XX WPI; 1999-095340/08.
XX New Apo-2Dcr polypeptide - used for modulation and diagnosis of
XX apoptosis, e.g. in neurodegeneration
XX Example 1; Page 39; 88pp; English.
XX This peptide is encoded by DNA21705, a cDNA clone obtained by
XX PCR amplification (see AAW84349-50) of human breast carcinoma cDNA.
XX The peptide shows homology to a peptide (see AAW88449) derived from
XX human tumor necrosis factor receptor 1 (TNFR1). DNA21705 was used
XX as a probe to screen a human foetal lung library, yielding a clone
XX (see AAW84347) encoding Apo-2Dcr, a novel member of the TNFR family
XX that binds to Apo-2 ligand and is involved in apoptosis. Apo-2Dcr
XX polypeptides can be used in methods for the modulation and
XX diagnosis of apoptosis e.g. in cases of neurodegeneration,
XX autoimmune diseases and inflammation.
XX Sequence 48 AA:
SO
Query Match 20.6%; Score 48; DB 20; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.6e-42;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 40 CNPCTEGVDYTNASNNEPSCFCTVCKSDQKHKSSCTWTRDTVCQCKE 87
DB 1 cnpctegvdytnasnepsctfctvcksdqkhhkssctmtrdtvcqcke 48
RESULT 19
ID AAW98200
XX AAW98200 standard; Protein; 386 AA.
AC AAW98200;
XX 05-JUL-1999 (first entry)
XX

```

DE RTD, inhibitor of Apo-2 ligand-induced apoptosis.  
 XX RTD: tumour necrosis factor receptor; trail receptor; Apo-2 ligand;  
 KW apoptosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key  
 FT Peptide  
 FT 1..55  
 FT /note= "signal peptide"  
 FT 56..386  
 FT /note= "mature protein"  
 FT 56..212  
 FT /note= "extracellular domain, specifically claimed  
 in Claim 6"  
 FT Domain  
 FT 213..232  
 FT /note= "transmembrane domain"  
 FT 233..386  
 FT /note= "intracellular domain"  
 FT Modified-site  
 FT 127  
 FT /note= "N-glycosylated"  
 FT Modified-site  
 FT 171  
 FT /note= "N-glycosylated"  
 FT Modified-site  
 FT 182  
 FT /note= "N-glycosylated"  
 FT Misc-difference  
 FT 310  
 FT /label= Ser, Leu  
 FT 99..139  
 FT /note= "cysteine-rich domain"  
 FT 141..180  
 FT /note= "cysteine-rich domain"  
 FT 1..212  
 FT /note= "extracellular domain polypeptide,  
 specifically claimed in Claim 7"  
 FT Protein  
 FT 99..139  
 FT /note= "extracellular domain polypeptide,  
 specifically claimed in Claim 8"  
 FT Protein  
 FT 141..180  
 FT /note= "extracellular domain polypeptide,  
 specifically claimed in Claim 9"  
 XX  
 PN WO9910484-A1.  
 PD 04-MAR-1999.  
 XX  
 PF 14-JUL-1998; 98WO-US14552.  
 XX  
 PR 26-AUG-1997; 97US-0918874.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Gurney A;  
 XX WPI: 1999-254218/21.  
 DR N-PSDB: AAX25093.  
 XX  
 PT A new polypeptide, designated RTD  
 XX  
 PS Claim 4; Page 40-52; 58pp; English.  
 XX  
 CC The present sequence is human RTD, a novel protein capable of  
 CC binding Apo-2 ligand. RTD is a receptor for tumour necrosis  
 CC factor, belonging to the family of trail receptors. It is an  
 CC inhibitor of Apo-2 ligand-induced apoptosis, and acts as a decoy  
 CC receptor, lacking an intracellular signalling death domain. RTD  
 CC polypeptides can be obtained by expressing the polypeptide  
 CC encoded by the cDNA insert of the vectors deposited as ATCC 209201  
 CC or ATCC 209202 (see also AAX25093). These cDNAs differ in sequence  
 CC at a single nucleotide, resulting in serine or leucine at amino  
 CC acid position 310 of RTD. Isolated RTD polypeptides, especially  
 CC the extracellular domain (ECD), chimeric molecules including RTD or  
 CC its ECD, and nucleic acids encoding such polypeptides are claimed,  
 CC as are antibodies, vectors, host cells (especially CHO, yeast and

CC E. coli cells), transgenic and knockout animals, and a method of  
 CC modulating apoptosis in mammalian cells by exposing the cells to  
 CC RTD polypeptide. This therapy can be accomplished e.g. using in  
 CC vivo or ex vivo gene therapy techniques. RTD chimeric molecules  
 CC comprising immunoglobulin sequences can be used to inhibit Apo-2  
 CC ligand activities, e.g. apoptosis or NF-kappa B induction or the  
 CC activity of another ligand to which RTD binds.  
 XX  
 SQ Sequence 386 AA;  
 XX  
 Query Match 6.0%; Score 14; DB 20; Length 386;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 37 TGACNPTCEGVDYT 50  
 DB 93 TGACNPTCEGVDYT 106  
 RESULT 20  
 AAY04144  
 ID AAY04144 standard; Protein: 386 AA.  
 AC  
 XX AAY04144;  
 XX  
 DT 15-JUN-1999 (first entry)  
 XX  
 DE Human Tango-74 protein.  
 XX  
 KW Human; Tango-71; Tango-73; Tango-74; Tango-76; Tango-83; diagnosis;  
 KW detection.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9907850-A1.  
 PD 18-FEB-1999.  
 XX  
 PF 06-AUG-1998; 98WO-US16502.  
 XX  
 PR 05-SEP-1997; 97US-0058108.  
 PR 06-AUG-1997; 97US-0054966.  
 XX  
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.  
 XX  
 PI Goodearl ADJ, Holtzman DA;  
 XX WPI: 1999-167426/14.  
 DR N-PSDB: AAX19957.  
 XX  
 PT New TANGO polypeptides and nucleic acids encoding them - useful as  
 PT diagnostic agents and for treating disorders caused by aberrant  
 PT expression of TANGO  
 XX  
 PS Claim 8; Fig 3; 84pp; English.  
 XX  
 CC The present sequence represents human Tango-74. Tango polypeptides are  
 CC useful for identifying compounds which bind the polypeptide via direct  
 CC binding, competition binding assays or Tango-71, -73, -74, 76 or -83-  
 CC mediated signal transduction. Tango polypeptides are also useful for  
 CC identifying modulating compounds by determining effect on Tango activity.  
 CC Tango polypeptides and nucleic acids are useful for diagnosing diseases  
 CC related to aberrant expression of Tango, and Tango polypeptides are  
 CC useful for raising antibodies which can be used in diagnostic assays for  
 CC detection of Tango, and also for generating anti-idiotypic antibodies for  
 CC prevention and protection.  
 CC  
 SQ Sequence 386 AA;  
 XX  
 Query Match 6.0%; Score 14; DB 20; Length 386;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-06;



Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 37 TGACNPCTEGVDYT 50  
 ||||||||||||||||  
 Db 93 tgacnpctegvdyt 106

## RESULT 21

ID AAM99018 standard; Protein: 386 AA.

XX AAM99018;

XX 12-MAY-1999 (first entry)

XX Human TRAIL receptor 4A.

XX Human; TRAIL; TRAIL receptor; immunoreactive; thrombotic microangiopathy;

KW HIV infection; tumour necrosis factor related apoptosis inducing ligand;

KW TNF related apoptosis inducing ligand; systemic lupus erythematosus;

KW multiple sclerosis.

XX Homo sapiens.

XX WO903992-A1.

XX 28-JAN-1999.

XX 10-JUL-1998; 98WO-US14410.

XX 15-JUL-1997; 97US-0892119.

XX (IMMV ) IMMUNEX CORP.

XX Degli-Esposti M.

XX WPI; 1999-132236/11.

XX N-PSDB; AAX18926.

XX New isolated TRAIL receptor polypeptides - used to develop products

PT for treating e.g. thrombotic microangiopathy, multiple sclerosis,

PT systemic lupus erythematosus or HIV infection

XX Claim 1; Fig 1; 51pp; English.

XX The present sequence is a human tumour necrosis factor (TNF)-related

CC apoptosis-inducing ligand (TRAIL) receptor designated TRAILR4A. TRAILR

CC proteins can be used for binding TRAIL, e.g. to measure or inhibit the

CC biological activity of TRAIL. TRAILR proteins can be used for treating

CC thrombotic microangiopathies, e.g. thrombotic thrombocytopenic purpura

CC (TTP) or haemolytic-uraemic syndrome (HUS), clotting of small blood

CC vessels in e.g. AIDS, multiple sclerosis or systemic lupus erythematosus

CC or for reducing TRAIL-mediated death of T cells in HIV-infected patients.

CC They can also be used to purify TRAIL or TRAIL-expressing cells or as

CC carriers for delivering agents to cells bearing TRAIL.

XX Sequence 386 AA;

Query Match 6.0%; Score 14; DB 20; Length 386;

Best Local Similarity 100.0%; Pred. No. 4.5e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 37 TGACNPCTEGVDYT 50

||||||||||||||

Db 93 tgacnpctegvdyt 106

RESULT 22  
 ID AAM99019 standard; Protein: 386 AA.  
 XX AAM99019;

XX 12-MAY-1999 (first entry)

XX Human TRAIL receptor 4B.

XX Human; TRAIL; TRAIL receptor; immunoreactive; thrombotic microangiopathy;

KW HIV infection; tumour necrosis factor related apoptosis inducing ligand;

KW TNF related apoptosis inducing ligand; systemic lupus erythematosus;

KW multiple sclerosis.

XX Homo sapiens.

XX WO903992-A1.

XX 28-JAN-1999.

XX 10-JUL-1998; 98WO-US14410.

XX 15-JUL-1997; 97US-0892119.

XX (IMMV ) IMMUNEX CORP.

XX Degli-Esposti M.

XX WPI; 1999-132236/11.

XX N-PSDB; AAX18927.

XX New isolated TRAIL receptor polypeptides - used to develop products

PT for treating e.g. thrombotic microangiopathy, multiple sclerosis,

PT systemic lupus erythematosus or HIV infection

XX Claim 1; Fig 2; 51pp; English.

XX The present sequence is a human tumour necrosis factor (TNF)-related

CC apoptosis-inducing ligand (TRAIL) receptor designated TRAILR4B. TRAILR

CC proteins can be used for binding TRAIL, e.g. to measure or inhibit the

CC biological activity of TRAIL. TRAILR proteins can be used for treating

CC thrombotic microangiopathies, e.g. thrombotic thrombocytopenic purpura

CC (TTP) or haemolytic-uraemic syndrome (HUS), clotting of small blood

CC vessels in e.g. AIDS, multiple sclerosis or systemic lupus erythematosus

CC or for reducing TRAIL-mediated death of T cells in HIV-infected patients.

CC They can also be used to purify TRAIL or TRAIL-expressing cells or as

CC carriers for delivering agents to cells bearing TRAIL.

XX Sequence 386 AA;

Query Match 6.0%; Score 14; DB 20; Length 386;

Best Local Similarity 100.0%; Pred. No. 4.5e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 37 TGACNPCTEGVDYT 50

||||||||||||||

Db 93 tgacnpctegvdyt 106

## RESULT 23

ID AAM92792 standard; Protein: 386 AA.

XX AAM92792;

XX 12-APR-1999 (first entry)

XX Human TNF receptor TR10 protein.

XX TR10; tumour necrosis factor receptor; TNF; human; agonist; treatment;

KW disease; apoptosis; inhibition; cancer; lymphoma; carcinoma; tumour;

KW autoimmune disease; viral infection; inflammation; graft rejection; AIDS;

KW graft versus host disease; antagonist; neurodegenerative disorder;

KW myelodysplastic syndrome; ischemic injury; liver disease; drug screening;

KW septic shock; cachexia; anorexia; detection; diagnosis.

OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..55  
 FT /label= signal\_peptide  
 FT Protein 56..386  
 FT /label= TR10  
 FT Domain 56..212  
 FT /label= extracellular\_domain  
 FT Domain 213..230  
 FT /label= transmembrane\_domain  
 FT Domain 231..386  
 FT /label= intracellular\_domain  
 XX  
 PN WO9854202-A1.  
 XX  
 PD 03-DEC-1998.  
 XX  
 PF 29-MAY-1998; 98WO-US10981.  
 XX  
 PR 09-DEC-1997; 97US-0069112.  
 PR 30-MAY-1997; 97US-0050936.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI N1 J, Rosen CA.  
 XX  
 DR WPI: 1999-059803/05.  
 DR N-PSDB; AAV72101.  
 XX  
 PT New isolated human tumour necrosis factor-like receptor TR10 - used  
 PT to develop products for treating, e.g. cancers, autoimmune  
 PT disorders, viral infections, inflammation, graft rejection,  
 PT neurodegenerative disorders or septic shock  
 XX  
 PS Claim 3; Fig 1A-D; 85pp; English.  
 XX  
 CC This sequence represents a novel human tumour necrosis factor (TNF)  
 CC receptor, TR10. TR10 polypeptides or agonists can be used for treating  
 CC diseases and disorders associated with inhibition of apoptosis, e.g.  
 CC cancers (e.g. follicular lymphomas, carcinomas with p53 mutations, and  
 CC hormone-dependent tumours, such as breast cancer, prostate cancer,  
 CC Kaposi's sarcoma and ovarian cancer), autoimmune disorders (e.g. systemic  
 CC lupus erythematosus and immune-related glomerulonephritis rheumatoid  
 CC arthritis), viral infections (e.g. herpes viruses, pox viruses and  
 CC adenoviruses), inflammation, graft versus host disease, acute graft  
 CC rejection and chronic graft rejection. Antagonists can be used for  
 CC treating diseases and disorders associated with increased apoptosis,  
 CC e.g. AIDS, neurodegenerative disorders (e.g. Alzheimer's disease,  
 CC Parkinson's disease, Amyotrophic lateral sclerosis, Retinitis pigmentosa,  
 CC cerebellar degeneration), myelodysplastic syndromes (e.g. aplastic  
 CC anemia), ischemic injury (e.g. as caused by myocardial infarction, stroke  
 CC and reperfusion injury), toxin-induced liver disease (e.g. as caused by  
 CC alcohol), septic shock, cachexia and anorexia. Antagonists can also be  
 CC used for treating inflammatory diseases and disorders, e.g. inflammatory  
 CC bowel disease, rheumatoid arthritis, osteoarthritis, psoriasis and  
 CC septicemia. The products can also be used for detection, diagnosis and  
 CC drug screening.  
 XX  
 SO Sequence 386 AA;

Query Match 6.0%; Score 14; DB 20; Length 386;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 TGACNPTCEGYDT 50  
 ||||||||||||  
 DB 93 tgaenptcegydyt 106

RESULT 24  
 AAB01341

ID AAB01341 standard; Protein; 386 AA.  
 XX  
 AC AAB01341;  
 XX  
 DT 25-SEP-2000 (first entry)  
 XX  
 DE TNF-related apoptosis inducing ligand (TRAIL) receptor-3.  
 XX  
 DE U144; death receptor; apoptosis; programmed cell death; FAS;  
 KW TNF-R1; TRAMP; DR-6; TRAIL; modulation; treatment; cancer; virus;  
 KW human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200034335-A2.  
 XX  
 PD 15-JUN-2000.  
 XX  
 PF 03-DEC-1999; 99WO-US26035.  
 XX  
 PR 04-DEC-1998; 98US-0205018.  
 XX  
 PA (SCHE) SCHERING CORP.  
 XX  
 PI Leong C, Phillips JH;  
 XX  
 DR WPI: 2000-423383/36.  
 XX  
 PT Purified or recombinant polypeptide for modulating apoptosis comprises  
 PT a sequence which binds to an antibody specific for U144 or its  
 PT fragments  
 XX  
 PS Disclosure; Page 73-74; 76pp; English.  
 XX  
 CC A pure or recombinant polypeptide which binds to a polyclonal antibody  
 CC specific for the mature U144 is useful for screening molecules which  
 CC block induction of apoptosis or interfere with antiapoptotic activity.  
 CC The polypeptide is also useful for modulating apoptosis and useful in  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, such as cancer or degenerative conditions and for  
 CC regulation of viral infection and replication. At least five  
 CC different death receptors are known, which include the CD95  
 CC (Fas/APO-1), the TNF receptor-1, TNF receptor apoptosis-mediated  
 CC protein (TRAMP), death receptor-6 (DR-6), and TNF-related  
 CC apoptosis-inducing ligand (TRAIL) receptors 1, 2 and 4.  
 XX  
 SO Sequence 386 AA;

Query Match 6.0%; Score 14; DB 21; Length 386;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 TGACNPTCEGYDT 50  
 ||||||||||||  
 DB 93 tgaenptcegydyt 106

RESULT 25  
 AAY69991  
 ID AAY69991 standard; Protein; 386 AA.  
 XX  
 AC AAY69991;  
 XX  
 DT 31-MAY-2000 (first entry)

DE Human receptor-associated protein from Incyte clone 3472455.  
 XX  
 DE Human receptor-associated protein; HRAP; Incyte clone 3472455;  
 KW cytosolic; immunomodulatory; antiinflammatory; cardiant; antianaemic;  
 KW antiarteriosclerotic; hepatotropic; antiarthritic antirheumatic;  
 KW antiallergic; antidiabetic; antidiabetic; dermatological;  
 KW neuroprotective; diagnosis; treatment; prevention; reproductive disorder;

KW cardiovascular; cell proliferative; autoimmune; inflammatory; allergy;  
 KW gastrointestinal; atherosclerosis; cirrhosis; leukaemia; cancer; AIDS;  
 KW arthritis; anaemia; asthma; dermatitis; diabetes; osteoporosis;  
 KW multiple sclerosis; irritable bowel syndrome.  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FT Modified-site 13 /note= "Potential phosphorylation site"  
 FT Modified-site 77 /note= "Potential phosphorylation site"  
 FT Modified-site 87 /note= "Potential phosphorylation site"  
 FT Modified-site 126 /note= "Potential phosphorylation site"  
 FT Modified-site 133 /note= "Potential phosphorylation site"  
 FT Modified-site 145 /note= "Potential phosphorylation site"  
 FT Modified-site 157 /note= "Potential phosphorylation site"  
 FT Modified-site 173 /note= "Potential phosphorylation site"  
 FT Modified-site 189 /note= "Potential phosphorylation site"  
 FT Modified-site 231 /note= "Potential phosphorylation site"  
 FT Modified-site 263 /note= "Potential phosphorylation site"  
 FT Modified-site 281 /note= "Potential phosphorylation site"  
 FT Modified-site 291 /note= "Potential phosphorylation site"  
 FT Modified-site 310 /note= "Potential phosphorylation site"  
 FT Modified-site 345 /note= "Potential phosphorylation site"  
 FT Modified-site 352 /note= "Potential phosphorylation site"  
 FT Modified-site 361 /note= "Potential phosphorylation site"  
 FT Modified-site 369 /note= "Potential phosphorylation site"  
 FT Modified-site 127 /note= "Potential phosphorylation site"  
 FT Modified-site 182 /note= "Potential N-glycosylation site"  
 FT Modified-site 277 /note= "Potential N-glycosylation site"  
 FT Binding-site 185..192 /note= "Potential N-glycosylation site"  
 FT Region 99..180 /label= ATP/GTP\_binding\_site  
 FT /label= "Signature sequence  
 FT /note= "TNFR/NGFR cysteine-rich region"  
 XX  
 PN MO200008155-A2.  
 XX  
 PD 17-FEB-2000.  
 XX  
 PF 06-AUG-1999; 99MO-US17777.  
 XX  
 PR 07-AUG-1998; 98US-0160065.  
 PR 01-SEP-1998; 98US-0098703.  
 XX  
 PA (INCYTE) INCYTE PHARM INC.  
 XX  
 PI Hillman JL, Yue H, Lal P, Tang YT, Gorgone GA, Guegler KJ;  
 PI Corley NC, Baughn MR;  
 XX  
 DR WPI: 2000-205710/18.  
 DR N-PSDB; AAZ50893.  
 XX

PT New human receptor-associated proteins (HRAP) useful for the diagnosis,  
 PT treatment and prevention of cell proliferative, autoimmune,  
 PT inflammatory, reproductive, cardiovascular, and gastrointestinal  
 PT disorders  
 XX  
 PS Claim 1; Page 78-79; 99pp; English.  
 XX  
 CC The present sequence is a human receptor-associated protein  
 CC (HRAP) from Incyte clone 3472455 obtained from LUNG0727 cDNA library.  
 CC This sequence is expressed in musculoskeletal, cardiovascular  
 CC and urologic tissues. HRAP has cytosolic, immunomodulatory,  
 CC antiinflammatory, cardiac, antiarteriosclerotic, hepatotropic,  
 CC antiarthritic, antirheumatic, osteopathic, antiallergic, antianemic,  
 CC antiasthmatic, antidiabetic, dermatological and neuroprotective  
 CC activities. The present sequence is useful in the diagnosis, treatment  
 CC and prevention of disorders associated with HRAP expression, especially  
 CC cell proliferative, autoimmune/inflammatory, reproductive,  
 CC cardiovascular and gastrointestinal disorders (e.g. atherosclerosis,  
 CC cirrhosis, leukaemia, cancer, AIDS, arthritis, allergies, anaemia,  
 CC asthma, dermatitis, diabetes, osteoporosis, multiple sclerosis and  
 CC irritable bowel syndrome).  
 XX  
 SQ Sequence 386 AA;  
 XX  
 Query Match 6.0%; Score 14; DB 21; Length 386;  
 Best Local Similarity 100.0%; Pred. No. 4.5e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 37 TGACNPGTEGVDPY 50  
 IIIIIIIIIIIIII  
 Db 93 tgaenpctegvdyt 106  
 XX  
 RESULT 26  
 AAU12341  
 ID AAU12341 standard; Protein: 386 AA.  
 XX  
 AC AAU12341;  
 XX  
 XX 24-OCT-2001 (first entry)  
 DT  
 XX  
 XX Human PRO288 polypeptide sequence.  
 DE  
 XX  
 KW Human secretory and transmembrane; PRO: mammalian; cancer; lung;  
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
 KW adipocyte; A-peptide; factor VIIA; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200140466-A2.  
 XX  
 PD 07-JUN-2001.  
 XX  
 PF 01-DEC-2000; 2000WO-US32678.  
 XX  
 PR 01-DEC-1999; 99MO-US28301.  
 PR 01-DEC-1999; 99MO-US28634.  
 PR 02-DEC-1999; 99MO-US28351.  
 PR 02-DEC-1999; 99MO-US28564.  
 PR 02-DEC-1999; 99MO-US28565.  
 PR 09-DEC-1999; 99US-0170262.  
 PR 16-DEC-1999; 99MO-US30095.  
 PR 20-DEC-1999; 99MO-US30911.  
 PR 20-DEC-1999; 99MO-US30999.  
 PR 30-DEC-1999; 99MO-US31243.  
 PR 06-JAN-2000; 2000WO-US00276.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 XX





PS Disclosure; SEQ ID NO 31485; 21pp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from *Drosophila*. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL01840-ABL16175) and the encoded proteins  
CC (AAB57737-AB572072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).  
XX  
SQ Sequence 109 AA;  
  
Query Match 3.4%; Score 8; DB 22; Length 109;  
Best Local Similarity 100.0%; Pred. No. 2.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 220 VGIIVLIIV 227  
|||||||  
Db 27 VGIIVLIIV 34  
  
RESULT 30  
AAB93909  
ID AAB93909 standard; Protein; 217 AA.  
XX  
AC AAB93909;  
XX  
DT 26-JUN-2001 (first entry)  
XX  
DE Human protein sequence SEQ ID NO:13873.  
XX  
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN EP1074617-A2.  
XX  
PD 07-FEB-2001.  
XX  
PF 28-JUL-2000; 2000EP-0116126.  
XX  
PR 29-JUL-1999; 99JP-0248036.  
XX  
PR 27-AUG-1999; 99JP-0300253.  
XX  
PR 11-JAN-2000; 2000JP-0118776.  
XX  
PR 02-MAY-2000; 2000JP-0183767.  
XX  
PR 09-JUN-2000; 2000JP-0241899.  
XX  
XX  
PA (HELI-) HELIX RES INST.  
XX  
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
XX  
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
XX  
XX  
DR WPI; 2001-318749/34.  
XX  
PT Primer sets for synthesizing polynucleotides, particularly the 5602  
XX  
PT full-length cDNAs defined in the specification, and for the detection  
XX  
PT and/or diagnosis of the abnormality of the proteins encoded by the  
XX  
PT full-length cDNAs -  
XX  
PS Claim 8; SEQ ID 13873; 2537pp + CD ROM; English.  
XX  
XX The present invention describes primer sets for synthesizing 5602  
XX full-length cDNAs defined in the specification. Where a primer set  
XX comprises: (a) an oligo-dT primer and an oligonucleotide complementary  
XX to the complementary strand of a polynucleotide which comprises one of  
XX the 5602 nucleotide sequences defined in the specification, where the  
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
XX of an oligonucleotide comprising a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end  
CC sequence and an oligonucleotide comprising a sequence complementary to a  
CC polynucleotide which comprises a 3'-end sequence, where the  
CC oligonucleotide comprises at least 15 nucleotides and the combination of  
CC the 5'-end sequence/3'-end sequence is selected from those defined in  
CC the specification. The primer sets can be used in antisense therapy and  
CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
CC particularly full-length cDNAs. The primers are also useful for the  
CC detection and/or diagnosis of the abnormality of the proteins encoded by  
CC the full-length cDNAs. The primers allow obtaining of the full-length  
CC cDNAs easily without any specialised methods. AA003166 to AA013628 and  
CC AA013633 to AA018742 represent human cDNA sequences; AAB92446 to  
CC AAB95893 represent human amino acid sequences; and AA013629 to AA013632  
CC represent oligonucleotides, all of which are used in the exemplification  
CC of the present invention.  
XX  
SQ Sequence 217 AA;  
  
Query Match 3.4%; Score 8; DB 22; Length 217;  
Best Local Similarity 100.0%; Pred. No. 4.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 141 TMNTSPGT 148  
|||||||  
Db 19 tmtspgt 26  
  
RESULT 31  
AAM41810  
ID AAM41810 standard; Protein; 272 AA.  
XX  
AC AAM41810;  
XX  
DT 22-OCT-2001 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 6741.  
XX  
KW Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;  
XX peripheral nervous system; neuropathy; central nervous system; CNS;  
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
XX leukaemia.  
XX  
OS Homo sapiens.  
XX  
XX  
XX WO200153312-A1.  
XX  
PN 26-JUL-2001.  
XX  
PD 26-DEC-2000; 2000WO-US34263.  
XX  
PF 21-JAN-2000; 2000US-0488725.  
XX  
PR 25-APR-2000; 2000US-052317.  
XX  
PR 09-JUL-2000; 2000US-0598042.  
XX  
PR 19-JUL-2000; 2000US-0620312.  
XX  
PR 03-AUG-2000; 2000US-0653450.  
XX  
PR 14-SEP-2000; 2000US-0662191.  
XX  
PR 19-OCT-2000; 2000US-0693036.  
XX  
PR 29-NOV-2000; 2000US-0727344.  
XX  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
XX  
PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;  
XX  
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
XX  
XX  
DR WPI; 2001-442253/47.  
XX  
DR N-PSDB; AAI60966.  
XX  
PT Novel nucleic acids and polypeptides, useful for treating disorders  
XX  
PT such as central nervous system injuries -



DR N-PSDB; AAV63095.  
XX  
XX DNA encoding tumour necrosis factor receptor TR6 - and corresponding  
PT polypeptide, antibody, agonist, antagonist, etc  
XX  
XX  
PS Disclosure; Page 30-31; 34pp; English.  
XX  
XX This sequence represents a novel human tumour necrosis factor related  
CC receptor, TR6. TR6 polypeptides and polynucleotides can be used in the  
CC treatment of chronic and acute inflammation, arthritis, septicemia,  
CC autoimmune diseases (e.g. inflammatory bowel disease, psoriasis),  
CC transplant rejection, graft vs. host disease, infection, stroke,  
CC ischaemia, acute respiratory disease syndrome, restenosis, brain injury,  
CC (acquired autoimmune disease syndrome) AIDS, bone diseases, cancer (e.g.  
CC lympho-proliferative disorders), atherosclerosis and Alzheimer's disease.  
XX  
XX  
SQ Sequence 303 AA;  
  
Query Match 3.4%; Score 8; DB 19; Length 303;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 95 SPEMCRKC 102  
Db 41 spemcrkc 48  
  
RESULT 34  
AAB48349  
ID AAB48349 standard; Protein: 303 AA.  
XX  
XX AAB48349;  
AC  
XX  
XX 20-APR-2001 (first entry)  
DT  
XX  
XX Partial amino acid sequence of human TR6.  
DE  
XX  
XX Tumour necrosis factor; TNF; TNF related receptor; TR6; human;  
KW antiinflammatory; immunosuppressive; cerebroprotective; vasotropic;  
KW antiasthmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic;  
KW nootropic; neuroprotective; antiarthritic; antirheumatic; antischismic;  
KW gene therapy; vaccine; TNF-alpha; bone disease; cancer.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200077191-A1.  
PN  
XX  
XX 21-DEC-2000.  
PD  
XX  
XX 12-JUN-2000; 2000WO-US16134.  
PE  
XX  
XX 15-JUN-1999; 99US-0333593.  
PR  
XX  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
PA  
XX  
XX Deen KC, Young PR, Marshall LA, Roshak AK, Tan KB, Truneh A;  
PI WPI; 2001-112223/12.  
DR N-PSDB; AAC84744.  
XX  
XX New tumor necrosis factor related receptor TR6 polynucleotides and  
PT polypeptides useful for e.g. for treating chronic and acute  
PT inflammation, arthritis, septicemia, autoimmune diseases, infection,  
PT cancer, bone diseases -  
XX  
XX Disclosure; Page 16-17; 47pp; English.  
XX  
XX The invention relates to a human tumour necrosis factor (TNF) related  
CC receptor, TR6. TR6 can be expressed by standard recombinant methodology.  
CC The TR6 polypeptides are useful for treating chronic and acute  
CC inflammation, rheumatoid arthritis, septicemia, autoimmune diseases  
CC (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft

CC vs. host disease, infection, stroke, ischaemia, acute respiratory disease  
CC syndrome, asthma, restenosis, brain injury, AIDS, bone diseases, cancer,  
CC atherosclerosis, and Alzheimer's disease. These may also be used to  
CC inhibit production of TNF-alpha and eicosanoids, as research reagents and  
CC materials for discovering treatments and diagnostics to animal and human  
CC diseases. The polypeptides may further be used as immunogens to produce  
CC antibodies immunospecific for the TR6 polypeptides. The polynucleotides  
CC may also be used as hybridization probes for cDNA and genomic DNA, for  
CC isolating full-length cDNAs and genomic clones encoding TR6 and of other  
CC genes having high sequence similarity to TR6 gene, and for chromosome  
CC identification. The present sequence represents a partial amino acid  
XX  
XX  
SQ Sequence 303 AA;  
  
Query Match 3.4%; Score 8; DB 22; Length 303;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 95 SPEMCRKC 102  
Db 41 spemcrkc 48  
  
RESULT 35  
AAV00934  
ID AAV00934 standard; Protein: 350 AA.  
XX  
XX AAV00934;  
AC  
XX  
XX 02-JUN-1999 (first entry)  
DT  
XX  
XX Human DR5s protein sequence.  
DE  
XX  
XX Human; DR5; TRAIL-R3; apoptosis related condition; cancer; therapy;  
KW autoimmune disease; viral infection; degenerative disorder;  
KW amyotrophic lateral sclerosis; retinitis pigmentosa; ischemic injury;  
KW cerebellar degeneration; myelodysplastic syndrome; splice variant.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO9909165-A1.  
PN  
XX  
XX 25-FEB-1999.  
PD  
XX  
XX 14-AUG-1998; 98WO-US16945.  
PE  
XX  
XX 15-AUG-1997; 97US-0055906.  
PR  
XX  
XX (IDUN-) IDUN PHARM INC.  
PA  
XX  
XX Alnemrl ES;  
PI WPI; 1999-181035/15.  
DR N-PSDB; AAX27281.  
XX  
XX Newly isolated polynucleotide encoding a mammalian TRAIL receptor  
PT protein - useful in for screening for (ant)agonists that modulate  
PT the apoptotic activity mediated by DR5 or TRAIL-R3 proteins  
XX  
XX Claim 16; Fig 5; 71pp; English.  
XX  
XX This sequence is the human TRAIL receptor DR5s of the invention. An  
CC antibody against the TRAIL receptors is useful for detecting mammalian  
CC DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in  
CC bioassays for screening for (ant)agonists of DR5 or TRAIL-R3 proteins.  
CC (Ant)agonists identified by the assay are useful for modulating the  
CC apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis  
CC related conditions which are treated in this way, include cancer  
CC (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus  
CC erythematosus and immune-mediated glomerulonephritis), viral infections  
CC (e.g. herpes virus, poxvirus and adenovirus), degenerative disorders



CC (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral  
 CC sclerosis, retinitis pigmentosa, cerebellar degeneration, myelodysplastic  
 CC syndromes (e.g. aplastic anaemia) and ischaemic injury (e.g. myocardial  
 CC infarction and stroke). The polynucleotides can also be used to treat  
 CC these diseases. Antisense oligonucleotides can be used to treat  
 CC used to form a composition that is useful for inhibiting expression of a  
 CC human DR5 or TRAIL-R3 protein.

SO Sequence 350 AA;

Query Match 3.4%; Score 8; DB 20; Length 350;  
 Best Local Similarity 100.0%; Pred. No. 6.9;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 SPENCRCRC 102  
 Db 149 spencrcrc 156

#### RESULT 36

ID AAW79261 standard; Protein; 411 AA.

XX AAW79261;

DT 15-FEB-1999 (first entry)

DE Tumour necrosis factor receptor related protein Tango-63e.

XX Tango-63e; tumour necrosis factor receptor related protein; human;  
 KW apoptosis; cancer; autoimmune disease; neurodegenerative disease.

XX Homo sapiens.

PN W09846643-A1.

XX 22-OCT-1998.

PF 16-APR-1998; 98WO-US07694.

XX 16-APR-1997; 97US-0843652.

PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.

XX Holtzman D;

XX WPI; 1998-594562/50.

DR N-PSDB; AAV62673.

PT Isolated tumour necrosis factor related proteins - used to develop  
 PT products for the diagnosis and treatment of apoptosis-related  
 PT disorders, e.g. cancers, autoimmune disorders or neurodegenerative  
 PT disorders

PS Claim 6; Fig 2; 88pp; English.

XX This is the amino acid sequence of Tango-63e, a new member of the  
 CC human tumour necrosis factor receptor superfamily. It was deduced  
 CC from a human prostate cDNA clone sequence (see AAV62673). Two  
 CC different forms of Tango-63, i.e. Tango-63e and Tango-63d (see  
 CC AAW79260), have been identified. These are identical with the  
 CC exception of the deletion of amino acids 183-211 of Tango-63d in  
 CC Tango-63e. The invention also encompasses nucleic acid molecules  
 CC encoding Tango-63d and -63e, vectors containing these nucleic acid  
 CC molecules, cells harboring recombinant DNA encoding Tango-63d and/or  
 CC -63e, fusion proteins that include Tango-63d and/or -63e, transgenic  
 CC animals that express Tango-63d and/or -63e, and recombinant knockout  
 CC animals that fail to express Tango-63d and/or -63e. Methods are  
 CC provided for the diagnosis and treatment of disorders associated  
 CC with either an abnormally high or an abnormally low rate of  
 CC apoptotic cell death. Inhibitors can be used for treating e.g.  
 CC cancers, autoimmune disorders (e.g. systemic lupus erythematosus

CC and immune-mediated glomerulonephritis), and viral infections (e.g.  
 CC herpesviruses, poxviruses, and adenoviruses). Agonists can be used  
 CC for treating e.g. neurodegenerative diseases, e.g. Alzheimer's  
 CC disease, Parkinson's disease, amyotrophic lateral sclerosis (ALS),  
 CC Huntington's disease, retinitis pigmentosa, spinal muscular atrophy,  
 CC various forms of cerebellar degeneration, anaemia, myelodysplastic  
 CC syndrome, ischaemic injury, myocardial infarction, cerebral ischaemia  
 CC or toxin-induced injury. In addition, T cell mediated diseases,  
 CC including AIDS, autoimmune diseases such as rheumatoid arthritis,  
 CC and type I diabetes, septic shock, cerebral malaria, graft  
 CC rejection, cytotoxicity, cachexia, and inflammation can be treated  
 CC by altering the expression or activity of the polypeptides. The  
 CC products can also be used for detection, diagnosis and screening  
 CC assays.

SO Sequence 411 AA;

Query Match 3.4%; Score 8; DB 19; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 SPENCRCRC 102  
 Db 149 spencrcrc 156

#### RESULT 37

ID AAW76827 standard; Protein; 411 AA.

XX AAW76827;

DT 25-JAN-1999 (first entry)

DE Human TR6 protein.

XX TR6; tumour necrosis factor related receptor; human; treatment; stroke;  
 KW inflammation; arthritis; septicemia; autoimmune disease; restenosis;  
 KW transplant rejection; infection; ischaemia; brain injury; bone disease;  
 KW acute respiratory disease syndrome; acquired autoimmune disease syndrome;  
 KW AIDS; cancer; atherosclerosis; Alzheimer's disease.

XX Homo sapiens.

OS Homo sapiens.

PN EP870827-A2.

XX 14-OCT-1998.

PF 23-DEC-1997; 97EP-0310562.

XX 22-AUG-1997; 97US-0916625.

PR 14-MAR-1997; 97US-0041230.

PR 09-MAY-1997; 97US-0853684.

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX Deen KC, Young PR;

XX WPI; 1998-523156/45.

DR N-PSDB; AAV63094.

PT DNA encoding tumour necrosis factor receptor TR6 - and corresponding  
 PT polypeptide, antibody, agonist, antagonist, etc

PS Claim 1; Page 27-29; 34pp; English.

XX This sequence represents a novel human tumour necrosis factor related  
 CC receptor. TR6 polypeptides and polynucleotides can be used in the  
 CC treatment of chronic and acute inflammation, arthritis, septicemia,  
 CC autoimmune diseases (e.g. inflammatory bowel disease, psoriasis),  
 CC transplant rejection, graft vs. host disease, infection, stroke,  
 CC ischaemia, acute respiratory disease syndrome, restenosis, brain injury,





PS Claim 16; Page 58-60; 71pp; English.  
 XX  
 CC This sequence is the human TRAIL receptor DR5 of the invention. An  
 CC antibody against the TRAIL receptors is useful for detecting mammalian  
 CC DR5 or TRAIL-R3 proteins in a sample. Recombinant cells are useful in  
 CC bioassays for screening for (ant)agonists of DR5 or TRAIL-R3 proteins.  
 CC (ant)agonists identified by the assay are useful for modulating the  
 CC apoptotic activity mediated by DR5 or TRAIL-R3 proteins. Apoptosis  
 CC related conditions which are treated in this way, include cancer  
 CC (e.g. lymphomas and carcinomas), autoimmune diseases (e.g. systemic lupus  
 CC erythematosus and immune-mediated glomerulonephritis), viral infections  
 CC (e.g. herpes virus, poxvirus and adenovirus), degenerative disorders  
 CC (e.g. Alzheimer's disease and Parkinson's disease), amyotrophic lateral  
 CC sclerosis, retinitis pigmentosa, cerebellar degeneration, myelodysplastic  
 CC syndromes (e.g. aplastic anaemia) and ischemic injury (e.g. myocardial  
 CC infarction and stroke). The polynucleotides to the DNA sequences can be  
 CC used to form a composition that is useful for inhibiting expression of a  
 CC human DR5 or TRAIL-R3 protein.  
 CC  
 XX Sequence 411 AA;  
 SQ  
 Query Match 3.4%; Score 8; DB 20; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 95 SPENCRC 102  
 |||||||  
 Db 149 spencrc 156

RESULT 42  
 AAW88410  
 ID AAW88410 standard; Protein: 411 AA.  
 XX  
 AC AAW88410;  
 DT 26-APR-1999 (first entry)  
 XX  
 XX Human Apo-2 ligand.  
 XX  
 KW Apo-2 ligand; Apo-2DCR; human; tumour necrosis factor receptor;  
 KW neurodegeneration; autoimmune disease; inflammation; cancer;  
 KW apoptosis; therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..53  
 FT /note= "signal peptide"  
 FT Protein 54..411  
 FT /note= "mature protein"  
 FT Domain 54..182  
 FT /note= "extracellular domain"  
 FT Domain 183..208  
 FT /note= "transmembrane domain"  
 FT Domain 209..411  
 FT /note= "intracellular domain"  
 FT Region 96..137  
 FT /note= "cysteine-rich region"  
 FT Region 138..179  
 FT /note= "cysteine-rich region"  
 FT Domain 324..391  
 FT /note= "death domain"  
 FT Misc-difference 410  
 FT /label= Met, Leu  
 FT /note= "encoded by WTG"  
 XX  
 PN WO9858062-A1.  
 XX  
 PD 23-DEC-1998.

PF 12-JUN-1998; 98WO-US12456.  
 XX  
 PR 18-JUN-1997; 97US-0878168.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AJ, Baker KP, Chuntharapai A, Gurney A;  
 PI Kim KJ, Wood WI;  
 XX  
 DR WPI: 1999-095340/08.  
 DR N-PSDB; AAW84352.  
 XX  
 PT New Apo-2DCR polypeptide - used for modulation and diagnosis of  
 PT apoptosis, e.g. in neurodegeneration  
 XX  
 PS Example 5; Page 61-62; 88pp; English.  
 XX  
 CC This polypeptide comprises human Apo-2 ligand. The amino acid  
 CC sequence was deduced from a nucleotide sequence (see AAW84352)  
 CC produced from overlapping cDNA clones obtained from human kidney  
 CC and pancreatic cDNA libraries. The invention relates to Apo-2DCR  
 CC (see AAW88408), a novel member of the tumour necrosis factor receptor  
 CC family that binds to Apo-2 ligand and is involved in apoptosis.  
 CC Apo-2DCR polypeptides are used to modulate apoptosis of mammalian  
 CC cells (claimed) e.g. in the treatment of neurodegeneration,  
 CC autoimmune diseases and inflammation. The Apo-2DCR polypeptides  
 CC are optionally used in conjunction with Apo-2 ligand, the  
 CC bioavailability of which is increased by antibody-mediated blockade  
 CC of Apo-2DCR.  
 CC  
 XX Sequence 411 AA;  
 SQ  
 Query Match 3.4%; Score 8; DB 20; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 95 SPENCRC 102  
 |||||||  
 Db 149 spencrc 156

RESULT 43  
 AAW83321  
 ID AAW83321 standard; Protein: 411 AA.  
 XX  
 AC AAW83321;  
 DT 16-MAR-1999 (first entry)  
 XX  
 XX Human Apo-2 protein.  
 XX  
 KW Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;  
 KW tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;  
 KW TNF cytokine.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 410  
 FT /label= unknown  
 FT /note= "encoded by WTG"  
 XX  
 PN WO9851793-A1.  
 XX  
 PD 19-NOV-1998.  
 XX  
 PF 14-MAY-1998; 98WO-US09704.  
 XX  
 PR 09-FEB-1998; 98US-0020746.  
 PR 15-MAY-1997; 97US-0857216.  
 XX  
 PA (GETH ) GENENTECH INC.

XX Adams CW, Ashkenazi AJ, Chuntharapai A, Kim RJ;  
 XX WPI: 1999-045228/04.  
 DR N-PSDB; AAV72526.  
 XX  
 PT Human Apo-2 polypeptide inducing apoptosis - useful to treat  
 PT conditions linked with decreased apoptosis e.g. cancer, and produce  
 PT antibodies to increase or decrease apoptosis  
 PS  
 PS Claim 1; Fig 1; 134pp; English.  
 XX  
 XX The present sequence represents human Apo-2. Apo-2 can be used  
 CC therapeutically to induce apoptosis in mammalian cells, and so is useful  
 CC to treat conditions associated with decreased apoptosis e.g. cancer.  
 CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor.  
 CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by  
 CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It  
 CC can be used to identify agents activating Apo-2, useful to treat  
 CC mammalian cancer cells, and to produce Apo-2 chimeras useful  
 CC therapeutically (e.g. those containing immunoglobulin sequences can be  
 CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope  
 CC tag polypeptide allow Apo-2 detection and purification using anti-tag  
 CC antibodies). It can be used to produce antibodies which can be combined  
 CC with a (particularly pharmaceutically acceptable) carrier in compositions  
 CC or used to produce dimeric molecules (especially homodimeric molecules  
 CC comprising first and second Apo-2 antibodies). Agonistic (especially  
 CC single-chain) antibodies can be administered to induce apoptosis in  
 CC mammalian cancer cells, and antagonistic antibodies used to block  
 CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2  
 CC antibodies may also be used diagnostically e.g. to detect Apo-2  
 CC expression in cells/tissues and in Apo-2 purification.  
 XX  
 SQ Sequence 411 AA;  
 QY 95 SPEMCRKC 102  
 DB 149 spemcrkc 156  
 |||||||  
 RESULT 44  
 AAB29790  
 ID AAB29790 standard; Protein: 411 AA.  
 AC AAB29790;  
 XX  
 XX 28-FEB-2001 (first entry)  
 DE Human death domain containing receptor-5 (DR5).  
 XX  
 XX Human death domain containing receptor-5; DR5; anti-DR5 antibody;  
 KW TRAIL binding; TNF-related apoptosis-inducing ligand; pro-apoptotic;  
 KW tumour necrosis factor receptor family; TNFR; graft-versus-host disease;  
 KW viral infection; cancer; leukaemia; immunodeficiency; autoimmune disease;  
 KW T-cell mediated immune response; osteoarthritis; psoriasis; septicaemia;  
 KW inflammatory bowel disease; parasitic infection; bacterial infection;  
 KW restenosis.  
 XX  
 OS Homo sapiens.  
 PN NO200066156-A1.  
 XX  
 PD 09-NOV-2000.  
 XX  
 PF 04-MAY-2000; 2000MO-US12041.  
 XX  
 PR 04-MAY-1999; 99US-0132498.  
 PR 07-MAY-1999; 99US-0133238.

PR 13-AUG-1999; 99US-0148939.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ni J, Gentz RL, Yu G, Rosen CA;  
 XX  
 XX WPI: 2000-687447/67.  
 DR N-PSDB; AAC81544.  
 XX  
 PT Treating graft-versus-host disease, viral infection, cancer, leukemia,  
 PT immunodeficiency, or an autoimmune disorder comprising administering an  
 PT antibody to death domain containing receptor (DR5) and a second agent -  
 XX  
 PS Claim 1; Fig 1A-B; 266pp; English.  
 XX  
 XX The invention relates to a novel method for treating graft-versus-host  
 CC disease, viral infection, cancer, leukemia, immunodeficiency, or an  
 CC autoimmune disorder. The method comprises administering an antibody  
 CC specific for human death domain containing receptor-5 (DR5); AAB29790  
 CC and a second agent selected from TRAIL (TNF-related apoptosis-inducing  
 CC ligand), a tumour necrosis factor (TNF), a TNF blocking agent, an  
 CC immunosuppressive agent, an antibiotic, an antiinflammatory agent, a  
 CC chemotherapeutic agent, or a cytokine. DR5 is a member of the TNF  
 CC receptor (TNFR) family, and is a mediator of apoptosis, being able to  
 CC bind TRAIL. The method of the invention is useful for the treatment of  
 CC graft-versus-host disease, viral infection, cancer, leukemia,  
 CC immunodeficiency, or an autoimmune disorder. The DR-5 antibody is useful  
 CC for treating or preventing diseases and conditions associated with  
 CC increased cell survival and/or insensitivity to apoptosis-inducing  
 CC agents. Examples of such diseases are solid tissue cancers and  
 CC leukemias. Antagonists of DR5 are useful for inhibiting T-cell mediated  
 CC immune responses, and preventing and/or treating diseases and conditions  
 CC associated with T-cell mediated immune responses such as graft-versus-  
 CC host responses, osteoarthritis, psoriasis, septicaemia, inflammatory  
 CC bowel disease, autoimmune diseases and leukaemia. DR5 nucleotides and  
 CC proteins are useful for diagnosis, prevention and/or treatment of  
 CC parasitic, bacterial, and viral infections, restenosis and autoimmune  
 CC disorders. The present sequence represents human DR5.  
 XX  
 SQ Sequence 411 AA;  
 QY 95 SPEMCRKC 102  
 DB 149 spemcrkc 156  
 |||||||  
 RESULT 45  
 AAY55805  
 ID AAY55805 standard; Protein: 411 AA.  
 AC AAY55805;  
 XX  
 XX 29-FEB-2000 (first entry)  
 DE Human Apo-2 polypeptide.  
 XX  
 XX Apo-2 polypeptide; immunization; antigen; polyclonal antibody; cancer;  
 KW monoclonal antibody; Apo-2L receptor; therapy; apoptosis; autoimmune;  
 KW immune-mediated cell death; neurodegenerative; inflammatory.  
 XX  
 OS Homo sapiens.  
 PN  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 410  
 FT /label= unknown  
 FT /note="encoded by WTG"  
 XX  
 PN W09964461-A2.

XX 16-DEC-1999.  
PD  
XX  
XX 10-JUN-1999; 99WO-US13197.  
XX  
XX  
XX 12-JUN-1998; 98US-0096637.  
PR  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Chuntharapal A, Kim KJ;  
PI  
XX WPI: 2000-097520/08.  
DR  
XX N-PSDB: AA239630.  
XX  
XX Preparation of antibodies using 2 or more different antigens, used for  
PT producing antibodies against Apo-2 ligand receptors useful for inducing  
PT apoptosis, particularly in cancer cells -  
XX  
XX  
XX Disclosure: Fig 5; 57pp; English.  
PS  
XX  
XX The invention provides a method for producing antibodies (Abs) by  
CC immunizing an animal with at least two different antigens. The method  
CC comprises: (a) immunizing an animal with at least two different antigens,  
CC to generate polyclonal Abs against each antigen in the animal; (b)  
CC preparing monoclonal Abs (Mabs) using immune cells of the above animal;  
CC and(c) screening the Mabs to identify one or more Mabs which bind to each  
CC antigen. The Abs obtained are Apo-2L receptor (ant)agonists and can be  
CC used for therapy. The Apo-2L receptor Abs can be used for enhancing  
CC immune-mediated cell death in cells expressing Apo-2L receptors.  
CC Agonistic Abs which specifically cross-react with 2 or more different  
CC Apo-2L receptors can be used for inducing apoptosis in mammalian cancer  
CC cells. Antagonistic Abs can be used for blocking apoptosis, e.g. in  
CC neurodegenerative disease, or to block potential autoimmune/inflammatory  
CC effects of Apo-2 resulting from NF-approx. KB activation. The Abs can also  
CC be used for detection, diagnosis and affinity purification. The method  
CC can reduce the number of animals that need to be immunized and sacrificed  
CC in order to make 2 or more Mabs with differing antigen-binding  
CC specificities. The present sequence represents a human Apo-2 polypeptide.  
XX  
XX Sequence 411 AA;  
SQ

Query Match 3.4%; Score 8; DB 21; Length 411;  
Best Local Similarity 100.0%; Pred. No. 8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 95 SPEMCRKC 102  
Db 149 spemcrkc 156  
IIIIIIII

RESULT 46  
AAU04038  
ID AAU04038 standard; Protein: 411 AA.  
XX  
XX AAU04038;  
AC  
XX  
XX 23-OCT-2001 (first entry)  
DT  
XX  
XX Human apoptotic protein, Apo-2.  
DE  
XX  
XX Human; Apo-2; Apo-2L receptor; immunogen; monoclonal antibody;  
KW cancer; tumour; apoptosis; lymphoma; blastoma; sarcoma; leukaemia;  
KM 3H3.14.5.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH MISC-difference 410 /label= OTHER  
FT /note= "Other= Leu or Met"  
FT  
XX  
PN US6252050-B1.

XX 26-JUN-2001.  
PD  
XX  
XX 10-JUN-1999; 99US-0329633.  
XX  
XX  
XX 12-JUN-1998; 98US-0089253.  
PR  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Chuntharapal A, Kim KJ;  
PI  
XX WPI: 2001-424490/45.  
DR  
XX N-PSDB: AAS07626.  
XX  
XX Novel human monoclonal antibody for inducing apoptosis in mammalian  
PT cancer cells, specifically cross-reacts with two or more different  
PT Apo-2 ligand receptors -  
XX  
XX  
XX Example 1; Fig 5; 29pp; English.  
PS  
XX  
XX The sequence represents human Apo-2, an apoptotic protein used as an  
CC immunogen to make the monoclonal antibodies of the invention. The  
CC invention relates to an isolated antibody which specifically cross-reacts  
CC with two or more different Apo-2 ligand (Apo-2L) receptors. Apoptosis by  
CC monoclonal antibody 3H3.14.5 after crosslinking with anti-mouse Ig was  
CC tested. Human 9D cells in complete RPMI medium were added. Cells were  
CC incubated with the monoclonal antibody in 100 micro on ice for 15  
CC minutes. Cells were then incubated with goat anti-mouse IgG FC complete  
CC RPMI medium overnight at 37 degrees C. After washing once with PBS, cells  
CC were resuspended in PBS containing 0.5% BSA and incubated with FITC-  
CC Annexin and propidium iodide for 15 minutes in the dark. Dead cells were  
CC detected by FACSscan. The 3H3.14.5 antibody was able to inhibit apoptosis  
CC induced by interaction between Apo-2L and Apo-2. This antibody was  
CC further capable of inducing apoptosis of 9D cells in the presence of an  
CC anti-PC antibody to cross-link antibodies. The antibodies are useful for  
CC inducing apoptosis in mammalian cancer cells for treating cancer  
CC including carcinoma, lymphoma, blastoma, sarcoma and leukaemia, and are  
CC useful in diagnostic assays for their antigen, e.g. detecting its  
CC expression in specific cells, tissues or serum and for affinity  
CC purification of antigen from recombinant cell culture or natural sources.  
XX  
XX Sequence 411 AA;  
SQ

Query Match 3.4%; Score 8; DB 22; Length 411;  
Best Local Similarity 100.0%; Pred. No. 8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 95 SPEMCRKC 102  
Db 149 spemcrkc 156  
IIIIIIII

RESULT 47  
AAB73442  
ID AAB73442 standard; Protein: 411 AA.  
XX  
XX AAB73442;  
AC  
XX  
XX 25-JUN-2001 (first entry)  
DT  
XX  
XX Human Apo-2 receptor precursor, SEQ ID NO:2.  
DE  
XX  
XX Human Apo-2 receptor; caspase-dependent apoptosis induction;  
KW programmed cell death; pro-apoptotic; death domain;  
KM agonistic antibody; nuclear factor kappa B;  
KW NF-kappa-B activation; cancer; tumour; lung cancer;  
KM colon cancer; glioma.  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..53  
FT

FT	Protein	/note- "Signal peptide"
FT		54..411
FT	Domain	/note- "Mature human Apo-2 receptor"
FT		54..182
FT		/note- "Extracellular domain. This domain is
FT		alternatively residues 1-182, or residues 1-130
FT	Disulfide-bond	81..94
FT	Domain	96..137
FT	Disulfide-bond	/note- "Cysteine-rich pseudorepeat domain #1"
FT	Binding-site	97..113
FT		106
FT	Binding-site	/note- "Binds Apo-2L"
FT		112
FT	Disulfide-bond	/note- "Binds Apo-2L"
FT		116..129
FT	Disulfide-bond	119..137
FT	Disulfide-bond	138..183
FT	Domain	/note- "Cysteine-rich pseudorepeat domain #2"
FT	Disulfide-bond	139..153
FT	Disulfide-bond	156..170
FT	Disulfide-bond	160..178
FT	Domain	183..208
FT		/note- "Transmembrane domain"
FT	Domain	209..411
FT		/note- "Intracellular domain"
FT	Domain	324..391
FT		/note- "Death domain"
FT	Misc-difference	410
FT		/label= Met, Leu
FT		/note- "Encoded by WTC. This residue is Met in kidney
FT		Apo-2, and is Leu in pancreatic Apo-2"
XX	WO200119861-A2.	
PD	22-MAR-2001.	
XX		
XX	14-SEP-2000; 2000WO-US25436.	
XX		
PR	15-SEP-1999; 99US-0396710.	
XX		
PA	(GETH ) GENENTECH INC.	
PI	Ashkenazi AJ, Chuntherapai A, Kim KJ;	
XX		
DR	WPI: 2001-266005/27.	
XX	N-PSDB; AAF84481.	
PT		
PT	Inducing apoptosis in mammalian cells for treating cancer, comprises	
PT	exposing mammalian cells or cancer cells expressing Apo-2 receptor, to	
PT	Apo-2 agonist antibody	
XX		
PS	Example 1; Fig 1; 90pp: English.	
XX		
CC	The invention relates to a method for inducing apoptosis in mammalian	
CC	cells which express the Apo-2 receptor protein (AAB3442, AAB3443).	
CC	The method involves exposing the cells to an Apo-2 agonistic antibody,	
CC	which induces Apo-2 receptor-mediated apoptosis. The Apo-2 receptor	
CC	(which referred to simply as Apo-2) is a member of the tumour	
CC	necrosis factor receptor (TNFR) family, and its natural ligand is the	
CC	Apo-2 ligand (Apo-2L, also known as TRAIL). The Apo-2 receptor is able	
CC	to trigger caspase-dependent apoptosis, and is also able to activate	
CC	NF-kappa-B (nuclear factor kappa B). The Apo-2 receptor is an	
CC	approximately 45 kD type I transmembrane protein, and contains a death	
CC	domain in the cytoplasmic region (residues 324-392). It exhibits	
CC	significantly more sequence identity to the apoptosis-linked receptor	
CC	DR4, which also binds Apo-2L, than other apoptosis-associated proteins.	
CC	The Apo-2 receptor agonist monoclonal antibodies used in the method of	
CC	the invention are JF11.39.7, 3H3.14, 5, 3D5.1.10 and 3H1.18.10. The	
CC	method of the invention is used to induce apoptosis in Apo-2-expressing	
CC	cells, particularly cancer cells. It may therefore be used for treating	
CC	mammalian cancers, especially lung cancer, colon cancer and glioma.	
CC	The present sequence represents human Apo-2 as encoded by cDNA isolated	
CC	in an exemplification of the invention.	

CC	Note:	The present sequence differs from the human Apo-2 receptor precursor given in AAB73443 in that residue 410 of this sequence can be Met or Leu, rather than Leu.
CC		
XX	Sequence	411 AA:
SQ		
Query Match	3.4%;	Score 8; DB 22; Length 411;
Best Local Similarity	100.0%;	Pred. No. 8;
Matches	8; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	95 SPKCRKC	102 
Db	149 spemcrkc	156
RESULT 48		
AAB73443		
ID	AAB73443 standard; Protein;	411 AA.
XX		
AC	AAB73443;	
XX		
DT	25-JUN-2001	(first entry)
DE	Human Apo-2 receptor precursor, SEQ ID NO:6.	
XX		
KW	Human Apo-2 receptor; caspase-dependent apoptosis induction;	
KW	programmed cell death; pro-apoptotic; death domain;	
KW	agonistic antibody; nuclear factor kappa B;	
KM	NF-kappa-B activation; cancer; tumour; lung cancer;	
KW	colon cancer; glioma.	
XX		
OS	Homo sapiens.	
XX		
RH	Key	Location/Qualifiers
FT	Peptide	1..53
FT	/note= "Signal peptide"	54..411
FT	Protein	/note= "Mature human Apo-2 receptor"
FT	/note=	54..182
FT	Domain	/note= "Extracellular domain. This domain is alternatively residues 1-182, or residues 1-130"
FT		
FT	Disulfide-bond	81..94
FT	Domain	96..137
FT	/note=	"Cysteine-rich pseudorepeat domain #1"
FT	Disulfide-bond	97..113
FT	Binding-site	106
FT	/note= "Binds Apo-2L"	112
FT	Binding-site	/note= "Binds Apo-2L"
FT	Disulfide-bond	115..129
FT	Disulfide-bond	119..137
FT	Domain	138..183
FT	/note=	"Cysteine-rich pseudorepeat domain #2"
FT	Disulfide-bond	139..153
FT	Disulfide-bond	156..170
FT	Disulfide-bond	160..178
FT	Domain	183..208
FT	/note=	"Transmembrane domain"
FT	Domain	209..411
FT	/note=	"Intracellular domain"
FT	Domain	324..391
FT	/note=	"Death domain"
FT	Misc-difference	410
FT	/note=	"Encoded by wrg"
WO200119861-AZ.		
XX		
PD	22-MAR-2001.	
XX		
PF	14-SEP-2000; 2000WO-US25436.	
XX		
PR	15-SEP-1999; 99US-0396710.	

XX (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Chuntherapai A, Kim KJ;  
 PI WPI: 2001-266005/27.  
 XX N-PSDB: AAF84481.  
 DR  
 XX Inducing apoptosis in mammalian cells for treating cancer, comprises  
 PT exposing mammalian cells or cancer cells expressing Apo-2 receptor, to  
 PT Apo-2 agonist antibody -  
 XX  
 XX Example 1: Fig 2A; 90pp: English.  
 PS  
 XX The invention relates to a method for inducing apoptosis in mammalian  
 CC cells which express the Apo-2 receptor protein (AAB73442, AAB73443).  
 CC The method involves exposing the cells to an Apo-2 agonistic antibody,  
 CC which induces Apo-2 receptor-mediated apoptosis. The Apo-2 receptor  
 CC (also referred to simply as Apo-2) is a member of the tumour  
 CC neurosis factor receptor (TNFR) family, and its natural ligand is the  
 CC Apo-2 ligand (Apo-2L, also known as TRAIL). The Apo-2 receptor is able  
 CC to trigger caspase-dependent apoptosis, and is also able to activate  
 CC NF-kappa B (nuclear factor kappa B). The Apo-2 receptor is an  
 CC approximately 45 kD type I transmembrane protein, and contains a death  
 CC domain in the cytoplasmic region (residues 324-392). It exhibits  
 CC significantly more sequence identity to the apoptosis-linked receptor  
 CC DR4, which also binds Apo-2L, than other apoptosis-associated proteins.  
 CC The Apo-2 receptor agonist monoclonal antibodies used in the method of  
 CC the invention are 3F11.39.7, 3H3.14, 5, 3D5.1.10 and 3H1.18.10. The  
 CC method of the invention is used to induce apoptosis in Apo-2-expressing  
 CC cells, particularly cancer cells. It may therefore be used for treating  
 CC mammalian cancers, especially lung cancer, colon cancer and glioma.  
 CC The present sequence represents human Apo-2 as given in figure 2A.  
 CC Note: The present sequence differs from the human Apo-2 receptor  
 CC precursor given in AAB73442 in that residue 410 of this sequence is Leu,  
 CC rather than Met or Leu.  
 CC  
 XX Sequence 411 AA;  
 SQ

Query Match 3.4%; Score 8; DB 22; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 SPENCRCRC 102  
 |||||  
 Db 149 spencrcrc 156

RESULT 49  
 AAB48348  
 ID AAB48348 standard; Protein: 411 AA.  
 XX  
 AC AAB48348;  
 XX  
 DT 20-APR-2001 (first entry)  
 XX  
 DE Human tumour necrosis factor related receptor TR6.  
 XX  
 KW Tumour necrosis factor: TNF; TNF related receptor: TR6; human;  
 KW antiinflammatory; immunosuppressive; cerebroprotective; vasotropic;  
 KW antisthmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic;  
 KW neurotropic; neuroprotective; antiarthritic; antineumatic; antischismic;  
 KW gene therapy; vaccine; TNF-alpha; bone disease; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 290..324  
 FT /note= "death domain"  
 XX  
 PN W0200077191-A1.  
 XX

PD 21-DEC-2000.  
 XX  
 XX 12-JUN-2000; 2000WO-US16134.  
 XX  
 XX 15-JUN-1999; 99US-0333593.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA  
 PI Deen KC, Young PR, Marshall LA, Roshak AK, Tan KB, Truneh A;  
 XX WPI: 2001-112223/12.  
 XX N-PSDB: AAC84743.  
 DR  
 XX New tumor necrosis factor related receptor TR6 polynucleotides and  
 PT polypeptides useful for e.g. for treating chronic and acute  
 PT inflammation, arthritis, septicemia, autoimmune diseases, infection,  
 PT cancer, bone diseases -  
 XX  
 XX Claim 10: Page 14-15; 47pp: English.  
 PS  
 XX This represents a human tumour necrosis factor (TNF) related receptor,  
 CC TR6. TR6 can be expressed by standard recombinant methodology. The TR6  
 CC polypeptides are useful for treating chronic and acute inflammation,  
 CC rheumatoid arthritis, septicemia, autoimmune diseases (e.g. inflammatory  
 CC bowel disease, psoriasis), transplant rejection, graft vs. host disease,  
 CC infection, stroke, ischemia, acute respiratory disease syndrome, asthma,  
 CC restenosis, brain injury, AIDS (acquired immunodeficiency syndrome), bone  
 CC diseases, cancer, atherosclerosis, and Alzheimer's disease. These may  
 CC also be used to inhibit production of TNF-alpha and eicosanoids, as  
 CC research reagents and materials for discovering treatments and  
 CC diagnostics to animal and human diseases. The polypeptides may further be  
 CC used as immunogens to produce antibodies immunospecific for the TR6  
 CC polypeptides. The polynucleotides may also be used as hybridization  
 CC probes for cDNA and genomic DNA, for isolating full-length cDNAs and  
 CC genomic clones encoding TR6 and of other genes having high sequence  
 CC similarity to TR6 gene, and for chromosome identification.  
 CC  
 XX Sequence 411 AA;  
 SQ

Query Match 3.4%; Score 8; DB 22; Length 411;  
 Best Local Similarity 100.0%; Pred. No. 8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 95 SPENCRCRC 102  
 |||||  
 Db 149 spencrcrc 156

RESULT 50  
 AAB48352  
 ID AAB48352 standard; Protein: 424 AA.  
 XX  
 AC AAB48352;  
 XX  
 DT 20-APR-2001 (first entry)  
 XX  
 DE TR6-Ig fusion protein sequence.  
 XX  
 KW Tumour necrosis factor: TNF; TNF related receptor: TR6; human;  
 KW antiinflammatory; immunosuppressive; cerebroprotective; vasotropic;  
 KW antisthmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic;  
 KW neurotropic; neuroprotective; antiarthritic; antineumatic; antischismic;  
 KW gene therapy; vaccine; TNF-alpha; bone disease; cancer; fusion protein.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..53  
 FT /note= "leader sequence"  
 FT Protein 1..184  
 FT /note= "TR6 receptor"  
 FT Cleavage-site 187..190  
 FT



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FT      /note="factor Xa protease cleavage site"
FT      Protein
FT      191..424
FT      /note="IgG-gamma1 hinge Fc region"
XX
XX      WO200077191-A1.
XX
XX      21-DEC-2000.
XX
XX      12-JUN-2000; 2000WO-US16134.
XX
XX      15-JUN-1999; 99US-0333593.
XX
XX      (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX      Deen KC, Young PR, Marshall LA, Roshak AK, Tan KB, Truneh A;
XX      WPI; 2001-112223/12.
XX
XX      New tumor necrosis factor related receptor TR6 polynucleotides and
XX      polypeptides useful for e.g. for treating chronic and acute
XX      inflammation, arthritis, septicemia, autoimmune diseases, infection,
XX      cancer, bone diseases
XX
XX      Claim 28; Page 17; 47pp; English.
XX
XX      The invention relates to a human tumour necrosis factor (TNF) related
XX      receptor, TR6. TR6 can be expressed by standard recombinant methodology.
XX      The TR6 polypeptides are useful for treating chronic and acute
XX      inflammation, rheumatoid arthritis, septicemia, autoimmune diseases
XX      (e.g. inflammatory bowel disease, psoriasis), transplant rejection, graft
XX      vs. host disease, infection, stroke, ischemia, acute respiratory disease
XX      syndrome, asthma, restenosis, brain injury, AIDS, bone diseases, cancer,
XX      atherosclerosis, and Alzheimer's disease. These may also be used to
XX      inhibit production of TNF-alpha and eicosanoids, as research reagents and
XX      materials for discovering treatments and diagnostics to animal and human
XX      diseases. The polypeptides may further be used as immunogens to produce
XX      antibodies immunospecific for the TR6 polypeptides. The polynucleotides
XX      may also be used as hybridization probes for cDNA and genomic DNA, for
XX      isolating full-length cDNAs and genomic clones encoding TR6 and of other
XX      genes having high sequence similarity to TR6 gene, and for chromosome
XX      identification. The present sequence represents a TR6-Ig fusion protein
XX      sequence where the N-terminal amino acids (1-184) of TR6 is fused to a
XX      factor Xa protease cleavage site and the hinge Fc region of a human
XX      IgG-gamma1 heavy chain.
XX
XX      Sequence 424 AA;
XX
XX      Query Match 3.4%; Score 8; DB 22; Length 424;
XX      Best Local Similarity 100.0%; Pred. No. 8.2;
XX      Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      95 SPEMCRKC 102
OY      |||||||
DB      149 SPEMCRKC 156

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Search completed: August 13, 2002, 08:37:59  
 Job time: 388 sec



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## OM protein - protein search, using sw model

Run on: August 13, 2002, 08:35:56 ; Search time 19.29 seconds  
(without alignments)  
1160.644 Million cell updates/sec

Title: US-09-826-212-2\_COPY\_27\_259  
Perfect score: 233  
Sequence: 1 TTARQEEVPQQTVAPOQOORH.....YLSCTIVGILVLLIVFV 233

Scoring table:  
OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 5

Total number of hits satisfying chosen parameters: 8656

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	8	3.4	464	2 D72058	transcription term
2	8	3.4	464	2 G86566	transcription term
3	8	3.4	491	2 AC1185	B. subtilis YdbB p
4	8	3.4	494	2 AB1543	B. subtilis YdbB p
5	8	3.4	685	2 G82022	methionine--trna l
6	8	3.4	801	2 T29018	hypothetical prote
7	7	3.0	155	2 S71258	major latex protei
8	7	3.0	165	2 T21313	hypothetical prote
9	7	3.0	184	2 H90386	hypothetical prote
10	7	3.0	199	2 H72242	flagellar L-ring p
11	7	3.0	201	2 D70519	probable lppc prot
12	7	3.0	219	2 E75477	hypothetical prote
13	7	3.0	255	2 T05958	cold acclimation p
14	7	3.0	256	2 H82517	hypothetical prote
15	7	3.0	256	2 B82661	hypothetical prote
16	7	3.0	256	2 B82648	hypothetical prote
17	7	3.0	262	2 T01305	hypothetical prote
18	7	3.0	263	2 T15453	hypothetical prote
19	7	3.0	266	2 T46853	yibQ protein [lipo
20	7	3.0	268	2 T06802	cold acclimation p
21	7	3.0	283	2 S27708	daunorubicin resis
22	7	3.0	313	2 T45537	moab protein [lipo
23	7	3.0	365	2 C81050	cytochrome c oxida
24	7	3.0	366	2 F81826	probable cytochrom
25	7	3.0	374	2 T50265	phosphate transpor
26	7	3.0	390	2 T50265	phosphate transpor
27	7	3.0	390	2 A53773	La/SS-B homolog D-
28	7	3.0	390	2 A53781	ribonucleoprotein
29	7	3.0	397	2 H71116	hypothetical prote

30	7	3.0	431	2 S64704	ornithine decarbox
31	7	3.0	450	2 T21515	hypothetical prote
32	7	3.0	464	2 S12591	beta-1-adrenergic
33	7	3.0	466	2 S36794	beta-1-adrenergic
34	7	3.0	471	1 S08325	flavonol 3-O-gluc
35	7	3.0	471	2 S01052	flavonol 3-O-gluc
36	7	3.0	477	1 QRH0B1	beta-1-adrenergic
37	7	3.0	480	2 T53053	beta-1-adrenergic
38	7	3.0	485	2 F95238	PTS system membra
39	7	3.0	508	2 G98102	hypothetical prote
40	7	3.0	542	2 UC7391	Ca2+-binding prote
41	7	3.0	548	2 D90493	hypothetical prote
42	7	3.0	548	2 E70546	hypothetical prote
43	7	3.0	556	2 T42100	serine/threonine p
44	7	3.0	556	2 T36502	serine/threonine p
45	7	3.0	589	2 H83085	conserved hypotet
46	7	3.0	599	1 H65057	sulfite reductase
47	7	3.0	599	2 C91081	sulfite reductase
48	7	3.0	599	2 D85926	sulfite reductase
49	7	3.0	669	2 T47484	receptor like prot
50	7	3.0	694	2 T12712	NADH dehydrogenase
51	7	3.0	744	2 T13502	NADH dehydrogenase
52	7	3.0	837	2 T02761	outer atm dynein 1
53	7	3.0	838	2 T20125	hypothetical prote
54	7	3.0	840	2 G98169	hypothetical prote
55	7	3.0	840	2 AF3117	hypothetical prote
56	7	3.0	964	2 AG3433	diguanylate cyclas
57	7	3.0	971	2 H97454	hypothetical prote
58	7	3.0	971	2 AB2673	conserved hypotet
59	7	3.0	1036	2 T38734	hypothetical prote
60	7	3.0	1110	2 T51116	NE-180 - sea lamp
61	7	3.0	1177	2 A87060	DNA polymerase III
62	7	3.0	1179	2 T35093	DNA-directed DNA p
63	7	3.0	1184	2 H70761	probable dinapolye
64	7	3.0	1318	2 T21266	hypothetical prote
65	7	3.0	1742	2 S76110	hypothetical prote
66	7	3.0	2938	2 T30249	cell proliferation
67	7	3.0	3739	2 T17410	polyketide synthas
68	6	2.6	22	2 T46633	transcription term
69	6	2.6	36	2 E95059	hypothetical prote
70	6	2.6	37	2 B95134	hypothetical prote
71	6	2.6	41	2 S29626	p36 protein - slim
72	6	2.6	44	2 G82408	hypothetical prote
73	6	2.6	50	2 G69094	ribosomal protein
74	6	2.6	53	2 H97844	hypothetical prote
75	6	2.6	54	2 A71635	hypothetical prote
76	6	2.6	56	2 H85964	hypothetical prote
77	6	2.6	59	2 E83866	hypothetical prote
78	6	2.6	62	2 H69301	conserved hypotet
79	6	2.6	62	2 C97847	hypothetical prote
80	6	2.6	65	2 A90826	Icd-like protein l
81	6	2.6	66	2 C97928	hypothetical prote
82	6	2.6	77	2 C89651	hypothetical prote
83	6	2.6	82	2 A95220	conserved hypotet
84	6	2.6	83	2 T23070	hypothetical prote
85	6	2.6	85	2 B91279	suppressor of inh
86	6	2.6	85	2 S77937	exoskeletal protei
87	6	2.6	85	2 B86120	suppressor of inh
88	6	2.6	86	2 T23886	hypothetical prote
89	6	2.6	87	2 T22131	hypothetical prote
90	6	2.6	89	2 A33542	islet amyloid poly
91	6	2.6	90	2 T22136	hypothetical prote
92	6	2.6	93	2 S44477	NADH dehydrogenase
93	6	2.6	94	2 E89840	hypothetical prote
94	6	2.6	95	2 H84945	50S ribosomal prot
95	6	2.6	98	2 PH0871	Ig heavy chain V r
96	6	2.6	98	2 S26910	Ig heavy chain V r
97	6	2.6	98	2 S26938	Ig heavy chain V r
98	6	2.6	98	2 S26912	Ig heavy chain V r
99	6	2.6	98	2 S26920	Ig heavy chain V r
100	6	2.6	100	2 G98083	hypothetical prote
101	6	2.6	104	2 S69899	Ig heavy chain V r
102	6	2.6	104	2 F48652	integral membrane

103	6	2.6	104	2	H90197	hypothetical prote
104	6	2.6	104	2	AH1551	hypothetical prote
105	6	2.6	105	2	S6794.1	Ig heavy chain var
106	6	2.6	106	2	A87676	SUGC protein [limp
107	6	2.6	109	2	PH1668	Ig heavy chain V r
108	6	2.6	109	2	T42436	FMFamide-Like pep
109	6	2.6	110	1	RebY22	60s acidic ribosom
110	6	2.6	110	2	PH1669	Ig heavy chain V r
111	6	2.6	110	2	T37490	ribosomal protein
112	6	2.6	110	2	T6537	FMFamide-Like pep
113	6	2.6	111	2	E72524	probable ribosomal
114	6	2.6	112	2	EB6141	protein T25K16.9 [
115	6	2.6	112	2	ES4462	probable membrane
116	6	2.6	113	2	A45252	P1LV variable regi
117	6	2.6	117	1	HVH0HG	Ig heavy chain pre
118	6	2.6	117	2	S31680	Ig heavy chain V r
119	6	2.6	117	2	S18551	Ig heavy chain V r
120	6	2.6	118	2	G72772	hypothetical prote
121	6	2.6	119	2	A97730	hypothetical prote
122	6	2.6	119	2	T17003	dormancy-associate
123	6	2.6	120	2	S31999	Ig heavy chain V r
124	6	2.6	121	2	S20783	Ig heavy chain V r
125	6	2.6	121	2	H71086	hypothetical prote
126	6	2.6	124	2	C84953	mutator mutr prote
127	6	2.6	125	2	H70101	gIPE protein (gIPE
128	6	2.6	126	2	I44151	Ig heavy chain V r
129	6	2.6	128	2	G71730	hypothetical prote
130	6	2.6	129	2	S46393	Ig heavy chain V r
131	6	2.6	133	2	B97706	hypothetical prote
132	6	2.6	133	2	E72763	immunoglobulin lam
133	6	2.6	134	2	A26986	hypothetical prote
134	6	2.6	135	2	C82297	DNA polymerase III
135	6	2.6	135	2	S49530	anti-Sm antibody V
136	6	2.6	136	2	C81436	biopolymer transpo
137	6	2.6	136	2	AB1127	hypothetical prote
138	6	2.6	136	2	AG1487	hypothetical prote
139	6	2.6	139	2	S78306	photosystem I ferr
140	6	2.6	139	2	A81938	probable membrane
141	6	2.6	141	2	A32124	photosystem I chal
142	6	2.6	141	2	C83529	hypothetical prote
143	6	2.6	142	2	A32483	Ig heavy chain V r
144	6	2.6	143	2	T48769	hypothetical prote
145	6	2.6	144	2	G81048	biopolymer transpo
146	6	2.6	144	2	B70111	V-type ATPase, sub
147	6	2.6	149	2	C84053	sodium-glutamate/a
148	6	2.6	150	2	S58488	DNA polymerase III
149	6	2.6	150	2	T10641	carbonic anhydrase
150	6	2.6	155	2	A82110	bacterioferritin c
151	6	2.6	155	2	AC1172	hypothetical prote
152	6	2.6	155	2	AE1529	hypothetical prote
153	6	2.6	155	2	C86206	hypothetical prote
154	6	2.6	156	2	AB2717	conserved hypotet
155	6	2.6	157	2	T35610	wh1e protein II -
156	6	2.6	157	2	D84987	smg protein [impor
157	6	2.6	157	2	AG2775	protein-export mem
158	6	2.6	158	2	D81820	hypothetical prote
159	6	2.6	161	2	G75059	hypothetical prote
160	6	2.6	162	2	E97555	hypothetical prote
161	6	2.6	162	2	E90497	hypothetical prote
162	6	2.6	167	2	A86941	conserved hypotet
163	6	2.6	170	2	S43476	histone-like DNA-b
164	6	2.6	172	2	H75384	osmotically-induci
165	6	2.6	172	2	T32120	hypothetical prote
166	6	2.6	173	2	AB1684	hypothetical prote
167	6	2.6	173	2	T38617	zinc finger protei
168	6	2.6	174	2	JE0305	propanediol dehydr
169	6	2.6	176	2	T18921	hypothetical prote
170	6	2.6	176	2	B64505	hypothetical prote
171	6	2.6	183	2	S24960	gene C98 protein -
172	6	2.6	185	1	S32238	ribosomal protein
173	6	2.6	185	2	B64615	hypothetical prote
174	6	2.6	189	2	E97498	outer membrane ser
175	6	2.6	190	2	E64775	probable lipoprote
176	6	2.6	190	2	C90692	glycoprotein/polys
177	6	2.6	190	2	G85542	glycoprotein/polys
178	6	2.6	193	2	AE0492	probable membrane
179	6	2.6	194	2	AF0082	conserved hypotet
180	6	2.6	194	2	T14746	hypothetical prote
181	6	2.6	194	2	A97351	hypothetical secre
182	6	2.6	195	1	MUBPM1	lysozyme (EC 3.2.1
183	6	2.6	195	2	S34993	nitrite reductase
184	6	2.6	196	2	D70637	hypothetical prote
185	6	2.6	197	1	S41182	phage-related repl
186	6	2.6	197	2	S52798	hypothetical prote
187	6	2.6	198	2	A10970	probable Tetr-Iam1
188	6	2.6	198	2	AF11887	hypothetical prote
189	6	2.6	198	2	B83717	NADP-dependent alc
190	6	2.6	200	2	D83997	hypothetical prote
191	6	2.6	204	2	T20407	hypothetical prote
192	6	2.6	205	2	T02247	photosystem I chal
193	6	2.6	205	2	T26846	hypothetical prote
194	6	2.6	208	1	R3R78	ribosomal protein
195	6	2.6	208	2	S42110	ribosomal protein
196	6	2.6	208	2	S25022	ribosomal protein
197	6	2.6	208	2	A87269	hypothetical prote
198	6	2.6	209	2	JX0266	platelet aggregati
199	6	2.6	211	2	C70665	probable uret prot
200	6	2.6	211	2	D69529	conserved hypotet
201	6	2.6	212	1	A1SP2	photosystem I chal
202	6	2.6	214	2	AB1407	phloose-phosphate
203	6	2.6	214	2	AB1783	ribulose-phosphate
204	6	2.6	214	2	T11966	lipoate biosynthes
205	6	2.6	215	2	T36448	probable methyltra
206	6	2.6	218	1	A40181	23K integral membr
207	6	2.6	218	2	H84084	hypothetical prote
208	6	2.6	218	2	H84340	circadian regulato
209	6	2.6	219	1	XMECAD	deda protein - Esc
210	6	2.6	219	2	A98029	hypothetical prote
211	6	2.6	219	2	B85873	hypothetical prote
212	6	2.6	219	2	AE0802	deda protein (ds9-
213	6	2.6	220	2	T04082	probable ribosomal
214	6	2.6	221	2	T04088	ribosomal protein
215	6	2.6	221	2	S44651	f42h10.4 protein -
216	6	2.6	222	2	A27270	myosin light chain
217	6	2.6	223	2	E89567	protein T08A9.3 [i
218	6	2.6	224	1	A64599	hydrogenase (EC 1.
219	6	2.6	224	2	S69635	hypothetical prote
220	6	2.6	225	2	B28456	histone H1.11L - c
221	6	2.6	225	2	G89662	protein E01G6.2 [i
222	6	2.6	226	2	S46353	nef protein - simi
223	6	2.6	226	2	E86326	protein F18014.3 [
224	6	2.6	226	2	T35236	hypothetical prote
225	6	2.6	227	2	H86940	probable membrane
226	6	2.6	228	2	T41834	OVV-E25 P25 orF94
227	6	2.6	228	2	G72861	occlusion-derived
228	6	2.6	230	2	T32999	hypothetical prote
229	6	2.6	230	2	T18613	hypothetical prote
230	6	2.6	231	2	I50467	MHC class II beta
231	6	2.6	232	2	T03678	plasma membrane pr
232	6	2.6	239	2	S73912	5-guanylate kinase
233	6	2.6	239	2	T02984	myb-related protei
234	6	2.6	245	2	T68673	gene X123 protein
235	6	2.6	245	2	AG2203	glucose inhibited
236	6	2.6	247	2	A71847	carbonic anhydrase
237	6	2.6	247	2	T43324	synaptogyrin homol
238	6	2.6	247	2	T21406	hypothetical prote
239	6	2.6	248	2	AG1571	cobalamin (5'-phos
240	6	2.6	249	2	T40405	hypothetical prote
241	6	2.6	251	2	T35285	probable integral
242	6	2.6	251	2	G95361	probable ABC trans
243	6	2.6	254	2	T10185	MADS-box protein C
244	6	2.6	254	2	A87582	conjugal transfer
245	6	2.6	256	2	T10376	hypothetical prote
246	6	2.6	256	2	AE0285	conserved hypotet
247	6	2.6	257	2	G70453	indole-3-glycerol
248	6	2.6	257	2	T12092	G-box-binding prot

249	6	2.6	258	2	AD2531	hypothetical prote	322	6	2.6	326	2	S74844	lmbp protein - Syn
250	6	2.6	260	2	T10642	carbonic anhydrase	323	6	2.6	327	2	S49619	crta protein - Rho
251	6	2.6	261	2	E70957	probable lprf prot	324	6	2.6	327	2	T50744	spherulene monoox
252	6	2.6	261	2	AB3070	conserved hypochet	325	6	2.6	328	2	S32369	gamma-SNAP protein
253	6	2.6	262	2	AB0715	aminoglycoside-res	326	6	2.6	329	2	G82900	aspartate-ammonia
254	6	2.6	264	2	C97402	probable acyltrans	327	6	2.6	329	2	A10574	ferric enterobacti
255	6	2.6	264	2	AC2620	1-acyl-sn-glycerol	328	6	2.6	330	2	C64792	ferric enterobacti
256	6	2.6	266	2	AE0979	probable transcrip	329	6	2.6	330	2	C95844	probable sugar ABC
257	6	2.6	268	2	AH1646	hypothetical prote	330	6	2.6	330	2	D90707	ferric enterobacti
258	6	2.6	269	1	C69651	prolipoprotein dia	331	6	2.6	330	2	H85557	ferric enterobacti
259	6	2.6	269	2	T21407	hypothetical prote	332	6	2.6	330	2	A89637	hypothetical prote
260	6	2.6	270	2	G90595	conserved hypochet	333	6	2.6	337	2	G95915	probable sugar ABC
261	6	2.6	270	2	A43711	replication protei	334	6	2.6	339	2	C83335	probable oxidoredu
262	6	2.6	270	2	S28682	replication protei	335	6	2.6	339	2	H64348	hypothetical prote
263	6	2.6	270	2	E87659	hypothetical prote	336	6	2.6	341	2	T16091	hypothetical prote
264	6	2.6	271	2	S12783	Ox40 antigen precu	337	6	2.6	343	2	E64363	acidic ribosomal p
265	6	2.6	273	2	H71212	hypothetical prote	338	6	2.6	343	2	T50179	yeast bud pattern
266	6	2.6	274	2	T12791	hypothetical prote	339	6	2.6	344	2	F72524	probable acidic ri
267	6	2.6	275	2	A32057	nitrogenase (EC 1.	340	6	2.6	345	2	H90515	lipote-protein II
268	6	2.6	275	2	C69808	transporter homolo	341	6	2.6	347	2	A75537	hypothetical prote
269	6	2.6	275	2	A97226	uncharacterized co	342	6	2.6	347	2	A46567	tetracycline resis
270	6	2.6	276	2	AI2392	hypothetical prote	343	6	2.6	348	2	T35968	conserved hypochet
271	6	2.6	279	2	AG0421	sugar transport sy	344	6	2.6	348	2	AD0654	probable protease
272	6	2.6	279	2	T51515	synthaxin homolog F	345	6	2.6	349	2	H97006	probable permease,
273	6	2.6	280	2	H75194	hypothetical prote	346	6	2.6	350	2	H82777	conserved hypochet
274	6	2.6	281	2	A41400	myristylated alani	347	6	2.6	353	2	A75027	oligopeptide trans
275	6	2.6	281	2	F84313	hypothetical prote	348	6	2.6	353	2	D75328	conserved hypochet
276	6	2.6	283	2	G84458	probable protein P	349	6	2.6	353	2	S38080	hypothetical prote
277	6	2.6	284	2	T39544	suppressor protein	350	6	2.6	355	2	T05390	probable cysteine
278	6	2.6	284	2	H72370	conserved hypochet	351	6	2.6	356	2	S42388	torso-like protein
279	6	2.6	287	2	T42085	MPF4 protein homol	352	6	2.6	357	2	H83388	probable permease
280	6	2.6	290	2	S64312	hypothetical prote	353	6	2.6	357	2	D86707	ABC transporter pe
281	6	2.6	292	2	T18584	f15c11.2 - Caemorb	354	6	2.6	359	2	E86706	hypothetical prote
282	6	2.6	294	2	S71642	dolichyl phosphate	355	6	2.6	362	2	S37220	fiber protein - hu
283	6	2.6	294	2	D70525	probable beta-1 -	356	6	2.6	362	2	S40932	fiber protein - hu
284	6	2.6	296	2	T46617	probable chemotaxi	357	6	2.6	364	2	I46604	MHC PD14 transplan
285	6	2.6	297	2	F86839	phosphate ABC tran	358	6	2.6	364	2	J01488	bradykinin B2 rece
286	6	2.6	297	2	A45335	cytochrome-c oxida	359	6	2.6	366	2	A60363	MHC class I histoc
287	6	2.6	297	2	S38477	lytic enzyme lyso	360	6	2.6	366	2	I46603	MHC PD14 transpla
288	6	2.6	299	2	T12505	hypothetical prote	361	6	2.6	369	2	T30592	conserved hypochet
289	6	2.6	299	2	D98238	helix-turn-helix d	362	6	2.6	369	2	T05013	hypothetical prote
290	6	2.6	300	2	AH1357	hypothetical prote	363	6	2.6	370	2	A75371	threonine 3-dehydr
291	6	2.6	300	2	AH1727	hypothetical prote	364	6	2.6	371	2	D96771	unknown protein FI
292	6	2.6	301	2	A87445	integral membrane	365	6	2.6	372	1	Q0BE88	glycoprotein I pre
293	6	2.6	307	2	JC5927	synthaxin 16 - huma	366	6	2.6	372	2	F43674	u57 protein - huma
294	6	2.6	308	2	H65035	hypothetical prote	367	6	2.6	372	2	C96771	unknown protein FI
295	6	2.6	308	2	H64409	hypothetical prote	368	6	2.6	372	2	S67770	probable membrane
296	6	2.6	308	2	T17248	hypothetical prote	369	6	2.6	372	2	A83714	Iron (III) transpo
297	6	2.6	310	2	S65966	succinate--CoA lig	370	6	2.6	372	2	B98331	probable transamin
298	6	2.6	310	2	B83331	catechol 1,2-dioxy	371	6	2.6	372	2	AC2952	aspartate aminotra
299	6	2.6	311	2	B69191	conserved hypochet	372	6	2.6	374	2	T10165	site-specific DNA-
300	6	2.6	312	1	Q0BE31	probable membrane	373	6	2.6	375	2	F75467	probable lipoprote
301	6	2.6	312	1	H91237	hypothetical prote	374	6	2.6	378	2	B99469	glycosyltransferas
302	6	2.6	312	2	D90504	conserved hypochet	375	6	2.6	380	2	T23546	hypothetical prote
303	6	2.6	312	2	H81432	probable membrane	376	6	2.6	381	2	H96731	hypothetical prote
304	6	2.6	312	2	H78664	hypothetical 34.1k	377	6	2.6	381	2	T40341	hypothetical prote
305	6	2.6	313	2	D86085	hypothetical prote	378	6	2.6	382	2	T24963	hypothetical prote
306	6	2.6	313	2	B69588	L-arabinose transp	379	6	2.6	383	1	ALRZOC	alpha-amylase (EC
307	6	2.6	315	1	S63990	thioredoxin reduct	380	6	2.6	388	2	JC6543	P2X4 receptor - hu
308	6	2.6	315	2	JC5201	chemoreceptor T856	381	6	2.6	391	2	C84268	aspartate aminotra
309	6	2.6	316	2	A11935	hypothetical prote	382	6	2.6	391	2	A42973	serum protein MSE5
310	6	2.6	317	2	T20302	phosphoglycerate d	383	6	2.6	392	2	E75042	transporter (major
311	6	2.6	318	2	AG1084	phosphoglycerate d	384	6	2.6	392	2	F96707	hypothetical prote
312	6	2.6	318	2	AG1441	phosphoglycerate d	385	6	2.6	395	2	S73531	CDP-diacylglyceri
313	6	2.6	318	2	AB0476	probable periplasm	386	6	2.6	396	2	T26967	hypothetical prote
314	6	2.6	318	2	B95844	probable sugar ABC	387	6	2.6	399	1	D64327	H+-transporting tw
315	6	2.6	319	2	EH98330	hypothetical prote	388	6	2.6	400	2	AD3293	opgc protein [limp
316	6	2.6	319	2	AH2952	hypothetical prote	389	6	2.6	401	2	H69833	conserved hypochet
317	6	2.6	319	2	H98216	hypothetical prote	390	6	2.6	405	2	S23260	hypothetical prote
318	6	2.6	320	2	C95970	probable sugar upt	391	6	2.6	408	2	A46712	glycoprotein Iia -
319	6	2.6	324	2	S05396	bifunctional cycla	392	6	2.6	409	2	AD0646	aminotripeptidase
320	6	2.6	325	2	T02117	hypothetical prote	393	6	2.6	411	2	D82524	transcription term
321	6	2.6	326	2	AE0658	psp operon transcr	394	6	2.6	413	2	AB3174	aminotransferase,

355	6	2.6	413	2	AC3614	468	6	2.6	476	2	D87386	sodium-dicarboxyla
356	6	2.6	414	1	C70859	469	6	2.6	476	2	S59339	proline oxidase -
397	6	2.6	417	2	E95327	470	6	2.6	478	2	T33942	hypothetical prote
398	6	2.6	419	2	D49917	471	6	2.6	480	2	C75614	probable xanthine
399	6	2.6	419	2	F82991	472	6	2.6	481	2	F87715	transcription term
400	6	2.6	419	2	F81927	473	6	2.6	484	2	T33504	hypothetical prote
401	6	2.6	419	2	F81667	474	6	2.6	484	2	F71317	probable antigen,
402	6	2.6	419	2	F81177	475	6	2.6	487	2	B96815	hypothetical prote
403	6	2.6	419	2	S74329	476	6	2.6	491	2	S61715	clathrin-associate
404	6	2.6	420	2	JW0076	477	6	2.6	491	2	AH1140	transmembrane prot
405	6	2.6	420	2	B64060	478	6	2.6	491	2	A86824	sensor protein kin
406	6	2.6	420	2	D71833	479	6	2.6	492	2	C82217	conserved hypotnet
407	6	2.6	420	2	D64682	480	6	2.6	493	2	AC1856	diaminobutyrate--p
408	6	2.6	421	2	G97698	481	6	2.6	493	2	JC5621	epidermal growth f
409	6	2.6	421	2	AH2924	482	6	2.6	494	1	A29079	lymphocyte surface
410	6	2.6	421	2	AF3252	483	6	2.6	494	2	E75486	hypothetical prote
411	6	2.6	421	2	T35515	484	6	2.6	495	2	A44489	GT box-binding pro
412	6	2.6	422	2	JC6035	485	6	2.6	497	1	WZBER3	host shutoff vario
413	6	2.6	422	2	T24865	486	6	2.6	497	2	JC2054	complement regulat
414	6	2.6	423	2	T38056	487	6	2.6	497	2	F82747	conserved hypotnet
415	6	2.6	423	2	E84122	488	6	2.6	498	1	VGXPLM	surface glycoprote
416	6	2.6	423	2	AB1769	489	6	2.6	498	1	VGXPLM	surface glycoprote
417	6	2.6	423	2	AG1393	490	6	2.6	498	2	G97062	glycerol kinase, G
418	6	2.6	427	2	A47051	491	6	2.6	500	2	F86845	glycerol kinase, G
419	6	2.6	428	2	S10013	492	6	2.6	501	2	AG0939	H+-transporting AT
420	6	2.6	429	1	A31950	493	6	2.6	502	1	K1EGL	glycerol kinase (I
421	6	2.6	429	1	AG3150	494	6	2.6	502	2	C91235	glycerol kinase (I
422	6	2.6	431	2	C82219	495	6	2.6	502	2	T18562	hypothetical prote
423	6	2.6	433	2	T36609	496	6	2.6	503	2	T64086	glycerol kinase (E
424	6	2.6	434	2	S12775	497	6	2.6	504	2	A83901	hypothetical prote
425	6	2.6	434	2	B72328	498	6	2.6	505	2	C82422	hypothetical prote
426	6	2.6	435	2	T39719	499	6	2.6	505	2	H83196	glycerol kinase VC
427	6	2.6	436	2	T39299	500	6	2.6	507	2	JG0165	glycerol kinase PA
428	6	2.6	439	2	C84981	501	6	2.6	507	2	T33024	Lmt1 protein - hum
429	6	2.6	440	2	H97705	502	6	2.6	508	2	A33378	hypothetical prote
430	6	2.6	442	2	C69785	503	6	2.6	508	2	T29988	fasciclin III prec
431	6	2.6	445	1	S54140	504	6	2.6	509	2	C86082	hypothetical prote
432	6	2.6	445	2	AD0962	505	6	2.6	510	2	S57808	glycerol kinase (I
433	6	2.6	445	2	C69596	506	6	2.6	516	2	A95134	cellulase (EC 3.2.
434	6	2.6	446	2	E85691	507	6	2.6	517	2	A10510	voltage-gated chlo
435	6	2.6	448	2	A69747	508	6	2.6	518	2	T10621	probable crotonobe
436	6	2.6	449	2	T30982	509	6	2.6	519	2	C71346	hypothetical prote
437	6	2.6	449	2	S49904	510	6	2.6	521	2	E98002	probable transcrip
438	6	2.6	450	2	F71351	511	6	2.6	522	2	H90633	conserved hypotnet
439	6	2.6	453	2	D84018	512	6	2.6	522	2	S40558	probable crotonobe
440	6	2.6	453	2	S73800	513	6	2.6	522	2	H85484	probable carnitine
441	6	2.6	455	2	A55972	514	6	2.6	525	2	B48058	RNA-binding protei
442	6	2.6	455	2	S51116	515	6	2.6	526	2	D75391	Algp-related prote
443	6	2.6	457	2	E71656	516	6	2.6	526	2	T39445	probable transcrip
444	6	2.6	457	2	E98213	517	6	2.6	535	2	S78598	probable transcrip
445	6	2.6	457	2	AD3073	518	6	2.6	536	2	A99199	D-ribulokinase (EC
446	6	2.6	458	2	E65068	519	6	2.6	536	2	AH3087	D-ribulokinase (EC
447	6	2.6	458	2	A85938	520	6	2.6	537	2	A46611	ribitol kinase (Im
448	6	2.6	458	2	E91092	521	6	2.6	539	2	F75497	mosin-binding pro
449	6	2.6	458	2	G97794	522	6	2.6	542	2	E90604	probable arginine
450	6	2.6	461	2	B64992	523	6	2.6	543	2	T50905	hypothetical prote
451	6	2.6	461	2	S60253	524	6	2.6	543	2	E93403	protochlorophyllid
452	6	2.6	462	1	DEECXB	525	6	2.6	544	2	AF1900	probable extracell
453	6	2.6	462	1	C71296	526	6	2.6	544	2	C42653	hydrogenase chain
454	6	2.6	462	2	A85766	527	6	2.6	544	2	A71260	dihydroliipoamide S
455	6	2.6	462	2	D90917	528	6	2.6	546	2	D86811	hypothetical prote
456	6	2.6	463	2	S27491	529	6	2.6	547	1	S52489	mannosyl-glycopro
457	6	2.6	464	2	A33523	530	6	2.6	547	2	H83018	choline oxidase (E
458	6	2.6	464	2	A71509	531	6	2.6	547	2	A47178	dihydroliipoamide a
459	6	2.6	466	2	AD3550	532	6	2.6	547	2	A10990	methvl-accepting t
460	6	2.6	466	2	S16333	533	6	2.6	547	2	A32803	glucan 1,4-alpha-m
461	6	2.6	466	2	AB2540	534	6	2.6	549	2	B45154	SMF2 protein - yea
462	6	2.6	468	2	A69468	535	6	2.6	551	2	F83015	hypothetical prote
463	6	2.6	470	2	F85164	536	6	2.6	551	2	S05667	glucan 1,4-alpha-m
464	6	2.6	471	2	S01037	537	6	2.6	551	2	T49900	2-oxoglutarate/mal
465	6	2.6	473	2	T04482	538	6	2.6	561	2	T06075	hypothetical prote
466	6	2.6	473	2	A54691	539	6	2.6	564	2	T23269	hypothetical prote
467	6	2.6	474	2	D75285	540	6	2.6	564	2	A38271	serotonin receptor

541	6	2.6	564	2	A48141	614	6	2.6	725	2	T33498	hypothetical prote
542	6	2.6	567	2	F87594	615	6	2.6	726	2	T47700	delta-1-pyrroline-
543	6	2.6	567	2	A71619	616	6	2.6	726	2	T50684	pyrroline-5-carbox
544	6	2.6	573	2	H82257	617	6	2.6	729	2	UC7501	oligopeptide trans
545	6	2.6	573	2	F86663	618	6	2.6	735	2	SS4147	alpha adducin - ra
546	6	2.6	575	1	WQECPI	619	6	2.6	753	2	F69338	pyruvate,water dik
547	6	2.6	575	1	WQEBPI	620	6	2.6	758	2	A29253	finger protein hun
548	6	2.6	575	1	H91039	621	6	2.6	764	2	A40027	thylotropin recept
549	6	2.6	575	2	C85858	622	6	2.6	764	2	A47456	down-regulated in
550	6	2.6	575	2	AC0364	623	6	2.6	772	2	T13078	KRAA092 protein -
551	6	2.6	578	2	T51230	624	6	2.6	778	2	B86218	protein T2767.20 l
552	6	2.6	585	2	T20979	625	6	2.6	778	2	B70667	hypothetical prote
553	6	2.6	592	2	T21536	626	6	2.6	800	2	A84293	helicase [imported
554	6	2.6	598	2	T48822	627	6	2.6	803	2	T46179	hypothetical prote
555	6	2.6	603	2	G82738	628	6	2.6	809	2	T40574	guanine nucleotide
556	6	2.6	608	2	B87282	629	6	2.6	814	2	T00953	hypothetical prote
557	6	2.6	610	1	S30234	630	6	2.6	827	1	A31642	villin [validated]
558	6	2.6	613	2	B91024	631	6	2.6	829	1	E87305	TonB-dependent rec
559	6	2.6	613	2	D64999	632	6	2.6	835	2	I55603	reduced hepatic gl
560	6	2.6	613	2	C85868	633	6	2.6	836	2	E89453	protein F35H12.3 l
561	6	2.6	616	2	C82641	634	6	2.6	839	2	F75518	hypothetical prote
562	6	2.6	620	2	F90969	635	6	2.6	849	2	C90834	tail length tape m
563	6	2.6	620	2	E85742	636	6	2.6	853	1	TLBPHL	minor tail protein
564	6	2.6	631	2	B98137	637	6	2.6	853	2	S49876	gamma-adaptin - sm
565	6	2.6	635	1	WMBEW6	638	6	2.6	859	1	VCLJST	env polypotein pr
566	6	2.6	638	1	XXAV	639	6	2.6	859	2	B90768	probable tail leng
567	6	2.6	638	2	T36309	640	6	2.6	859	2	B85718	probable tail comp
568	6	2.6	643	2	T30746	641	6	2.6	859	2	S02196	DNA-directed RNA p
569	6	2.6	643	2	B25817	642	6	2.6	865	1	S02196	envelope polypote
570	6	2.6	648	2	A71342	643	6	2.6	869	2	S53098	hypothetical prote
571	6	2.6	648	2	E98216	644	6	2.6	872	2	T30237	regulatory protein
572	6	2.6	648	2	AD3070	645	6	2.6	876	1	A57987	nitrate reductase
573	6	2.6	650	2	AB0585	646	6	2.6	877	2	S72541	hypothetical prote
574	6	2.6	656	2	B70766	647	6	2.6	881	2	T28013	hypothetical prote
575	6	2.6	658	2	T41309	648	6	2.6	883	2	C86729	hypothetical prote
576	6	2.6	660	1	Q0BE3	649	6	2.6	885	1	VGBESA	glycoprotein B pre
577	6	2.6	662	2	S55274	650	6	2.6	885	2	JC4732	beta-N-acetylhexos
578	6	2.6	662	2	T16845	651	6	2.6	887	2	C86453	COS protein F9L11.
579	6	2.6	664	2	H83962	652	6	2.6	889	2	H84506	probable retroelem
580	6	2.6	665	1	VCMVVR	653	6	2.6	892	2	H71558	probable translati
581	6	2.6	665	1	VCMVVR	654	6	2.6	894	2	T13029	beta-adaptin homol
582	6	2.6	669	1	VCWWEK	655	6	2.6	898	2	T42131	probable toxR-regu
583	6	2.6	669	2	A46511	656	6	2.6	900	2	F32827	hypothetical prote
584	6	2.6	671	2	A46295	657	6	2.6	919	2	T83827	hypothetical prote
585	6	2.6	673	2	C82346	658	6	2.6	923	2	C86453	conserved hypotet
586	6	2.6	673	2	G85095	659	6	2.6	923	2	AC2705	hypothetical prote
587	6	2.6	677	2	E95417	660	6	2.6	923	2	C97487	hypothetical prote
588	6	2.6	682	2	T47473	661	6	2.6	925	2	T41350	meiotic recombina
589	6	2.6	682	2	F70421	662	6	2.6	925	2	T22388	hypothetical prote
590	6	2.6	684	2	G69015	663	6	2.6	943	2	B83068	probable oxidoredu
591	6	2.6	685	2	A81246	664	6	2.6	946	2	B87316	TonB-dependent rec
592	6	2.6	685	2	T06334	665	6	2.6	948	2	S52739	H+-transporting AT
593	6	2.6	686	2	T06334	666	6	2.6	965	2	S55658	tegment protein 6
594	6	2.6	687	2	S33475	667	6	2.6	970	2	F64230	spore germination
595	6	2.6	687	2	T02459	668	6	2.6	972	2	T22488	hypothetical prote
596	6	2.6	688	2	A43491	669	6	2.6	980	2	G75523	probable cell divi
597	6	2.6	689	2	B43491	670	6	2.6	981	2	T32707	hypothetical prote
598	6	2.6	693	2	T19598	671	6	2.6	983	2	A87063	conserved large me
599	6	2.6	694	2	T47474	672	6	2.6	986	2	S71750	import intermediat
600	6	2.6	700	2	A42599	673	6	2.6	999	1	IJH0G3	desmoglein 3 precu
601	6	2.6	703	1	ALBSX1	674	6	2.6	1008	2	S72698	transport protein
602	6	2.6	707	2	S43297	675	6	2.6	1024	2	H87599	TonB-dependent rec
603	6	2.6	708	2	A56163	676	6	2.6	1025	2	H86250	hypothetical prote
604	6	2.6	710	2	T22377	677	6	2.6	1027	2	T46481	hypothetical prote
605	6	2.6	710	2	S72497	678	6	2.6	1031	2	C81302	probable type I si
606	6	2.6	712	1	VCLUS4	679	6	2.6	1033	2	T31084	RNA-directed DNA p
607	6	2.6	716	2	C90100	680	6	2.6	1047	2	T114897	probable ATPase (E
608	6	2.6	716	2	T03695	681	6	2.6	1049	2	C95883	probable efflux pr
609	6	2.6	717	2	T50685	682	6	2.6	1057	2	H83273	ribonuclease E PA2
610	6	2.6	717	2	S66637	683	6	2.6	1061	2	H97361	hypothetical prote
611	6	2.6	719	2	T12258	684	6	2.6	1061	2	A12579	conserved hypotet
612	6	2.6	719	2	T05384	685	6	2.6	1067	2	T28663	hypothetical prote
613	6	2.6	723	2	T30094	686	6	2.6	1091	2	S33556	protein-tyrosine k
									1099	2	A56155	tumor suppressor p

667	6	2.6	1111	2	T29070	hypothetical prote
668	6	2.6	1135	1	GNVUH7	M polypeptide - Ha
689	6	2.6	1135	1	GNVUH7	M polypeptide - Ha
690	6	2.6	1135	2	J02163	hypothetical 126.5
691	6	2.6	1135	2	J02163	M polypeptide - Ha
692	6	2.6	1141	2	A44093	cAMP-inhibited cAMP
693	6	2.6	1150	2	S58775	myl protein - smu
694	6	2.6	1166	2	S37692	probable tumor sup
695	6	2.6	1169	2	S38181	flocculation prote
696	6	2.6	1182	2	T29097	pro-pol-durpase po
697	6	2.6	1188	2	F64367	pyruvate, water dik
698	6	2.6	1203	2	T51029	related to pathway
699	6	2.6	1207	2	H87475	urea amidolyase-re
700	6	2.6	1224	2	F96795	hypothetical prote
701	6	2.6	1233	2	T30989	serine/threonine p
702	6	2.6	1244	2	T19068	hypothetical prote
703	6	2.6	1246	2	G89287	protein H39E23.1 l
704	6	2.6	1271	2	A45555	glutamate rich pro
705	6	2.6	1274	2	S35050	cardiac myosin-b1n
706	6	2.6	1280	2	G96796	hypothetical prote
707	6	2.6	1295	2	G96549	hypothetical prote
708	6	2.6	1299	2	T47182	hypothetical prote
709	6	2.6	1307	2	T21283	hypothetical glyci
710	6	2.6	1329	2	E70917	cell division prot
711	6	2.6	1329	2	A64828	cell division prot
712	6	2.6	1342	2	G90750	cell division prot
713	6	2.6	1342	2	E85614	hypothetical prote
714	6	2.6	1386	2	T00257	hypothetical prote
715	6	2.6	1421	2	T02501	hypothetical prote
716	6	2.6	1477	2	S64616	YOR1 protein - yea
717	6	2.6	1501	2	C84512	probable retroelem
718	6	2.6	1579	2	S25329	carboxypeptidase y
719	6	2.6	1750	2	E86151	hypothetical prote
720	6	2.6	1816	2	F83901	hypothetical prote
721	6	2.6	1884	2	JC4975	plexin 2 precursor
722	6	2.6	1902	1	A48585	lactocoeptin (EC 3.4
723	6	2.6	1902	2	B45754	lactocoeptin (EC 3.4
724	6	2.6	1952	2	T48814	hypothetical prote
725	6	2.6	1957	2	T38077	hypothetical colle
726	6	2.6	1962	2	A32634	lactocoeptin (EC 3.4
727	6	2.6	2187	2	T30826	nascent polyepid
728	6	2.6	2499	1	A30788	mannose 6-phosphat
729	6	2.6	2747	2	B49132	fat facets (fat) s
730	6	2.6	2783	2	T34416	hypothetical prote
731	6	2.6	2897	2	B48666	cell proliferation
732	6	2.6	3104	2	S20473	fatty-acid synthas
733	6	2.6	3256	2	A48666	cell proliferation
734	6	2.6	3388	1	GNMWP	genome polypeptin
735	6	2.6	3391	1	GNMVA	genome polypeptin
736	6	2.6	3391	1	GNMVA	genome polypeptin
737	6	2.6	3391	1	GNMVA	genome polypeptin
738	6	2.6	3391	1	GNMVA	genome polypeptin
739	6	2.6	3391	1	GNMVA	genome polypeptin
740	6	2.6	3391	1	GNMVA	genome polypeptin
741	6	2.6	3391	1	GNMVA	genome polypeptin
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745	6	2.6	3391	1	GNMVA	genome polypeptin
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747	6	2.6	3391	1	GNMVA	genome polypeptin
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759	6	2.6	3391	1	GNMVA	genome polypeptin



833	5	2.1	71	2	G83792	hypothetical prote	906	5	2.1	89	2	S03805	hypothetical prote
834	5	2.1	71	2	G83556	hypothetical prote	907	5	2.1	89	2	D97038	probable membrane
835	5	2.1	72	2	S41611	high-potential lro	908	5	2.1	89	2	AC1576	carbon dioxide con
836	5	2.1	72	2	T32629	hypothetical prote	909	5	2.1	89	2	AH1222	carbon dioxide con
837	5	2.1	72	2	T03390	hypothetical prote	910	5	2.1	90	1	WMBPMB	gene m protein - p
838	5	2.1	72	2	T21081	hypothetical prote	911	5	2.1	90	2	D84247	hypothetical prote
839	5	2.1	72	2	A36460	glucocorticoid rec	912	5	2.1	90	2	F69511	hypothetical prote
840	5	2.1	72	2	F95408	hypothetical prote	913	5	2.1	91	1	A46539	monocyte chemotatr
841	5	2.1	73	2	F90556	acyl carrier prote	914	5	2.1	91	1	G71562	ferredoxin [2Fe-2S
842	5	2.1	73	2	T12883	hypothetical prote	915	5	2.1	91	2	G72088	ferredoxin [2Fe-2S
843	5	2.1	74	2	E69028	hypothetical prote	916	5	2.1	91	2	E81715	ferredoxin [2Fe-2S
844	5	2.1	74	2	T48037	hypothetical prote	917	5	2.1	91	2	H86701	hypothetical prote
845	5	2.1	75	2	T26916	hypothetical prote	918	5	2.1	91	2	H86536	ferredoxin IV [imp
846	5	2.1	75	2	G97116	probable nucleic a	919	5	2.1	91	2	S34669	hypothetical prote
847	5	2.1	75	2	AD3131	hypothetical prote	920	5	2.1	91	2	F59093	hypothetical prote
848	5	2.1	76	2	A69391	DNA-directed RNA p	921	5	2.1	91	2	F83654	pro-sigma K proces
849	5	2.1	76	2	S41722	excisionase - Sacc	922	5	2.1	92	2	A84637	hypothetical prote
850	5	2.1	76	2	G84788	hypothetical prote	923	5	2.1	92	2	C75348	hypothetical prote
851	5	2.1	76	2	B75271	hypothetical prote	924	5	2.1	92	2	T45441	hypothetical prote
852	5	2.1	76	2	T45877	hypothetical prote	925	5	2.1	92	2	A40533	cAMP-dependent pro
853	5	2.1	76	2	F83739	hypothetical prote	926	5	2.1	92	2	D71151	hypothetical prote
854	5	2.1	76	2	AG0163	hypothetical prote	927	5	2.1	92	2	B85911	hypothetical prote
855	5	2.1	77	2	S52636	metallothionein -	928	5	2.1	93	2	S78712	probable DNA topoi
856	5	2.1	77	2	S57862	metallothionein 2b	929	5	2.1	93	2	S25466	r-cell receptor al
857	5	2.1	78	2	T12021	acyl carrier prote	930	5	2.1	93	2	S50649	hypothetical prote
858	5	2.1	78	2	PQ0053	hypothetical prote	931	5	2.1	93	2	C86764	hypothetical prote
859	5	2.1	78	2	E61547	p27 protein - huma	932	5	2.1	93	2	F84175	hypothetical prote
860	5	2.1	78	2	AC0694	conserved hypotet	933	5	2.1	93	2	S04157	outer membrane pro
861	5	2.1	78	2	AB1133	hypothetical orf 1	934	5	2.1	93	2	S33842	acyl-CoA thioester
862	5	2.1	79	2	U02128	metallothionein -	935	5	2.1	93	2	AC0592	probable membrane
863	5	2.1	79	2	F90575	hypothetical prote	936	5	2.1	93	2	B86305	FcII.4 protein - A
864	5	2.1	79	2	S08454	hypothetical prote	937	5	2.1	94	2	H70654	hypothetical prote
865	5	2.1	79	2	A97847	ubiquitin-like ty	938	5	2.1	94	2	A69105	hypothetical prote
866	5	2.1	80	2	T10087	metallothionein-1i	939	5	2.1	94	2	C97181	uncharacterized se
867	5	2.1	80	2	A84528	hypothetical prote	940	5	2.1	95	2	T06905	ribosomal protein
868	5	2.1	80	2	I68668	transcription fact	941	5	2.1	95	2	T25253	hypothetical prote
869	5	2.1	80	2	T68256	ORF MSV095 hypot	942	5	2.1	96	1	U00349	11.5K protein - Ch
870	5	2.1	81	2	JN0710	ubiquitin-like ty	943	5	2.1	96	1	ERBP62	gene 6 protein - p
871	5	2.1	82	2	T07076	metallothionein ty	944	5	2.1	96	2	T17865	hypothetical prote
872	5	2.1	82	2	H90491	conserved hypotet	945	5	2.1	96	2	F97645	hypothetical prote
873	5	2.1	82	2	A47482	pillin-like coloniz	946	5	2.1	96	2	AD2869	conserved hypotet
874	5	2.1	82	2	C81840	hypothetical prote	947	5	2.1	97	2	PH1090	Ig lambda chain V
875	5	2.1	83	2	A36505	oxalacetate decar	948	5	2.1	97	2	F65108	hypothetical 10.8
876	5	2.1	83	2	S76476	hypothetical prote	949	5	2.1	97	2	S60889	hypothetical prote
877	5	2.1	83	2	AE0870	endonuclease fragm	950	5	2.1	97	2	G72117	conserved hypotet
878	5	2.1	83	2	S06077	H+-transporting At	951	5	2.1	97	2	B90725	hypothetical prote
879	5	2.1	84	2	A53578	esculentin-1b prec	952	5	2.1	97	2	C91136	hypothetical prote
880	5	2.1	84	2	T23177	hypothetical prote	953	5	2.1	97	2	B86506	hypothetical prote
881	5	2.1	85	1	IMECE3	immunity protein (	954	5	2.1	97	2	F64809	CT031 hypothetical
882	5	2.1	85	2	S68906	alpha-toxin Bot XI	955	5	2.1	97	2	S72866	ylge protein - Esc
883	5	2.1	85	2	S49177	colicin E4 immunit	956	5	2.1	97	2	T25342	hypothetical prote
884	5	2.1	85	2	T30462	hypothetical prote	957	5	2.1	97	2	C85576	hypothetical prote
885	5	2.1	85	2	A10316	sec-independent pr	958	5	2.1	97	2	F85961	hypothetical prote
886	5	2.1	85	2	AD2497	hypothetical prote	959	5	2.1	98	2	S55622	hypothetical prote
887	5	2.1	86	2	S54912	Ig heavy chain V r	960	5	2.1	98	2	H81072	hypothetical prote
888	5	2.1	86	2	T34975	hypothetical prote	961	5	2.1	98	2	S72990	hypothetical prote
889	5	2.1	86	2	C90666	probable DNA bindi	962	5	2.1	98	2	S26981	pvs protein 1 - Ki
890	5	2.1	86	2	H75364	hypothetical prote	963	5	2.1	98	2	T29026	Ig lambda chain V
891	5	2.1	86	2	S37381	chitin-binding ant	964	5	2.1	99	2	PH1089	Ig lambda chain V
892	5	2.1	86	2	G85516	probable RNA bindi	965	5	2.1	99	2	S14582	Ig lambda chain V
893	5	2.1	87	2	T17591	hypothetical prote	966	5	2.1	99	2	S14583	Ig lambda chain V
894	5	2.1	87	2	T27890	hypothetical prote	967	5	2.1	99	2	S14584	Ig lambda chain V
895	5	2.1	88	2	S69489	bombyxin B-8 precu	968	5	2.1	99	2	S14585	Ig lambda chain V
896	5	2.1	88	2	S02720	outer membrane pro	969	5	2.1	99	2	S14586	Ig lambda chain V
897	5	2.1	88	2	S61552	mammary tumor prot	970	5	2.1	99	2	E89267	hypothetical prote
898	5	2.1	88	2	B75116	hypothetical prote	971	5	2.1	99	2	PH1087	Ig lambda chain V
899	5	2.1	88	2	AG0910	conserved hypotet	972	5	2.1	100	2	PH1088	Ig lambda chain V
900	5	2.1	88	2	AC2561	hypothetical prote	973	5	2.1	100	2	AT1298	cobalt transport p
901	5	2.1	88	2	T01863	guanylate kinase-r	974	5	2.1	100	2	T41217	hypothetical prote
902	5	2.1	89	2	I54187	small proline-rich	975	5	2.1	100	2	F86836	transcription regu
903	5	2.1	89	2	A46709	probable transcrip	976	5	2.1	100	2	D22848	hypothetical ORF-1
904	5	2.1	89	2	D90802		977	5	2.1	100	2		
905	5	2.1	89	2			978	5	2.1	101	2	S07706	r-cell receptor al

979 5 2.1 101 2 D43255 hypothetical prote  
980 5 2.1 101 2 AC3467 sarcosine oxidase  
981 5 2.1 101 2 T26641 hypothetical prote  
982 5 2.1 101 2 B97851 hypothetical prote  
983 5 2.1 102 2 B34770 ORF2 protein - sai  
984 5 2.1 102 2 A37887 apolipoprotein A-I  
985 5 2.1 102 2 B23594 apolipoprotein A-I  
986 5 2.1 102 2 A23594 apolipoprotein A-I  
987 5 2.1 102 2 A24846 apolipoprotein A-I  
988 5 2.1 102 2 I48250 apolipoprotein A-I  
989 5 2.1 102 2 S45406 probable membrane  
990 5 2.1 102 2 T45810 hypothetical prote  
991 5 2.1 102 2 C96595 hypothetical prote  
992 5 2.1 102 2 T49565 hypothetical prote  
993 5 2.1 103 2 T03541 probable cobalt tr  
994 5 2.1 103 2 T34790 hypothetical prote  
995 5 2.1 103 2 E72635 hypothetical prote  
996 5 2.1 103 2 AD3217 conserved hypothet  
997 5 2.1 104 2 ERBP69 early protein gp6  
998 5 2.1 104 2 PH1053 Ig light chain V r  
999 5 2.1 104 2 G75090 hypothetical prote  
1000 5 2.1 104 2 A85838 probable outer mem

## ALIGNMENTS

RESULT 1  
D72058  
transcription termination factor Rho CP0137 [imported] - Chlamydia pneumoniae (strain  
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 11-May-2000  
R:Accession: D72058; H81608  
R:Kalmay, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Ollinger, L.; Grimwood, J.;  
Nature Genet. 21, 385-389, 1999  
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.  
A:Reference number: A72000; MUID:99206606  
A:Accession: D72058  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-464 <RNA>  
A:Cross-references: GB:AE001645; GB:AE001363; NID:g4376896; PIDN:AD18749.1; PID:g437690  
A:Experimental source: strain CWL029  
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,  
C.; Dodson, R.; Wain, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
Nucleic Acids Res. 28, 1397-1406, 2000  
A:Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39.  
A:Reference number: A81500; MUID:20150255  
A:Accession: H81608  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-464 <RNA>  
A:Cross-references: GB:AE002175; GB:AE002161; NID:g7189069; PIDN:AF38020.1; PID:g718907  
A:Experimental source: strain AR39, HL cells  
C:Genetics:  
A:Gene: rho; CP0137  
C:Superfamily: transcription termination factor rho  
C:Keywords: transcription termination

Query Match 3.4%; Score 8; DB 2; Length 464;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 223 IVLVLLI 230  
|  
Db 248 IVLVLLI 255

RESULT 2  
G86566  
transcription termination factor [imported] - Chlamydia pneumoniae (strain J138)  
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
A:Accession: G86566  
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.;  
Nucleic Acids Res. 28, 2311-2314, 2000  
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.  
A:Reference number: A86491; MUID:20330349  
A:Accession: G86566  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-464 <SNO>  
A:Cross-references: GB:BA000008; NID:g8978982; PIDN:BA98817.1; GSPDB:GN00142  
A:Experimental source: strain J138  
C:Genetics:  
A:Gene: rho  
C:Superfamily: transcription termination factor rho  
C:Keywords: transcription termination

Query Match 3.4%; Score 8; DB 2; Length 464;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 223 IVLVLLI 230  
|  
Db 248 IVLVLLI 255

RESULT 3  
AC1185  
B. subtilis ydbB protein homolog lmo0883 [imported] - Listeria monocytogenes (strain  
C:Species: Listeria monocytogenes  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001  
R:Accession: AC1185  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec  
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Eshti,  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maitournam, A.;  
Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla  
A:Title: Comparative genomes of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AC1185  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-491 <GTA>  
A:Cross-references: GB:NC\_003210; PIDN:CAC98961.1; PID:g16410286; GSPDB:GN00177  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: lmo0883  
C:Superfamily: Bacillus subtilis hypothetical protein ydbB

Query Match 3.4%; Score 8; DB 2; Length 491;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 221 GIIVIVL 228  
|  
Db 228 GIIVIVL 235

RESULT 4  
AB1543  
B. subtilis ydbB protein homolog lln0882 [imported] - Listeria innocua (strain C1p11  
C:Species: Listeria innocua  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001  
R:Accession: AB1543  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec  
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Eshti,  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maitournam, A.;  
Ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla

A>Title: Comparative genomics of *Listeria* species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AB1543  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-494 <GLA>  
A:Cross-references: GB:AL592022; PIDN:CAC96114.1; PID:g16413332; GSPDB:GN00178  
A:Experimental source: strain C1p11262  
C:Genetics:  
A:Gene: 110882  
C:Superfamily: *Bacillus subtilis* hypothetical protein ydbT

Query Match 3.4%; Score 8; DB 2; Length 494;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 221 GIIVLIVL 228  
DB 231 GIIVLIVL 238

RESULT 5  
G82022  
methionine--tRNA ligase (EC 6.1.1.10) NMA0275 [imported] - *Neisseria meningitidis* (strain  
C:Species: *Neisseria meningitidis*  
C>Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: G82022  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel,  
; Holtzoyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A>Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.  
A:Reference number: AB1775; MUID:2022556  
A:Accession: G82022  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-685 <PAR>  
A:Cross-references: GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83583.1; PID:g737903  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: metG: NMA0275  
C:Superfamily: methionine--tRNA ligase  
C:Keywords: ligase

Query Match 3.4%; Score 8; DB 2; Length 685;  
Best Local Similarity 100.0%; Pred. No. 5.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 TPAPAAEE 155  
DB 561 TPAPAAEE 568

RESULT 6  
T29018  
hypothetical protein ZK84.1 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 17-Mar-2000  
C:Accession: T29018  
R:Kirsten, J.  
submitted to the EMBL Data Library, April 1995  
A:Description: The sequence of *C. elegans* cosmid ZK84.  
A:Reference number: Z20553  
A:Accession: T29018  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-801 <KIR>  
A:Cross-references: EMBL:U23181; PIDN:AAC48204.1; GSPDB:GN00020; CESP:ZK84.1  
A:Experimental source: strain Bristol N2; clone ZK84  
C:Genetics:  
A:Gene: CESP:ZK84.1  
A:Map position: 2

A:introns: 22/2; 45/3; 108/1  
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo

Query Match 3.4%; Score 8; DB 2; Length 801;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAAEET 156  
DB 267 PAPAAEET 274

RESULT 7  
S71258  
major latex protein type 3 - *Arabidopsis thaliana*  
C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
C>Date: 28-Oct-1996 #sequence\_revision 27-Feb-1997 #text\_change 20-Jun-2000  
C:Accession: S71258  
R:Grellet, F.; Cooke, R.; Laudie, M.; Raynal, M.; Delseny, M.  
submitted to the EMBL Data Library, October 1995  
A:Reference number: S71258  
A:Accession: S71258  
A:Molecule type: mRNA  
A:Residues: 1-155 <GRE>  
A:Cross-references: EMBL:X91961; NID:g1107494; PID:g1107495  
C:Superfamily: wound-induced protein Sn-1

Query Match 3.0%; Score 7; DB 2; Length 155;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 91 RENSPE 97  
DB 123 RENSPE 129

RESULT 8  
T21313  
hypothetical protein F23H12.3 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T21313  
R:Kershaw, J.  
submitted to the EMBL Data Library, June 1996  
A:Reference number: Z19405  
A:Accession: T21313  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-165 <NTL>  
A:Cross-references: EMBL:Z74472; PIDN:CAA98941.1; GSPDB:GN00023; CESP:F23H12.3  
A:Experimental source: clone F23H12  
C:Genetics:  
A:Gene: CESP:F23H12.3  
A:Map position: 5  
A:introns: 22/3; 56/3; 95/3  
C:Superfamily: *Caenorhabditis elegans* hypothetical protein F23H12.3

Query Match 3.0%; Score 7; DB 2; Length 165;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 221 GIIVLIV 227  
DB 89 GIIVLIV 95

RESULT 9  
H90386  
hypothetical protein SSO2176 [imported] - *Sulfolobus solfataricus*  
C:Species: *Sulfolobus solfataricus*

C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
 C/Accession: H90386  
 R/She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Anayez, M.J.; Chan-  
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi Ngoc, H.P.; Redder, H.  
 arrett, R.A.; Ragan, M.A.; SENSE, C.W.; Van der Oost, J.  
 submitted to Genbank, April 2001  
 A/Description: *Sulfolobus solfataricus* complete genome.  
 A/Reference number: A99139  
 A/Accession: H90386  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-184 <KUR>  
 A/Cross-references: GB:AE006641; NID:g13815473; PIDN:AAK42351.1; GSPDB:GN00155  
 C/Genetics:  
 A/Gene: SS02176

Query Match 3.0%; Score 7; DB 2; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 20;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 225 LIVLIV 231  
 |||||  
 Db 164 LIVLIV 170

RESULT 10  
 H72242  
 flagellar L-ring protein - Thermotoga maritima (strain MSB8)  
 C/Species: Thermotoga maritima  
 C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
 C/Accession: H72242  
 R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;  
 C.M.  
 Nature 399, 323-329, 1999  
 A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
 A/Reference number: A72200; MUID:99287316  
 A/Accession: H72242  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-199 <ARN>  
 A/Cross-references: GB:AE001800; GB:AE000512; NID:g4982090; PIDN:AAD36607.1; PID:g498210  
 A/Experimental source: strain MSB8  
 C/Genetics:  
 A/Gene: TM1540

Query Match 3.0%; Score 7; DB 2; Length 199;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 226 IIVLIV 232  
 |||||  
 Db 6 IIVLIV 12

RESULT 11  
 D70519  
 Probable lppc protein - Mycobacterium tuberculosis (strain H37Rv)  
 C/Species: Mycobacterium tuberculosis  
 C/Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
 C/Accession: D70519  
 R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
 Rajandream, M.A.; Rogers, J.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
 Nature 393, 537-544, 1998  
 A/Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A/Reference number: A70500; MUID:98295967  
 A/Accession: D70519  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA

A/Residues: 1-201 <COL>  
 A/Cross-references: GB:D97193; GB:AL123456; NID:g3261816; PIDN:CAB10030.1; PID:g32482  
 A/Experimental source: strain H37Rv  
 C/Genetics:  
 A/Gene: lppc

Query Match 3.0%; Score 7; DB 2; Length 201;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 TPAPAE 154  
 |||||  
 Db 48 TPAPAE 54

RESULT 12  
 E75477  
 hypothetical protein - Deinococcus radiodurans (strain R1)  
 C/Species: Deinococcus radiodurans  
 C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
 C/Accession: E75477  
 R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.  
 M.; Shen, M.; Vamathevan, J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.;  
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 Science 286, 1571-1577, 1999  
 A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
 A/Reference number: A75250; MUID:20036896  
 A/Accession: E75477  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-219 <WHI>  
 A/Cross-references: GB:AE001932; GB:AB000513; NID:g6458481; PIDN:AAF10355.1; PID:g645  
 A/Experimental source: strain R1  
 C/Genetics:  
 A/Gene: DR0772  
 A/Map position: 1

Query Match 3.0%; Score 7; DB 2; Length 219;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 147 GTPAPAA 153  
 |||||  
 Db 205 GTPAPAA 211

RESULT 13  
 T05958  
 cold acclimation protein homolog - barley  
 C/Species: Hordeum vulgare (barley)  
 C/Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 08-Oct-1999  
 C/Accession: T05958  
 R/Grossi, M.; Gull, M.; Stanca, A.M.; Cattivelli, L.  
 Plant Sci. 105, 71-80, 1995  
 A/Title: Characterization of two barley genes that respond rapidly to dehydration str  
 A/Reference number: Z15371  
 A/Accession: T05958  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-255 <GRO>  
 A/Cross-references: EMBL:X84056; NID:g642245; PIDN:CAA58875.1; PID:g642246  
 A/Experimental source: cv. Georgie, leaf  
 C/Genetics:  
 A/Gene: paf93

Query Match 3.0%; Score 7; DB 2; Length 255;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAAEE 155

Db 206 PAPAEE 212

## RESULT 14

H82517 hypothetical protein Xf2765 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C/Accession: H82517

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20355717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: H82517

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-256 <SIM>

A:Cross-references: GB:AE004082; GB:AE003849; NID:g9108003; PIDN:AAF85550.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Relnach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H.

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F.

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv

M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: Xf2765

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 256;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAEE 155

Db 65 PAPAEE 71

## RESULT 15

H82661 hypothetical protein Xf1591 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C/Accession: H82661

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20355717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: H82661

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-256 <SIM>

A:Cross-references: GB:AE003987; GB:AE003849; NID:g9106634; PIDN:AAF84400.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Relnach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H.

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F.

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv

M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: Xf1591

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 256;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAEE 155

Db 65 PAPAEE 71

## RESULT 16

H82648 hypothetical protein Xf1697 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000

C/Accession: H82648

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20355717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: H82648

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-256 <SIM>

A:Cross-references: GB:AE003994; GB:AE003849; NID:g9106756; PIDN:AAF84506.1; GSPDB:GN

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Relnach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv

M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: Xf1697

Query Match

Best Local Similarity 100.0%; Score 7; DB 2; Length 256;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAEE 155

Db 65 PAPAEE 71

## RESULT 17

T01305 hypothetical protein T14P8.5 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 14-May-1999

C/Accession: T01305

R:Kitajima, J.; Elliott, G.; Cloud, J.

submitted to the EMBL Data Library, May 1998

A:Description: The sequence of A. thaliana T14P8.

A:Reference number: Z14290

A:Accession: T01305  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-262 <KAL>  
A:Cross-references: EMBL:AF069298; NID:g3193282; PID:g3193303  
A:Experimental source: cultivar Columbia  
C:Genetics:  
A:Map position: 4  
A:Introns: 6/2; 68/3; 121/1; 163/3; 226/1  
A:Note: T14P8.5

Query Match 3.0%; Score 7; DB 2; Length 262;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 APAAEET 156  
|||  
Db 249 APAAEET 255

RESULT 18  
T13453  
hypothetical protein C08A9.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 18-Feb-2000  
C:Accession: T13453  
R:Latrelle, P.  
submitted to the EMBL Data Library, December 1995  
A:Description: The sequence of C. elegans cosmid C08A9.  
A:Reference number: Z18353  
A:Accession: T13453  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-263 <LAT>  
A:Cross-references: EMBL:U02844; NID:g1125797; PID:g1125799; PIDN:AAB53817.1; GSPDB:GN04  
A:Experimental source: strain Bristol N2; clone C08A9  
C:Genetics:  
A:Gene: CESP:C08A9.3  
A:Map position: X  
A:Introns: 45/3; 79/3; 128/2

Query Match 3.0%; Score 7; DB 2; Length 263;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 VLIVLLI 230  
|||  
Db 116 VLIVLLI 122

RESULT 19  
T46853  
Y1bD protein [imported] - Rhodobacter sphaeroides  
C:Species: Rhodobacter sphaeroides  
C:Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 21-Jul-2000  
C:Accession: T46853  
R:MacKenzie, C.; Simons, A.E.; Kaplan, S.  
Genetics 153, 525-538, 1999  
A:Title: Multiple chromosomes in bacteria. The Yin and Yang of trp gene localization in  
A:Reference number: Z24108; MUID:99442363  
A:Accession: T46853  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-266 <MAC>  
A:Cross-references: EMBL:AF108766; NID:g4185542; PIDN:AAD09126.1; PID:g4185554  
A:Experimental source: strain 2.4.1  
C:Genetics:  
A:Gene: y1bQ  
A:Map position: I

Query Match 3.0%; Score 7; DB 2; Length 266;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAAEE 155  
|||  
Db 37 PAPAAEE 43

RESULT 20  
T06802  
cold acclimation protein WCOR410b - wheat  
C:Species: Triticum aestivum (common wheat)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 08-Oct-1999  
C:Accession: T06802  
R:Danyluk, J.; Sarhan, F.  
submitted to the EMBL Data Library, October 1996  
A:Reference number: Z15826  
A:Accession: T06802  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-268 <DAN>  
A:Cross-references: EMBL:U73210; NID:g1657842; PIDN:AAB18201.1; PID:g1657843  
A:Experimental source: cv. Norstar; seedling; shoot  
C:Genetics:  
A:Gene: WCOR410b

Query Match 3.0%; Score 7; DB 2; Length 268;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAAEE 155  
|||  
Db 219 PAPAAEE 225

RESULT 21  
S27708  
daunorubicin resistance protein - Streptomyces peucetius  
C:Species: Streptomyces peucetius  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Oct-1999  
C:Accession: S27708  
R:Guilfoile, P.G.; Hutchinson, C.R.  
submitted to the EMBL Data Library, August 1991  
A:Description: A bacterial analog of the mdr gene of mammalian tumor cells is present  
A:Reference number: S27706  
A:Accession: S27708  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-283 <GUL>  
A:Cross-references: EMBL:M73758; NID:g153228; PIDN:AA74718.1; PID:g153231  
C:Superfamily: Streptomyces peucetius daunorubicin resistance protein  
C:Keywords: transmembrane protein

Query Match 3.0%; Score 7; DB 2; Length 283;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 172 MTTSPTG 178  
|||  
Db 1 MTTSPTG 7

RESULT 22  
T45537  
mobB protein [imported] - Agrobacterium tumefaciens plasmid pTi15955  
C:Species: Agrobacterium tumefaciens  
C:Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 21-Jul-2000  
C:Accession: T45537  
R:Lyti, S.M.; Jafri, S.; Wians, S.C.  
Mol. Microbiol. 31, 339-347, 1999

A>Title: Mannophilic acid and agropinic acid catabolism region of the octopine-type T1 p  
A:Reference number: Z23002; MUID:99141607  
A:Accession: T45537  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-313 <LTY>  
A:Cross-references: EMBL:AF03413; NID:g2665704; PIDN:AB88473.1; PID:g2665713  
A:Experimental source: strain 15955  
C:Genetics:  
A:Gene: moab  
A:Genome: plasmid pT15955  
C:Superfamily: oligopeptide permease protein oppb

Query Match 3.0%; Score 7; DB 2; Length 313;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 226 TVLLIVF 232  
| | | | |  
Db 149 TVLLIVF 155

RESULT 23  
C81050  
cytochrome c oxidase, chain III NMB1723 [imported] - Neisseria meningitidis (strain MC58  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: C81050  
R:Nettelin, H.; Saunders, N.J.; Heideberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Mastignani, V.; Pizzi, M.  
Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
A>Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: AB1000; MUID:20157555  
A:Accession: C81050  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-365 <TET>  
A:Cross-references: GB:AE002522; GB:AE002098; NID:g7226972; PIDN:AAF42068.1; PID:g722697  
C:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB1723

Query Match 3.0%; Score 7; DB 2; Length 365;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 TPAPAAE 154  
| | | | |  
Db 321 TPAPAAE 327

RESULT 24  
F81826  
probable cytochrome c NMA1977 [imported] - Neisseria meningitidis (strain Z2491 serogrou  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: F81826  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
R.; Holtz, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A>Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: AB1775; MUID:20222556  
A:Accession: F81826  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-365 <PAR>  
A:Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85197.1; PID:g738066  
C:Experimental source: serogroup A, strain Z2491  
C:Genetics:

A:Gene: NMA1976; NMA1977

Query Match 3.0%; Score 7; DB 2; Length 365;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 TPAPAAE 154  
| | | | |  
Db 321 TPAPAAE 327

RESULT 25  
T01169  
phosphate transport protein, mitochondrial - maize  
C:Species: Zea mays (maize)  
C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 20-Jun-2000  
C:Accession: T01169  
R:Takabatake, R.; Hata, S.; Taniguchi, M.; Kouchi, H.; Sugiyama, T.; Izui, K.  
submitted to the EMBL Data Library, July 1998  
A:Description: Isolation and Characterization of cDNAs Encoding Mitochondrial Phospha  
A:Reference number: Z14251  
A:Accession: T01169  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-366 <TAK>  
A:Cross-references: EMBL:AB016064; PIDN:BAA31583.1  
C:Experimental source: strain H84; root  
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology  
C:Keywords: mitochondrion

Query Match 3.0%; Score 7; DB 2; Length 366;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 TPAPAAE 154  
| | | | |  
Db 353 TPAPAAE 359

RESULT 26  
T50265  
probable phosphate/phosphoenolpyruvate translocator protein - fission yeast (Schizosa  
C:Species: Schizosaccharomyces pombe  
C:Date: 09-Jun-2000 #sequence\_revision 20-Oct-2000 #text\_change 20-Oct-2000  
C:Accession: T50265; T38158  
R:Saunders, D.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, December 1999  
A:Reference number: Z25052  
A:Accession: T50265  
A:Molecule type: DNA  
A:Residues: 1-258 <SNU>  
A:Cross-references: EMBL:AL13498; PIDN:CAB63500.1; GSPDB:GN00066; SPDB:SPAC890.09  
A:Experimental source: strain 972h-7; cosmid c890  
R:Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.  
submitted to the EMBL Data Library, March 1996  
A:Reference number: Z21775  
A:Accession: T38158  
A:Molecule type: DNA  
A:Residues: 229-374 <DEV>  
A:Cross-references: EMBL:Z70043; NID:g1220275; PIDN:CAA93888.1; GSPDB:GN00066; SPDB:S  
A:Experimental source: strain 972h-7; cosmid c22E12  
C:Genetics:  
A:Gene: SPAC22E12.01; SPDB:SPAC890.09  
A:Map position: 1

Query Match 3.0%; Score 7; DB 2; Length 374;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 TVLLIVL 228

Db 52 IIVLVL 58

# RESULT 27

A53773  
la/SS-B homolog D-la - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 21-Jul-2000  
C:Accession: A53773  
R:Baiz, C.; Li, Z.; Tolias, P.P.  
Mol. Cell. Biol. 14, 5123-5129, 1994  
A:Title: Developmental characterization of a Drosophila RNA-binding protein homologous to  
A:Reference number: A53773; MUID:94309632  
A:Accession: A53773  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-390 <BAI>  
A:Cross-references: GB:U07652; NID:g464019; PIDN:AAA20518.1; PID:g464020  
C:Genetics:  
A:Gene: FlyBase:La  
A:Cross-references: FlyBase:FBgn0011638  
C:Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology  
C:Keywords: leucine zipper; RNA binding

Query Match 3.0%; Score 7; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAEE 155  
Db 36 PAPAEE 42

# RESULT 28

A53781  
ribonucleoprotein la - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C>Date: 19-Jan-1996 #sequence\_revision 19-Jan-1996 #text\_change 20-Sep-1999  
C:Accession: A53781  
R:Yoo, C.J.; Molin, S.L.  
Mol. Cell. Biol. 14, 5412-5424, 1994  
A:Title: la proteins from Drosophila melanogaster and Saccharomyces cerevisiae: a yeast  
A:Reference number: A53781; MUID:94309661  
A:Accession: A53781  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-390 <YOO>  
A:Cross-references: GB:U32988; NID:g488469; PID:g488470  
C:Genetics:  
A:Gene: FlyBase:La  
A:Cross-references: FlyBase:FBgn0011638  
C:Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology  
C:Keywords: RNA binding

Query Match 3.0%; Score 7; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAEE 155  
Db 36 PAPAEE 42

# RESULT 29

H7116  
hypothetical protein PH0703 - Pyrococcus horikoshii  
C:Species: Pyrococcus horikoshii  
C>Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 20-Jun-2000  
C:Accession: H7116  
R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Hainawa, Y.; Hino, Y.; Yamamoto, S.; Sekin

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu  
DNA Res. 5, 55-76, 1998  
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
A:Reference number: A71000; MUID:98344137  
A:Accession: H7116  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-397 <KAW>  
A:Cross-references: GB:AP000003; NID:g3236130; PIDN:BAA29794.1; PID:g3257111  
A:Experimental source: strain OT3  
A:Note: this accession replaces an interim accession for a sequence replaced by GenBa  
C:Genetics:  
A:Gene: PH0703

Query Match 3.0%; Score 7; DB 2; Length 397;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 227 VLLIVFV 233  
Db 133 VLLIVFV 139

# RESULT 30

S64704  
ornithine decarboxylase (EC 4.1.1.17) - Jimsonweed  
C:Species: Datura stramonium (Jimsonweed; common thornapple)  
C>Date: 06-Dec-1996 #sequence\_revision 06-Dec-1996 #text\_change 08-Sep-2000  
C:Accession: S64704; MUID:957484  
R:Michael, A.J.; Furze, J.M.; Rhodes, M.J.C.; Burtin, D.  
Biochem. J. 314, 241-248, 1996  
A:Title: Molecular cloning and functional identification of a plant ornithine decarbo  
A:Reference number: S64704; MUID:96195135  
A:Accession: S64704  
A:Molecule type: mRNA  
A:Residues: 1-431 <MIC>  
A:Cross-references: EMBL:X87847; NID:g871007; PIDN:CAA61121.1; PID:g871008  
C:Superfamily: ornithine decarboxylase  
C:Keywords: carbon-carbon lyase; carboxy-lyase; phosphoprotein; polyamine biosynthesi  
F;94/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match 3.0%; Score 7; DB 2; Length 431;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 TPAPAE 154  
Db 25 TPAPAE 31

# RESULT 31

T21515  
hypothetical protein F28G4.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T21515  
R:Wall, M.  
submitted to the EMBL Data Library, March 1997  
A:Reference number: Z19433  
A:Accession: T21515  
A:Molecule type: DNA  
A:Residues: 1-450 <WTL>  
A:Cross-references: EMBL:Z93381; PIDN:CAB07607.1; GSPDB:GN00023; CESP:F28G4.4  
A:Experimental source: clone F28G4  
C:Genetics:  
A:Gene: CESP:F28G4.4  
A:Map position: 5  
A:introns: 28/3; 52/3; 74/3; 104/3; 233/3; 293/3



Query Match 3.0%; Score 7; DB 2; Length 450;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 LIVLIV 230  
|||  
Db 11 LIVLIV 17

## RESULT 32

S12591  
beta-1-adrenergic receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 20-Jun-2000  
C:Accession: S12591; S40185; A36618  
R:Shimomura, H.; Terada, A.  
Nucleic Acids Res. 18, 4591, 1990  
A:Title: Primary structure of the rat beta-1 adrenergic receptor gene.  
A:Reference number: S12591; MUID:90356399  
A:Accession: S12591  
A:Molecule type: DNA  
A:Residues: 1-464 <SH1>  
A:Cross-references: EMBL:D00634  
R:Shimomura, H.; Terada, A.  
Submitted to the EMBL Data Library, July 1991  
A:Reference number: S40185  
A:Accession: S40185  
A:Molecule type: DNA  
A:Residues: 1-25, 'A', 26-174, 'R', 175-464 <SH2>  
A:Cross-references: EMBL:D00634; NID:g220670; PIDN:BAA0057.1; PID:g220671  
R:Michida, C.A.; Bunzow, J.R.; Searles, R.P.; Van Tol, H.; Testier, B.; Neve, K.A.; Teal, J. Biol. Chem. 265, 12960-12965, 1990  
A:Title: Molecular cloning and expression of the rat beta-1-adrenergic receptor gene.  
A:Reference number: A36618; MUID:90330633  
A:Accession: A36618  
A:Molecule type: DNA  
A:Residues: 1-26, 'A', 27-160, 'L', 162-174, 'R', 175-264, 'T', 266-464 <MAC>  
A:Cross-references: GB:J05561; NID:g203073; PIDN:AAA40792.1; PID:g203074  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

Query Match 3.0%; Score 7; DB 2; Length 464;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 225 LIVLIV 231  
|||  
Db 66 LIVLIV 72

## RESULT 33

S36794  
beta-1-adrenergic receptor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 09-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 13-Aug-1999  
C:Accession: S36794  
R:Jasper, J.R.; Link, R.E.; Chruschinski, A.J.; Kobilka, B.K.; Bernstein, D.  
Biochim. Biophys. Acta 1178, 307-309, 1993  
A:Title: Primary structure of the mouse beta(1)-adrenergic receptor gene.  
A:Reference number: S36794; MUID:93372116  
A:Accession: S36794  
A:Molecule type: DNA  
A:Status: preliminary  
A:Residues: 1-466 <JAS>  
A:Cross-references: EMBL:L10084; NID:g293278; PIDN:AAA02929.1; PID:g293279  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; phosphoprotein; transmembrane protein

Query Match 3.0%; Score 7; DB 2; Length 466;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 225 LIVLIV 231  
|||  
Db 67 LIVLIV 73

## RESULT 34

S08325  
flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (allele BzMcC2) - maize  
N:Alternate names: UDPglucose flavonoid glucosyl-transferase  
C:Species: Zea mays (maize)  
C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S08325  
R:Futtek, D.; Schiefelbein, J.W.; Johnston, F.; Nelson Jr., O.E.  
Plant Mol. Biol. 11, 473-481, 1988  
A:Title: Sequence comparisons of three wild-type Bronze-1 alleles from Zea mays.  
A:Reference number: S08324  
A:Accession: S08325  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-471 <FUR>  
A:Cross-references: EMBL:X13501; NID:g22361; PIDN:CAA31856.1; PID:g295854  
C:Genetics:  
A:Gene: Bz1  
A:Introns: 175/1  
C:Superfamily: flavonol O3-glucosyltransferase  
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 3.0%; Score 7; DB 1; Length 471;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 APAEET 156  
|||  
Db 83 APAEET 89

## RESULT 35

S01052  
flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (allele Bz-Mcc) - maize  
N:Alternate names: UDPglucose flavonoid glucosyltransferase  
C:Species: Zea mays (maize)  
C>Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 18-Jun-1999  
C:Accession: S01052; S08324  
R:Raiston, E.J.; English, J.J.; Dooner, H.K.  
Genetics 119, 185-197, 1988  
A:Title: Sequence of three bronze alleles of maize and correlation with the genetic f  
A:Reference number: S01037; MUID:88284304  
A:Accession: S01052  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-471 <RAL>  
A:Cross-references: EMBL:X07940; NID:g22204; PIDN:CAA30761.1; PID:g22205  
R:Futtek, D.; Schiefelbein, J.W.; Johnston, F.; Nelson Jr., O.E.  
Plant Mol. Biol. 11, 473-481, 1988  
A:Title: Sequence comparisons of three wild-type Bronze-1 alleles from Zea mays.  
A:Reference number: S08324  
A:Accession: S08324  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-471 <FUR>  
A:Cross-references: EMBL:X13500; NID:g22364; PIDN:CAA31855.1; PID:g1030071  
C:Genetics:  
A:Gene: Bz1  
A:Map position: 9  
A:Introns: 175/1  
C:Superfamily: flavonol O3-glucosyltransferase  
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 3.0%; Score 7; DB 2; Length 471;  
Best Local Similarity 100.0%; Pred. No. 43;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 APAEET 156  
|||||||  
Db 83 APAEET 89

RESULT 36  
ORNUB1  
beta-1-adrenergic receptor - human  
C:Species: Homo sapiens (man)  
C>Date: 22-Jan-1993 #sequence\_revision 18-Aug-1995 #text\_change 22-Jun-1999  
C:Accession: A39911  
R:Fielle, T.; Collins, S.; Daniel, K.W.; Caron, M.G.; Lefkowitz, R.J.; Kobilka, B.K.  
Proc. Natl. Acad. Sci. U.S.A. 84, 7920-7924, 1987  
A:Title: Cloning of the cDNA for the human beta-1-adrenergic receptor.  
A:Reference number: A39911; MUID:88068509

A:Accession: A39911  
A:Molecule type: mRNA  
A:Residues: 1-477 <FRI>  
A:Cross-references: GB:J03019; NID:g178199; PIDN:AAA51667.1; PID:g178200  
C:Genetics:

A:Gene: GDB:ADRB1; ADRB1R  
A:Cross-references: GDB:119654; OMIM:109630  
A:Map position: 10q25-10q25

C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein  
F:58-84/Domain: transmembrane #status predicted <TM1>  
F:94-121/Domain: transmembrane #status predicted <TM2>  
F:133-154/Domain: transmembrane #status predicted <TM3>  
F:177-199/Domain: transmembrane #status predicted <TM4>  
F:224-245/Domain: transmembrane #status predicted <TM5>  
F:325-346/Domain: transmembrane #status predicted <TM6>  
F:358-377/Domain: transmembrane #status predicted <TM7>  
F:15/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 3.0%; Score 7; DB 1; Length 477;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVLIV 231  
|||||||  
Db 67 LIVLIV 73

RESULT 37  
I53053  
beta 1 adrenergic receptor - rhesus macaque  
C:Species: Macaca mulatta (rhesus macaque)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999  
C:Accession: I53053  
R:Searles, R.P.; Nipper, V.J.; Machida, C.A.  
DNA Seq. 4, 231-241, 1994  
A:Title: The rhesus macaque beta 1-adrenergic receptor gene: structure of the gene and  
A:Reference number: I53053; MUID:95078456  
A:Accession: I53053  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-480 <RES>  
A:Cross-references: EMBL:X75540; NID:g510532; PIDN:CAA53228.1; PID:g510533  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: neurotransmitter receptor

Query Match 3.0%; Score 7; DB 2; Length 480;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVLIV 231  
|||||||  
Db 67 LIVLIV 73

RESULT 38  
F95238  
PTS system, membrane component, probable [imported] - Streptococcus pneumoniae (strain

C:Species: Streptococcus pneumoniae  
C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001  
C:Accession: F95238  
R:Rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapf  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venster, J.C.; Dougherty, B.A.; Morris  
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: F95238  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-485 <KUR>  
A:Cross-references: GB:AE005672; PIDN:AAK76103.1; PID:g14973548; GSPDB:GN00164; TIGR:  
A:Experimental source: strain TIGR4  
C:Genetics:  
A:Gene: SP2038

Query Match 3.0%; Score 7; DB 2; Length 485;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 IVLIVF 232  
|||||||  
Db 358 IVLIVF 364

RESULT 39  
G98102  
hypothetical protein PTS-EII [imported] - Streptococcus pneumoniae (strain R6)  
C:Species: Streptococcus pneumoniae  
C>Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 22-Oct-2001  
C:Accession: G98102  
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.  
e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.  
y, P.; Sun, P.M.; Winkler, M.E.  
J. Bacteriol. 183, 5709-5717, 2001  
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.  
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.  
A:Reference number: A97872; MUID:21429245; PMID:11544234  
A:Accession: G98102  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-508 <KUR>  
A:Cross-references: GB:AE007317; PIDN:AAU00652.1; PID:g15459539; GSPDB:GN00174  
C:Genetics:  
A:Gene: PTS-EII

Query Match 3.0%; Score 7; DB 2; Length 508;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 IVLIVF 232  
|||||||  
Db 381 IVLIVF 387

RESULT 40  
JC7391  
Ca2+-binding protein, DD4 - prawn  
N:Alternate names: DD4 protein  
C:Species: Marsupenaeus japonicus  
C>Date: 17-Nov-2000 #sequence\_revision 17-Nov-2000 #text\_change 18-Jul-2001  
C:Accession: JC7391  
R:Endo, H.; Persson, P.; Watanabe, T.  
Biochem. Biophys. Res. Commun. 276, 286-291, 2000

A:Title: Molecular cloning of the crustacean Dd4 cDNA encoding a Ca<sup>2+</sup>-binding protein.  
A:Reference number: JC7391; MUID:20462952; PMID:11006119  
A:Accession: JC7391  
A:Molecule type: mRNA  
A:Residues: 1-542 <END>  
C:Comment: This protein, acidic and proline-rich, is involved in the calcification process.  
C:Genetics:  
A:Gene: dd4  
C:Keywords: calcium binding

Query Match 3.0%; Score 7; DB 2; Length 542;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 132 TVERPAA 138  
|||||||  
Db 13 TVERPAA 19

## RESULT 41

hypothetical protein SSO3099 [imported] - Sulfolobus solfataricus  
C:Species: Sulfolobus solfataricus  
C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
C:Accession: D90493  
R:She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Anayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.  
arrest, R.A.; Ragan, M.A.; Sengen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A:Description: Sulfolobus solfataricus complete genome.  
A:Reference number: A99139  
A:Accession: D90493  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-548 <KUR>  
A:Cross-references: GB:AE006641; NID:913816517; PIDN:AAK43203.1; GSPDB:GN00155  
C:Genetics:  
A:Gene: SSO3099

Query Match 3.0%; Score 7; DB 2; Length 548;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 221 GIIVLIIV 227  
|||||||  
Db 530 GIIVLIIV 536

## RESULT 42

hypothetical protein RV0538 - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
C:Accession: E70546  
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garrier, T.; Churcher, C.; Harris, D.; Gordon, S.  
Rajandream, M.A.; Rogers, J.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
Nature 393, 537-544, 1998  
A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987  
A:Accession: E70546  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-548 <COL>  
A:Cross-references: GB:Z95558; GB:AL123456; NID:93261781; PIDN:CAB08989.1; PID: e316975;  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: RV0538

Query Match 3.0%; Score 7; DB 2; Length 548;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 QOTVAPQ 16  
|||||||  
Db 517 QOTVAPQ 523

## RESULT 43

T42100  
serine/threonine protein kinase (Ec 2.7.1.-) - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000  
C:Accession: T42100  
R:Bakal, C.J.; Davies, J.E.  
submitted to the EMBL Data Library, September 1998  
A:Description: Cloning, nucleotide sequence and expression of a serine/threonine prot  
A:Reference number: 222067  
A:Accession: T42100  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-556 <BAK>  
A:Cross-references: EMBL:AF094711; PIDN:AAC64406.1  
C:Genetics:  
A:Note: pksc  
C:Superfamily: Synechocystis sp. protein kinase, 58K; protein kinase homology  
C:Keywords: phosphotransferase; serine/threonine-specific protein kinase

Query Match 3.0%; Score 7; DB 2; Length 556;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 147 GTPAPAA 153  
|||||||  
Db 347 GTPAPAA 353

## RESULT 44

T36502  
serine/threonine protein kinase - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000  
C:Accession: T36502  
R:Saunders, D.C.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.  
submitted to the EMBL Data Library, July 1999  
A:Reference number: 221608  
A:Accession: T36502  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-556 <SAU>  
A:Cross-references: EMBL:AL096822; PIDN:CAB46944.1; GSPDB:GN00070; SCQDB:SCGD3.22  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: pksc; SCQDB:SCGD3.22  
C:Superfamily: Synechocystis sp. protein kinase, 58K; protein kinase homology

Query Match 3.0%; Score 7; DB 2; Length 556;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 147 GTPAPAA 153  
|||||||  
Db 347 GTPAPAA 353

## RESULT 45

H83085  
conserved hypothetical protein PA4491 [imported] - Pseudomonas aeruginosa (strain PAO  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C;Accession: H83085  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lartig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen  
A;Reference number: A82950; MUID:20437337  
A;Accession: H83085  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-589 <SNO>  
A;Cross-references: GB:AE004862; GB:AE004091; NID:q9950716; PIDN:AA07879.1; GSPDB:GN001  
A;Experimental source: strain PA01  
C;Genetics:  
A;Gene: PA4491  
C;Superfamily: *Escherichia coli* yfaA protein

Query Match 3.0%; Score 7; DB 2; Length 589;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 147 TPAPAA 153  
|||||  
Db 12 TPAPAA 18

RESULT 46  
H65057  
sulfite reductase (NADPH) (EC 1.8.1.2) flavoprotein beta chain - *Escherichia coli*  
C;Species: *Escherichia coli*  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 15-Oct-1999  
C;Accession: H65057; B34231; I41185  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of *Escherichia coli* K-12.  
A;Reference number: A64720; MUID:9742617  
A;Accession: H65057  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-599 <BIAT>  
A;Cross-references: GB:AE000360; GB:U00096; NID:q2367157; PIDN:AA075806.1; PID:q1789123;  
A;Experimental source: strain K-12, substrain MG1655  
R;Ostrowski, J.; Barber, M.J.; Rueger, D.C.; Miller, B.E.; Siegel, L.M.; Kredich, N.M.  
J. Biol. Chem. 264, 15796-15808, 1989  
A;Title: Characterization of the flavoprotein moieties of NADPH-sulfite reductase from *S. typhimurium* and comparison with NADPH-cytochrome P-450 reductase.  
A;Reference number: A92735; MUID:89380164  
A;Accession: B34231  
A;Molecule type: DNA  
A;Residues: 1-155; 'T', 157-267, 'L', 269-507, 'E', 509-599 <OST>  
A;Cross-references: GB:M23008; NID:q145679; PIDN:AAA23650.1; PID:q145680; GB:J05025; GB:R;London, J.A.; Loughlin, R.E.  
Gene 122, 17-25, 1992  
A;Title: Mutagenesis and regulation of the *cysJ* promoter of *Escherichia coli* K-12.  
A;Reference number: I41185; MUID:93083978  
A;Accession: I41185  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-29 <RES>  
A;Cross-references: GB:M65058; NID:q145677; PIDN:AAA23649.1; PID:q145678  
C;Genetics:  
A;Gene: *cysJ*  
C;Superfamily: sulfite reductase (NADPH); flavodoxin homology; NADPH--ferrithemoprotein F;64-598/Domain: NADPH--ferrithemoprotein reductase homology <FEH>  
F;66-205/Domain: flavodoxin homology <FLX>

Query Match 3.0%; Score 7; DB 1; Length 599;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 148 TPAPAAE 154  
|||||  
Db 54 TPAPAAE 60

RESULT 47  
C91081  
sulfite reductase (NADPH) beta subunit [imported] - *Escherichia coli* (strain O157:H7,  
C;Species: *Escherichia coli*  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 24-Aug-2001  
C;Accession: C91081  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.  
gasawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: C91081  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-599 <HAY>  
A;Cross-references: GB:BA000007; PIDN:BA837042.1; PID:q13363090; GSPDB:GN00154  
A;Experimental source: strain O157:H7, substrain RIMD 0509952  
C;Genetics:  
A;Gene: ECs3619  
C;Superfamily: sulfite reductase (NADPH); flavodoxin homology; NADPH--ferrithemoprotein  
C;Keywords: flavoprotein

Query Match 3.0%; Score 7; DB 2; Length 599;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 148 TPAPAAE 154  
|||||  
Db 54 TPAPAAE 60

RESULT 48  
D85926  
sulfite reductase (NADPH) beta subunit [imported] - *Escherichia coli* (strain O157:H7,  
C;Species: *Escherichia coli*  
C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 27-Nov-2001  
C;Accession: D85926  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206531  
A;Accession: D85926  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-599 <SNO>  
A;Cross-references: GB:AE005174; NID:q12517225; PIDN:AA057872.1; GSPDB:GN00145; UMG:  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: *cysJ*  
C;Superfamily: sulfite reductase (NADPH); flavodoxin homology; NADPH--ferrithemoprotein  
C;Keywords: flavoprotein

Query Match 3.0%; Score 7; DB 2; Length 599;  
Best Local Similarity 100.0%; Pred. No. 52;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 148 TPAPAAE 154  
|||||  
Db 54 TPAPAAE 60

RESULT 49  
T47484  
receptor like protein kinase - *Arabidopsis thaliana*

N;Alternate names: protein F9K21.20  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 02-Sep-2000  
 C;Accession: T47484  
 R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K.  
 submitted to the Protein Sequence Database, February 2000  
 A;Reference number: Z24467  
 A;Accession: T47484  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-669 <J0R>  
 A;Cross-references: EMBL:AL138657  
 A;Experimental source: cultivar Columbia; BAC clone F9K21  
 C;Genetics:  
 A;Map position: 3  
 A;Note: F9K21.20  
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homold

Query Match 3.0%; Score 7; DB 2; Length 669;  
 Best Local Similarity 100.0%; Pred. No. 57;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 VLIYVLI 230  
 |||||  
 Db 287 VLIYVLI 293

## RESULT 50

T12712  
 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Clerodendrum incisum chloroplast  
 C;Species: chloroplast Clerodendrum incisum  
 C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 11-Jan-2000  
 C;Accession: T12712  
 R;Steeane, D.A.; Scotland, R.W.; Mabbertley, D.J.; Wagstaff, S.J.; Reeves, P.A.; Olmstead,  
 submitted to the EMBL Data Library, July 1996  
 A;Description: Phylogenetic relationships of Clerodendrum s.l. (Lamiaceae) inferred from  
 A;Reference number: Z17577  
 A;Accession: T12712  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-694 <SFE>  
 A;Cross-references: EMBL:L49156; NID:g1448957; PID:g1448958; PIDN:AAB04624.1  
 C;Genetics:  
 A;Genome: chloroplast  
 A;Note: ndhF  
 C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5  
 C;Keywords: chloroplast; membrane-associated complex; NAD; oxidoreductase

Query Match 3.0%; Score 7; DB 2; Length 694;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 VGIIVLI 226  
 |||||  
 Db 95 VGIIVLI 101

Search completed: August 13, 2002, 08:38:52  
 Job time: 176 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 13, 2002, 08:38:01 ; Search time 11.26 Seconds  
(without alignments)  
801.213 Million cell updates/sec

Title: US-09-826-212-2\_COPY\_27\_259  
Perfect score: 233  
Sequence: 1 TTAROEVEVPOQTVAPOQORH.....YLCTIVGIIVLLIVFV 233

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 5

Total number of hits satisfying chosen parameters: 3416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	233	100.0	259	1	T10C_HUMAN
2	14	6.0	386	1	T10D_HUMAN
3	8	3.4	440	1	T10B_HUMAN
4	7	3.0	199	1	FLGH_THEMA
5	7	3.0	205	1	YJ11_MYCTU
6	7	3.0	275	1	TFZD_ARTSF
7	7	3.0	283	1	DRBR_STRPE
8	7	3.0	374	1	YDB1_SCHPO
9	7	3.0	390	1	LA_DROME
10	7	3.0	431	1	DCOR_DATST
11	7	3.0	466	1	BLAR_MOUSE
12	7	3.0	466	1	BLAR_MOUSE
13	7	3.0	468	1	BLAR_PIG
14	7	3.0	468	1	T10A_HUMAN
15	7	3.0	471	1	UF01_MAIZE
16	7	3.0	471	1	UF02_MAIZE
17	7	3.0	473	1	BLAR_CANFA
18	7	3.0	474	1	BLAR_FELCA
19	7	3.0	477	1	BLAR_HUMAN
20	7	3.0	480	1	BLAR_MOUSE
21	7	3.0	584	1	PARF_PARTE
22	7	3.0	598	1	CYSJ_ECOLI
23	7	3.0	1036	1	YANZ_SCHPO
24	7	3.0	1177	1	DP3A_MYCLE
25	7	3.0	1179	1	DP3A_STRCO
26	7	3.0	1184	1	DP3A_MYCTU
27	7	3.0	1637	1	MRSP_STRAU
28	7	3.0	1835	1	CCAL_RAT
29	7	3.0	1856	1	MGA_HUMAN
30	6	2.6	50	1	RS14_METHN
31	6	2.6	54	1	TATA_RICPR
32	6	2.6	62	1	Y416_ARCFU
33	6	2.6	89	1	IAPP_FELCA

34	6	2.6	95	1	RL25_BUCAI	P57238 buchnera ap
35	6	2.6	110	1	RLA1_ALTPA	P49148 alternaria
36	6	2.6	110	1	RLA2_SCHPO	P08094 schizosacch
37	6	2.6	111	1	RL12_ARPE	O9999 aeropyrum p
38	6	2.6	111	1	RLA2_BRAFL	O01725 brachiosteo
39	6	2.6	116	1	HV1B_HUMAN	P01743 homo sapien
40	6	2.6	124	1	MUTP_BUCAI	P57298 buchnera ap
41	6	2.6	128	1	Y192_RICPR	O9999 aeropyrum p
42	6	2.6	134	1	TYRT_STRGA	P55047 streptomyces
43	6	2.6	139	1	PSAD_OPOST	P49481 odontella s
44	6	2.6	139	1	PSAD_SKECO	O96800 skeletonema
45	6	2.6	140	1	PSAD_SYNY3	P19569 synchocyst
46	6	2.6	141	1	PSAD_GUTTH	O78502 guillardia
47	6	2.6	144	1	EXBD_NEIMA	O06434 neisseria m
48	6	2.6	144	1	EXBD_NEIMA	P95376 neisseria m
49	6	2.6	157	1	SMG_BUCAI	P57562 buchnera ap
50	6	2.6	157	1	WH16_STRCO	P23157 streptomyces
51	6	2.6	183	1	OLEC_BRANA	P29526 brassica na
52	6	2.6	185	1	RL10_STRGR	P36257 streptomyces
53	6	2.6	189	1	RL6_SULAC	O05637 sulfolobus
54	6	2.6	190	1	YBAY_ECOLI	P77171 escherichia
55	6	2.6	202	1	B3G1_MOUSE	O9999 aeropyrum p
56	6	2.6	202	1	LYCA_BPMV1	P33486 lactococcus
57	6	2.6	204	1	RS8_GRIJA	O92556 griffithsia
58	6	2.6	205	1	RS8_HORVU	P36213 hordeum vul
59	6	2.6	207	1	RS8_HUMAN	P09058 homo sapien
60	6	2.6	210	1	RS8_ARATH	O91153 arabidopsis
61	6	2.6	211	1	YREF_MYCTU	P50050 mycobacteri
62	6	2.6	211	1	YREF_MYCTU	O28047 archaeglob
63	6	2.6	212	1	PSAD_SPIOL	P12353 spinachia ol
64	6	2.6	214	1	LIPIB_CYACA	O19898 cyanidium c
65	6	2.6	218	1	IM23_SCHJA	P27591 schistosoma
66	6	2.6	219	1	DEDA_ECOLI	P09548 escherichia
67	6	2.6	220	1	RS8_ORYSA	P49199 oryza sativ
68	6	2.6	221	1	MLR_DROME	P18432 drosophila
69	6	2.6	221	1	RS8_DROME	O08009 zea mays (m
70	6	2.6	221	1	RS8_MAIZE	O81361 prunus arme
71	6	2.6	221	1	YL24_CAEEL	P34417 caenorhabdi
72	6	2.6	224	1	H11L_CHICK	P08287 gallus gall
73	6	2.6	228	1	VP25_NPVAC	P1483 autographa
74	6	2.6	230	1	YP23_CAEEL	O09282 caenorhabdi
75	6	2.6	239	1	KGDA_MYCPN	P73536 mycoplasma
76	6	2.6	245	1	X123_HUMAN	O15884 homo sapien
77	6	2.6	247	1	SNGL_CAEEL	O76785 caenorhabdi
78	6	2.6	250	1	YC97_HUMAN	O99355 homo sapien
79	6	2.6	252	1	AROD_SALEN	O19677 salmonella
80	6	2.6	252	1	AROD_SALEN	P58667 salmonella
81	6	2.6	252	1	CAH_NETGO	O50940 neisseria g
82	6	2.6	256	1	Y107_NPVOP	O10346 oryza pseu
83	6	2.6	257	1	TRPC_AQUAE	O67657 aquilex aeo
84	6	2.6	261	1	LPRE_MYCTU	P71798 mycobacteri
85	6	2.6	266	1	REAF_RAT	O63558 rattus norv
86	6	2.6	269	1	LGT_BACSU	O34752 bacillus su
87	6	2.6	270	1	REAF_HUMAN	P15927 homo sapien
88	6	2.6	270	1	REAF_MOUSE	O62193 mus musculu
89	6	2.6	271	1	TNR4_RAT	P15725 rattus norv
90	6	2.6	275	1	NH3_AZOVI	P16289 azotobacter
91	6	2.6	279	1	STX_ARATH	O39293 arabidopsis
92	6	2.6	280	1	MACS_CHICK	P16577 gallus gall
93	6	2.6	290	1	YGLD_YEAST	P53212 saccharomyc
94	6	2.6	293	1	YFIE_ECOLI	P33634 escherichia
95	6	2.6	294	1	DPM1_USYMA	P54856 ustilla go ma
96	6	2.6	295	1	MTLS_MOUSE	O94716 mus musculu
97	6	2.6	301	1	YJIE_ECOLI	P32667 escherichia
98	6	2.6	308	1	YB80_MERJA	O58280 methanococ
99	6	2.6	310	1	SUCA_DICDI	P36967 dictyostell
100	6	2.6	312	1	SNAG_BOVIN	P81127 bos taurus
101	6	2.6	312	1	VMEM_EBV	P03208 Epstein-bar
102	6	2.6	315	1	TRXB_CLOLI	P52223 clostridium
103	6	2.6	317	1	O2F1_HUMAN	O13667 homo sapien
104	6	2.6	317	1	O2F2_HUMAN	O95006 homo sapien
105	6	2.6	324	1	CYRK_STRVN	P16500 streptomyces
106	6	2.6	324	1	STXF_HUMAN	O14662 homo sapien

107	6	2.6	330	1	FEPG_ECOLI	P23877	escherichia	180	504	1	TPM5_DROME	P49456	drosophila
108	6	2.6	334	1	B3G1_HUMAN	O9P247	homo sapien	181	505	1	GLPK_PSEAE	O01330	pseudomonas
109	6	2.6	334	1	B3G1_RAT	O35769	r galactosyl	182	507	1	LAT1_HUMAN	O01600	homo sapien
110	6	2.6	338	1	RLA0_HUMAN	P54049	methanococc	183	508	1	FAS3_DROME	P15278	drosophila
111	6	2.6	339	1	Y392_MERJA	O57837	methanococc	184	508	1	BAE2_HUMAN	O93520	homo sapien
112	6	2.6	344	1	RLA0_AERPE	O57948	aeropyrum p	185	519	1	RHO_TREPA	O83321	treponema p
113	6	2.6	347	1	TCR_STRM	P14551	streptomyces	186	522	1	CAIC_ECOLI	P31552	escherichia
114	6	2.6	353	1	YK21_YEAST	O02209	saccharomyc	187	525	1	NAB2_YEAST	P32505	saccharomyc
115	6	2.6	356	1	TSI_DROME	P40689	drosophila	188	537	1	MYCH_CHICK	O05633	gallus gall
116	6	2.6	357	1	IF35_HUMAN	O00303	homo sapien	189	543	1	BCHB_RHOGE	O91993	rhodocyclus
117	6	2.6	362	1	FIIBP_ADRO9	P36846	human adeno	190	544	1	ODP2_ACHLA	P35499	achetlepiasm
118	6	2.6	366	1	DHLE_BACE	O59194	dacillus ce	191	547	1	Y966_TREPA	O83932	treponema p
119	6	2.6	367	1	BRB2_RABIT	O28612	oryctolagus	192	547	1	MCPC_SALTY	O02795	salmonella
120	6	2.6	372	1	BRB2_CAVPO	O70526	cavia porce	193	547	1	ODP2_PSEAE	O59638	pseudomonas
121	6	2.6	372	1	VGLI_HSV23	O67674	herpes simp	194	548	1	AMT4_PSEST	P13507	pseudomonas
122	6	2.6	372	1	VGLI_HSV2H	P13231	herpes simp	195	549	1	SMF2_YEAST	P88778	saccharomyc
123	6	2.6	374	1	MTEF_NEIGO	O59606	neisseria g	196	551	1	AMT4_PSESA	P22963	pseudomonas
124	6	2.6	377	1	DHLE_BACST	P13154	dacillus st	197	554	1	SHT1_DROME	P20905	drosophila
125	6	2.6	381	1	VATC_METUA	O37672	methanococc	198	554	1	ACH3_CABEL	P54244	caenorhabd1
126	6	2.6	383	1	AMC1_ORYSA	P27940	oryza sativ	199	564	1	FRP1_SCHPO	O04800	schizosacch
127	6	2.6	385	1	TGT_PASMU	P57831	pasteurella	200	569	1	SOT1_SPIOL	O41364	splinacla ol
128	6	2.6	388	1	P2X4_HUMAN	O99571	homo sapien	201	575	1	PTI_ECOLI	P08839	escherichia
129	6	2.6	391	1	BRB2_HUMAN	P30411	homo sapien	202	575	1	PTI_SALTY	P12654	escherichia
130	6	2.6	391	1	MSES_HUMAN	O00557	homo sapien	203	599	1	RP2P_DROST	P24629	drosophila
131	6	2.6	395	1	CDSA_MTCPN	P75160	m putative	204	604	1	VEI_HPV38	O80909	human papil
132	6	2.6	408	1	LMP1_BOVIN	O05204	bos taurus	205	606	1	SP2_HUMAN	O02086	homo sapien
133	6	2.6	410	1	NEUS_HUMAN	O99574	homo sapien	206	610	1	POUC_BRARE	P13367	brachydanio
134	6	2.6	410	1	NEUS_MOUSE	O35684	mus musculu	207	613	1	NUO1_ECOLI	P33607	escherichia
135	6	2.6	410	1	NEUS_RAT	O91182	rattus norv	208	620	1	MUT1_TREPA	O83325	treponema p
136	6	2.6	415	1	KLFP_MOUSE	O9EPW2	mus musculu	209	635	1	VP40_HSV11	P10210	herpes simp
137	6	2.6	419	1	RHO_NEIGO	O06447	neisseria g	210	637	1	ODP2_AZOVI	P10802	azotobacter
138	6	2.6	419	1	RHO_PSEFL	O52165	pseudomonas	211	640	1	SCAA_RABIT	O97741	oryctolagus
139	6	2.6	420	1	RHO_HAEIN	P44619	haemophilus	212	642	1	PHSA_STRAT	O53672	streptomyces
140	6	2.6	420	1	SECY_HELPJT	O92359	helicobacte	213	656	1	YK79_MYCTU	O10667	mycobacteri
141	6	2.6	420	1	SECY_HELPPT	O25879	helicobacte	214	660	1	YH11_EBY	P03181	epstein-bar
142	6	2.6	422	1	RHO_RHOSH	P52156	rhodobacter	215	662	1	ABPA_STRLI	P53627	streptomyces
143	6	2.6	427	1	RHO_BACSU	O03222	dacillus su	216	662	1	YRW3_CABEL	O09333	caenorhabd1
144	6	2.6	428	1	AMV1_ORYSA	P17654	oryza sativ	217	665	1	ATKB_TREAC	P57700	thermoplasm
145	6	2.6	433	1	RHO_CHRYI	P52152	chromatium	218	665	1	ENV_MLVAD	P11268	radiation m
146	6	2.6	434	1	Y830_THEMA	O9WZL7	thermotoga	219	665	1	ENV_MLVAK	P31794	radiation m
147	6	2.6	439	1	Y441_BUCAI	P57516	buchnera ap	220	669	1	ENV_MLVAV	P03386	akv murine
148	6	2.6	445	1	DSOX_ECOLI	P08555	escherichia	221	671	1	P5CS_VIGAC	P32206	delta 1-p
149	6	2.6	453	1	Y259_MYCPN	P75419	mycoplasma	222	684	1	P5PS_METTH	O27180	methanobact
150	6	2.6	455	1	ACHO_CHICK	P43679	gallus gall	223	700	1	FLHA_CAUCR	O03845	caulobacter
151	6	2.6	457	1	RHO_RICER	O9ZD24	rickettsia	224	703	1	CDGT_BACS2	P31746	caulobacter
152	6	2.6	458	1	ACHO_HUMAN	O05901	homo sapien	225	707	1	PET1_RABIT	P36836	oryctolagus
153	6	2.6	458	1	YGEH_ECOLI	P76639	escherichia	226	708	1	PET1_HUMAN	P46059	homo sapien
154	6	2.6	461	1	ATOC_ECOLI	O06065	escherichia	227	710	1	PET1_RAT	P51574	homo sapien
155	6	2.6	461	1	SE12_CABEL	P52166	caenorhabd1	228	712	1	ENV_HV2S2	P32536	human immun
156	6	2.6	461	1	Y4SH_RHISN	P55651	rhizobium s	229	716	1	P5CS_ORYSA	O04226	delta 1-p
157	6	2.6	461	1	Y40A_RHISN	O53195	rhizobium s	230	717	1	P5C1_ARATH	P54882	delta 1-p
158	6	2.6	462	1	PNTB_ECOLI	P07002	escherichia	231	719	1	P5CS_MESCR	P54361	delta 1-p
159	6	2.6	462	1	SYG_TREPA	O83678	treponema p	232	722	1	Z219_HUMAN	O9P234	homo sapien
160	6	2.6	463	1	YAD4_YEAST	P28003	saccharomyc	233	726	1	P5C2_ARATH	P54888	delta 1-p
161	6	2.6	463	1	YKAA_BACFI	P30267	dacillus fl	234	735	1	ADDA_MOUSE	O93408	rattus norv
162	6	2.6	464	1	ACHO_RAT	P12331	dacillus fl	235	735	1	ADDA_MOUSE	O63028	rattus norv
163	6	2.6	466	1	ACHP_CARAV	P18257	carassius a	236	753	1	PPSA_ARCFU	O29548	archaeoglob
164	6	2.6	467	1	BIAR_BOVIN	O9T166	bos taurus	237	757	1	HUNB_DROSE	O62538	drosophila
165	6	2.6	467	1	BIAR_SHEEP	O28927	ovis aries	238	758	1	HUNB_DROSE	P05084	drosophila
166	6	2.6	471	1	UEO3_MAIZE	P16167	zea mays (m	239	759	1	CHLD_ARATH	O93451	arabidopsis
167	6	2.6	473	1	PHDK_NOSK	O24723	nocardioide	240	759	1	HUNB_DROYA	O62541	drosophila
168	6	2.6	476	1	APM4_YEAST	P09368	saccharomyc	241	764	1	DRH_HUMAN	P14783	homo sapien
169	6	2.6	491	1	APM4_YEAST	O99186	saccharomyc	242	764	1	TSRH_CANFA	P40879	caus fami1
170	6	2.6	491	1	CD5_RAT	P51882	rattus norv	243	767	1	HUNB_DROOR	O62537	drosophila
171	6	2.6	493	1	PBI3_RAT	O35568	rattus norv	244	774	1	AD28_MOUSE	O93166	mus musculu
172	6	2.6	494	1	CD5_MOUSE	P13379	mus musculu	245	778	1	RG12_MOUSE	O61193	mus musculu
173	6	2.6	497	1	PSD3_SCHPO	O42897	schizosacch	246	826	1	VILI_HUMAN	P09337	homo sapien
174	6	2.6	497	1	VHS_HSVB	P28957	equine herp	247	826	1	VILI_MOUSE	O62468	mus musculu
175	6	2.6	498	1	VGLY_LCYVA	P09991	lymphocytic	248	830	1	SREC_HUMAN	O14016	caenorhabd1
176	6	2.6	501	1	GLPK_ECOLI	P08859	escherichia	249	836	1	YIAK_CABEL	O20072	caenorhabd1
177	6	2.6	502	1	GLPK_HAEIN	P44400	haemophilus	250	837	1	GCL2_HUMAN	O92830	homo sapien
178	6	2.6	502	1	GLPK_PASMU	P57944	pasteurella	251	853	1	ADG_USTWA	O99128	ustilago ma
179	6	2.6	503	1	GLPK_PSETO	O87924	pseudomonas	252	853	1	VMTB_LAMBD	P03736	bacterioph



253	6	2.6	859	1	ENV_HV2CA	P24105	human	immun	326	5	2.1	66	1	LHA2_RHOA	P35102	rhodopseudo
254	6	2.6	859	1	ENV_HV2ST	P20872	human	immun	327	5	2.1	66	1	MT3_MALDO	024059	malus domes
255	6	2.6	859	1	ENP1_METTM	P09846	methanobact		328	5	2.1	67	1	MTB_SPHGR	026496	sphaerectin
256	6	2.6	876	1	AREA_EMENTI	P17429	emeritella		329	5	2.1	67	1	REF1_STRGC	P47980	streptococc
257	6	2.6	885	1	CHB_SERNA	Q54468	serattia ma		330	5	2.1	67	1	SCL3_LEIOH	P56678	leiturus qui
258	6	2.6	885	1	VGLB_HSV2S	P24994	herpes simp		331	5	2.1	67	1	TATA_NEIMA	P57049	neisseria qul
259	6	2.6	892	1	IF2_CHLIR	O84098	chlamydia t		332	5	2.1	68	1	EPUB_STRPN	0003159	streptococc
260	6	2.6	904	1	VGLB_HSV1K	P06437	herpes simp		333	5	2.1	70	1	GBG1_DROME	P38040	droscophila
261	6	2.6	923	1	RELI_SCHPO	O92380	schizosacch		334	5	2.1	70	1	S1FA_SPTOL	P42552	splanactia ol
262	6	2.6	963	1	CHC1_HUMAN	Q9h158	homo sapien		335	5	2.1	72	1	HP11_ECTVA	P38911	ectothlorho
263	6	2.6	970	1	Y277_MYCGE	Q49409	mycoplasma		336	5	2.1	75	1	MER1_EUPRA	P10774	euploetes ra
264	6	2.6	999	1	DSG3_HUMAN	P32926	homo sapien		337	5	2.1	75	1	PM22_BOVIN	Q9t943	bos laurus
265	6	2.6	1002	1	YA37_ANASP	P58612	anabena sp		338	5	2.1	76	1	RPON_ARCFU	Q29135	archaeoglob
266	6	2.6	1008	1	MMLA_MYCLE	Q49619	mycobacteri		339	5	2.1	76	1	S1FA_ARATH	P03151	arabidopsi
267	6	2.6	1080	1	HDC_DROME	O9n288	droscophila		340	5	2.1	77	1	MT2B_ARATH	P38805	arabidopsi
268	6	2.6	1111	1	YTER_HAETN	O57352	haemophilus		341	5	2.1	77	1	MT2_VICRA	Q41657	vicia faba
269	6	2.6	1134	1	VGLM_HANTH	P16483	hantaa vir		342	5	2.1	79	1	MT2_CICAR	Q1657	cicer arlet
270	6	2.6	1135	1	VGLM_HANTV	P16853	hantaan vir		343	5	2.1	79	1	VG8_SPTVR	Q39493	spliroplasma
271	6	2.6	1135	1	VGLM_HANTV	P08668	hantaan vir		344	5	2.1	80	1	MT21_BRAJU	P56170	brassica ju
272	6	2.6	1141	1	CN3A_HUMAN	Q14432	homo sapien		345	5	2.1	80	1	MT25_BRAJU	P56172	brassica ju
273	6	2.6	1166	1	L2GL_DROPS	O08470	droscophila		346	5	2.1	80	1	MT2_RICCO	P30564	ricinus com
274	6	2.6	1169	1	YK82_YEAST	P36170	saccharomyc		347	5	2.1	80	1	NED8_HUMAN	Q15843	homo sapien
275	6	2.6	1171	1	TR12_STRCO	Q3KX9	streptomyc		348	5	2.1	81	1	NED8_HUMAN	P29595	mus musculu
276	6	2.6	1188	1	PPSA_METJA	Q57962	methanococc		349	5	2.1	81	1	CEP_VIBCH	Q9K333	vibririo chol
277	6	2.6	1244	1	YP83_CABEL	O09441	caenorhabdi		350	5	2.1	82	1	CEP_VIBCH	P66457	streptomyc
278	6	2.6	1274	1	MYPC_HUMAN	Q14896	homo sapien		351	5	2.1	82	1	MT2B_LYCES	O40158	lycoperisico
279	6	2.6	1311	1	AFRX_DROME	O9G95	droscophila		352	5	2.1	82	1	MT2B_LYCES	P13315	klebsiella
280	6	2.6	1329	1	FTSK_ECOLI	P46889	escherichia		353	5	2.1	83	1	OADG_KLEPN	P12991	vibririo algi
281	6	2.6	1477	1	YOR1_YEAST	P33049	saccharomyc		354	5	2.1	84	1	ATPL_VIBAL	P40848	rana esculie
282	6	2.6	1579	1	PEP1_YEAST	P32319	saccharomyc		355	5	2.1	84	1	ES1B_RANES	IMM3_ECOLI	mus musculu
283	6	2.6	1902	1	P1P_IACPA	P16271	lactococcu		356	5	2.1	84	1	SCXE_BUTOC	P02994	escherichia
284	6	2.6	1902	1	P2P_IACPA	O02470	lactobacill		357	5	2.1	85	1	AMP_AMACA	P17254	buthus occi
285	6	2.6	1902	1	P3P_IACIC	P15232	lactococcu		358	5	2.1	86	1	PTHP_STRBO	P27275	amaranthus
286	6	2.6	1957	1	YD86_SCIPO	Q10411	schizosacch		359	5	2.1	87	1	BXB8_BOMMO	Q6XKX8	streptococc
287	6	2.6	2499	1	MPRI_BOVIN	P08169	bos taurus		360	5	2.1	88	1	FXV3_MOUSE	P26742	domdyx mori
288	6	2.6	2747	1	FAF_DROME	P55824	droscophila		361	5	2.1	88	1	H82_NEIGO	Q61835	mus musculu
289	6	2.6	3256	1	K167_HUMAN	P46013	homo sapien		362	5	2.1	88	1	YK94_ARCFU	P11910	neisseria g
290	6	2.6	3388	1	POLG_DEN2P	P12823	d genome po		363	5	2.1	89	1	CORA_HUMAN	P25321	homo sapien
291	6	2.6	3391	1	POLG_DEN26	P29990	d genome po		364	5	2.1	89	1	CORR_HUMAN	P22559	homo sapien
292	6	2.6	3391	1	POLG_DEN27	P29991	d genome po		365	5	2.1	89	1	CORN_MACMU	P25332	macaca mula
293	6	2.6	3391	1	POLG_DEN2J	P07564	d genome po		366	5	2.1	89	1	YCO2_PARDE	P08302	paracoccus
294	6	2.6	3391	1	POLG_DEN2N	P14340	d genome po		367	5	2.1	90	1	VPM_BPYPD	P27369	bacterioph
295	6	2.6	3421	1	TEGU_HSVB	P2895	equine herp		368	5	2.1	90	1	YK94_ARCFU	O28166	archaeoglob
296	6	2.6	4303	1	PKD1_HUMAN	P98161	homo sapien		369	5	2.1	91	1	SY05_MOUSE	Q08812	mus musculu
297	6	2.6	4473	1	PLEI_CRIGR	O91355	crictetulus		370	5	2.1	91	1	V179_FOPPV	O91554	fowlpox vir
298	6	2.6	4544	1	LRP1_HUMAN	Q07954	homo sapien		371	5	2.1	92	1	PLM_CANFA	P06513	canis famli
299	6	2.6	4687	1	PLEI_RAT	P30427	rattus norv		372	5	2.1	92	1	PLM_HUMAN	O00168	homo sapien
300	5	2.1	14	1	UHA1_CANFA	P9503	canis famli		373	5	2.1	92	1	PLM_MOUSE	O08589	mus musculu
301	5	2.1	28	1	MT2_BRANA	Q96353	brassica na		374	5	2.1	92	1	PLM_MOUSE	P40089	saccharomyc
302	5	2.1	29	1	CX07_CONGE	P05483	conus geogr		375	5	2.1	93	1	LSM5_YEAST	RR8140	cyanophora
303	5	2.1	30	1	RNP_ODOVI	P19640	odocoleus		376	5	2.1	95	1	RM20_CVAPA	P06955	bacterioph
304	5	2.1	37	1	RSBY_GUTTH	O78433	guillardia		377	5	2.1	96	1	VG6_BPPZA	P19183	bacterioph
305	5	2.1	37	1	RK36_CVACA	Q9PLU9	cyandidium c		378	5	2.1	96	1	Y11K_BPCHP	Q92960	chlamydia p
306	5	2.1	38	1	H5_COLL	P02260	columba liv		379	5	2.1	97	1	Y121_CHLPN	P37343	escherichia
307	5	2.1	38	1	MFA2_USTMA	P31963	ustillago ma		380	5	2.1	97	1	YBGE_ECOLI	P42550	escherichia
308	5	2.1	39	1	VPV_HVIR	P12518	human immun		381	5	2.1	97	1	YBXY_ECOLI	O9u919	homo sapien
309	5	2.1	51	1	MLEV_MOUSE	P09542	mus musculu		382	5	2.1	99	1	NIC1_HUMAN	P22757	alcaligenes
310	5	2.1	52	1	LHA1_ECTHL	P80102	ectochlorho		383	5	2.1	101	1	YHOX_ALCEU	P08813	mus musculu
311	5	2.1	53	1	YBAM_ECOLI	P45807	escherichia		384	5	2.1	102	1	APAZ_MOUSE	P24258	herpesvirs
312	5	2.1	54	1	YH11_STRCO	P16248	streptomyc		385	5	2.1	102	1	COLL_HVSC	P22567	mus musculu
313	5	2.1	56	1	SCP2_MESMA	O9njp7	mesobutlus		386	5	2.1	102	1	RS24_AERPE	Q9GVC0	aeropyrum p
314	5	2.1	56	1	SCP3_MESMA	O9ubd1	mesobutlus		387	5	2.1	102	1	VAM5_MOUSE	P81311	methanococc
315	5	2.1	60	1	MT_BRARE	P52722	brachydanio		388	5	2.1	102	1	Y70A_METJA	P81101	saccharomyc
316	5	2.1	60	1	MT_CARAU	P52723	carassius a		389	5	2.1	102	1	YBUI_YEAST	P212902	gallus gall
317	5	2.1	61	1	AERC_AEROS	P09165	aeromonas s		390	5	2.1	103	1	CHIN_RHOCA	Q92067	mus musculu
318	5	2.1	61	1	Y106_NPVAC	P41659	autographa		391	5	2.1	103	1	HG15_CHICK	P32665	bacterioph
319	5	2.1	63	1	YFEG_ECOLI	P76571	escherichia		392	5	2.1	104	1	UGR2_MOUSE	P22031	anthracidari
320	5	2.1	64	1	MT3_PRUVAV	O48951	prunus aviu		393	5	2.1	104	1	VG6_BPAPH	P27075	candida mal
321	5	2.1	64	1	PMCH_RAT	P80250	rattus norv		394	5	2.1	104	1	LBG_ANTCR		
322	5	2.1	65	1	LHA2_ECTHL	P80103	ectochlorho		395	5	2.1	105	1	PSBX_GOSHI		
323	5	2.1	65	1	LHA3_RHOA	P35103	retodopseudo		396	5	2.1	105	1	R440_CANMA		
324	5	2.1	65	1	MT3_CARPA	Q96386	carlica papa		397	5	2.1	105	1	RL44_CANTR		
325	5	2.1	65	1	OMP_LOCOMI	P80045	locusta mig		398	5	2.1	105	1			

399	5	2.1	105	1	SUGE_CITFR	069279	citrobacter	472	5	2.1	133	1	TRK4_ECOLI	P17910	escherichia
400	5	2.1	105	1	VE7_HPVS0	P36826	human papil	473	5	2.1	134	1	ANP3_RHIDE	P5753	aribophila
401	5	2.1	105	1	YNCR_YEAST	P53967	saccharomyc	474	5	2.1	134	1	CVS1_RHIDE	Q4233	trichodopsis
402	5	2.1	106	1	PSIE_ECOLI	P27295	escherichia	475	5	2.1	134	1	E315_ADE03	P11316	human adeno
403	5	2.1	106	1	RLI2_SUISO	P96040	sulfolobus	476	5	2.1	134	1	E315_ADE07	P15136	human adeno
404	5	2.1	106	1	VATF_HALVO	Q48331	halobacteri	477	5	2.1	135	1	H2A_TRYCR	P35066	trypanosoma
405	5	2.1	108	1	YG16_YEAST	P53205	saccharomyc	478	5	2.1	135	1	VE6_PAPVE	P11331	european el
406	5	2.1	109	1	VATL_MAIZE	Q41773	zea mays (m	479	5	2.1	135	1	Y274_BUCAI	P57362	buchnera ap
407	5	2.1	109	1	YPER_SALTU	O92fi5	salmonella	480	5	2.1	135	1	YDOA_SCHPO	O14202	schizosacch
408	5	2.1	109	1	YQ31_BACAN	O9n01	bacillus an	481	5	2.1	135	1	VF72_ARCFU	O28700	archaeoglob
409	5	2.1	110	1	LV1C_MOUSE	P01725	mus musculus	482	5	2.1	136	1	ATPM_HUMAN	O99766	homo sapien
410	5	2.1	110	1	US36_HCMVA	P16842	human cytom	483	5	2.1	136	1	RS8E_AERPE	Q99740	aeropyrum p
411	5	2.1	111	1	RA2A_MAIZE	P46252	zea mays (m	484	5	2.1	136	1	YP09_DEIRA	Q9142	deinococcus
412	5	2.1	111	1	RLAI_CABEL	P91913	caenorhabdi	485	5	2.1	137	1	CPC_CUCSA	P29602	cucumis sat
413	5	2.1	111	1	RLA2_ARTSA	P02399	artemia sal	486	5	2.1	138	1	GRIM_DROME	Q4570	dtrosophila
414	5	2.1	112	1	RLAI_DROME	P08570	dtrosophila	487	5	2.1	140	1	BM88_PIG	O29028	sus scrofa
415	5	2.1	112	1	VG33_BPT4	P13338	bacteriopho	488	5	2.1	141	1	HBAD_CHICK	P02001	gallus gall
416	5	2.1	113	1	CY4C_PSEPU	P09787	pseudomonas	489	5	2.1	141	1	HBAD_MERGA	P81024	melaeagris g
417	5	2.1	113	1	DTLX_HUMAN	Q15763	homo sapien	490	5	2.1	141	1	HBA_STUVU	P01997	sturnus vul
418	5	2.1	113	1	NTRC_PSEST	P24039	pseudomonas	491	5	2.1	141	1	YEDD_SALTU	P01997	sturnus vul
419	5	2.1	113	1	RLI2_HALVO	P41197	halobacteri	492	5	2.1	142	1	RK40_SPIOL	P27664	splicina ol
420	5	2.1	113	1	Y465_AOUAE	O66767	aquifex aeo	493	5	2.1	143	1	RK2_SOYBN	P18663	glycine max
421	5	2.1	114	1	ET3_RABIT	P19998	oryctolagus	494	5	2.1	144	1	SOD1_HALME	O08461	halobacteri
422	5	2.1	114	1	RLAI_HUMAN	P05386	homo sapien	495	5	2.1	144	1	Y100_AOUAE	O67669	aquifex aeo
423	5	2.1	114	1	RLAI_MOUSE	P47955	mus musculu	496	5	2.1	146	1	HBH_BRATR	P14526	dradypus tr
424	5	2.1	114	1	VL03_FOWPV	P19944	rattus norv	497	5	2.1	146	1	HBH_BRATR	P02039	erinaeacus e
425	5	2.1	114	1	RA2B_ARATH	O915b7	fowlpox vir	498	5	2.1	146	1	HBE_RABIT	P02103	oryctolagus
426	5	2.1	115	1	RUBR_SYNY3	P51407	arabidopsis	499	5	2.1	146	1	SOD2_HALME	O08460	halobacteri
427	5	2.1	115	1	NU3C_NEPOL	P73066	synechocyst	500	5	2.1	146	1	Y142_AOUAE	O66557	aquifex aeo
428	5	2.1	116	1	LV1A_MOUSE	P01722	mus musculu	501	5	2.1	146	1	YB99_MERJA	O58599	methanococc
429	5	2.1	116	1	NU3C_MACRO	P2666	macropus ro	502	5	2.1	146	1	YG56_YEAST	P35311	saccharomyc
430	5	2.1	116	1	VAM5_HUMAN	O95183	homo sapien	503	5	2.1	147	1	HV1C_HUMAN	P01744	homo sapien
431	5	2.1	116	1	YJG7_YEAST	P40366	saccharomyc	504	5	2.1	147	1	PSAE_HORPI	PJ3194	hordeum vul
432	5	2.1	117	1	LV2A_MOUSE	P01728	mus musculu	505	5	2.1	147	1	UCRH_YEAST	P00127	saccharomyc
433	5	2.1	118	1	ATPZ_SYNP6	P08443	synechococc	506	5	2.1	147	1	Y1F3_MOUSE	O88784	saccharomyc
434	5	2.1	118	1	CBIN_STRCO	O54189	streptomyce	507	5	2.1	148	1	GP22_LITRCA	O01443	litomosoid
435	5	2.1	118	1	VPML_HAEIN	P44234	haemophilus	508	5	2.1	148	1	YEE5_ECOLI	P76362	escherichia
436	5	2.1	119	1	ID3_HUMAN	Q02535	homo sapien	509	5	2.1	150	1	LSPA_LACIC	Q48789	lactococcus
437	5	2.1	119	1	ORNT_ORNMO	P56409	ornithodoro	510	5	2.1	150	1	YTR1_AZOBP	P69694	azospirillum
438	5	2.1	119	1	RNP_CHESE	P40461	chelydra se	511	5	2.1	151	1	YVB2_RHIME	Q92361	rhizobium m
439	5	2.1	119	1	YPX3_BLYJ	P03414	bovine leuk	512	5	2.1	152	1	YCF8_YEAST	P25565	saccharomyc
440	5	2.1	120	1	CU19_ARADI	P80515	arateneus dia	513	5	2.1	153	1	HEMA_MUMPS	P33460	mumps virus
441	5	2.1	120	1	NU3C_NEPOL	O9TKx9	nephroselini	514	5	2.1	154	1	YAI6_ARCFU	O93246	archaeoglob
442	5	2.1	120	1	RBFA_BUCAI	P57457	buchnera ap	515	5	2.1	154	1	YGG9_YEAST	P53162	saccharomyc
443	5	2.1	120	1	Y041_UREPA	O9PRA4	ureaplasma	516	5	2.1	155	1	COX4_YEAST	P40407	saccharomyc
444	5	2.1	120	1	YD42_MYCTU	Q11012	mycoplasma	517	5	2.1	155	1	NU6M_ALBCO	P48922	albilaria c
445	5	2.1	121	1	GSP1_ERWCA	P31588	erwinia car	518	5	2.1	155	1	RL21_PYST	P19667	pyura stelo
446	5	2.1	122	1	RBS2_HYDMR	O59461	hydrogenovi	519	5	2.1	156	1	BCCP_PSEAE	P37789	pseudomonas
447	5	2.1	122	1	RL7_DEIRA	O9RSIO	deinococcus	520	5	2.1	157	1	BSAA_BACHD	O9297	bacillus ha
448	5	2.1	123	1	RP14_HUMAN	O95059	homo sapien	521	5	2.1	157	1	FLIN_PSEAE	O51466	pseudomonas
449	5	2.1	124	1	CMGG_BACSU	P25959	bacillus su	522	5	2.1	159	1	RL21_MOUSE	P40280	rattus norv
450	5	2.1	124	1	HYPA_MERJA	O57667	methanococc	523	5	2.1	160	1	RL21_MOUSE	P43334	caenorhabd1
451	5	2.1	125	1	RL7_RICCN	O92187	rickettisia	524	5	2.1	160	1	RL21_CABEL	P17657	bacteriopho
452	5	2.1	126	1	ACTR_PAPHA	O286928	papio hamad	525	5	2.1	161	1	VP12_BPREP	P17657	bacteriopho
453	5	2.1	126	1	CU24_ARADI	P80516	arateneus dia	526	5	2.1	161	1	PRI_ARATH	P33154	arabidopsis
454	5	2.1	126	1	PLAS_STNY3	P21697	synechocyst	527	5	2.1	161	1	YG22_HAEIN	P44275	haemophilus
455	5	2.1	127	1	LYC_COLDI	P00708	colymba liv	528	5	2.1	162	1	XYLB_AMPSP	P54271	ampullariel
456	5	2.1	127	1	Y55B_MYCGE	O9ZbH1	mycoplasma	529	5	2.1	162	1	YDYA_SCHPO	O13669	schizosacch
457	5	2.1	127	1	Y55B_MYCGE	P75047	mycoplasma	530	5	2.1	162	1	Y227_MERJA	O60266	methanococc
458	5	2.1	129	1	DYIA_CHIRE	O39591	chlamydomon	531	5	2.1	164	1	VATL_LYCES	O24011	lycopersico
459	5	2.1	129	1	LV1B_MOUSE	P01724	mus musculu	532	5	2.1	164	1	VATL_PHAU	O22532	physosolus a
460	5	2.1	129	1	LV1D_MOUSE	P01726	mus musculu	533	5	2.1	165	1	RS16_GAUCR	P81642	caulobacter
461	5	2.1	129	1	LV1E_MOUSE	P01727	mus musculu	534	5	2.1	165	1	SSB_PSEAE	P40947	pseudomonas
462	5	2.1	129	1	LV2B_MOUSE	P01729	mus musculu	535	5	2.1	165	1	VATL_ARYSA	O39039	arabidopsis
463	5	2.1	129	1	RT16_DROME	O96v63	dtrosophila	536	5	2.1	165	1	VATL_AYVSA	P23957	avena sativ
464	5	2.1	130	1	CHB1_ANTPO	P02848	anthraaea p	537	5	2.1	165	1	VATL_BETVU	O39457	beta vulgar
465	5	2.1	130	1	RS22_AGABT	P46792	agaricus bi	538	5	2.1	165	1	VATL_GOSHI	Q43434	gossypium h
466	5	2.1	130	1	TAT_HVNZ	P05909	human immun	539	5	2.1	165	1	VATL_KALDA	O64173	calanchoe d
467	5	2.1	130	1	TAT_HV2RO	P04605	human immun	540	5	2.1	165	1	VATL_ORYSA	Q40655	coryza sativ
468	5	2.1	131	1	CHHB_BOMBO	P05688	bombyx mori	541	5	2.1	165	1	VATL_TOBAC	O40585	nicotiana t
469	5	2.1	132	1	IMEP_STRNT	P01077	streptomyce	542	5	2.1	165	1	Y051_HAEIN	P44484	haemophilus
470	5	2.1	132	1	YJWM_ECOLI	P39394	escherichia	543	5	2.1	165	1	YREP_BUCTS	O31289	buchnera ap
471	5	2.1	133	1	TAT_HVZCA	P24109	human immun	544	5	2.1	166	1	HESS_RAT	O03082	rattus norv

545	5	2.1	166	1	RS5_ECOLI	P02356	eschlerichia	618	5	2.1	190	1	APOM_MOUSE	Q921r3	mus musculus
546	5	2.1	166	1	P542_MYCPN	P75270	mycoplasma	619	5	2.1	190	1	APOM_RAT	P14630	rattus norv
547	5	2.1	167	1	HES5_MOUSE	P70120	mus musculus	620	5	2.1	190	1	CAN2_FALTI	P46503	flatteria 11
548	5	2.1	167	1	MB12_MYCLE	O49771	mycobacteri	621	5	2.1	190	1	CC42_COTGL	O94103	colletotric
549	5	2.1	167	1	NU6M_MXGXL	O9g2w7	myxine glut	622	5	2.1	190	1	ESS1_YEAST	P22656	saccharomyc
550	5	2.1	167	1	YREP_BUCBP	O9ze44	buchnera ap	623	5	2.1	190	1	LEPW_BACST	P54506	bacillus su
551	5	2.1	168	1	ATPD_RAT	P35434	rattus norv	624	5	2.1	190	1	MAF_BACHD	O9K8h3	bacillus ha
552	5	2.1	168	1	VA34_VACCC	P21057	vaccinia vi	625	5	2.1	190	1	YREG_STRCO	P39g95	streptomyces
553	5	2.1	168	1	VA34_VACCV	P24761	vaccinia vi	626	5	2.1	191	1	CBP2_ARATH	P30187	arabidopsis
554	5	2.1	168	1	VA34_VARV	P33851	vaccinia vi	627	5	2.1	191	1	PGHD_BOVIN	O02853	bos taurus
555	5	2.1	168	1	VA40_VACCC	P21053	vaccinia vi	628	5	2.1	191	1	TF2D_ACECL	P4622D	acetabulari
556	5	2.1	168	1	VA40_VACCV	P24765	vaccinia vi	629	5	2.1	192	1	CSR2_HUMAN	O16537	homo sapien
557	5	2.1	168	1	Y22_MYCTU	O50706	mycobacteri	630	5	2.1	192	1	CSR2_RAT	O62908	rattus norv
558	5	2.1	169	1	GP38_CANFA	O95152	canis famli	631	5	2.1	192	1	MLEF_MOUSE	P09541	mus musculus
559	5	2.1	169	1	GPO_SYNY3	P74250	synecocyst	632	5	2.1	192	1	RHOI_DROME	P48188	drosophila
560	5	2.1	169	1	HUPJ_BRAJA	P48311	bradyrhizob	633	5	2.1	192	1	RHOI_CAEEL	Q22038	caenorhabd1
561	5	2.1	169	1	VPL_BPP2	P25475	bacilliothpa	634	5	2.1	192	1	RHO_APICA	P01122	aplysia cal
562	5	2.1	171	1	IF3_BACSU	P55872	bacillus su	635	5	2.1	192	1	RHO_DISOM	P22122	discopyge o
563	5	2.1	171	1	IR10_HCMVA	P16808	human cytom	636	5	2.1	192	1	Y678_AOUAE	O66906	aquilex aeo
564	5	2.1	171	1	RS4_MERTH	O26142	methanobact	637	5	2.1	192	1	YBCC_RHOCA	P26166	rhodobacter
565	5	2.1	171	1	SFME_ECOLI	P38052	eschlerichia	638	5	2.1	193	1	CSR2_CHICK	P50460	gallus gall
566	5	2.1	172	1	P1ME_SALTY	P37926	salmonella	639	5	2.1	193	1	CSR2_COTUA	O05138	colurnix co
567	5	2.1	172	1	GP38_MOUSE	O62011	mus musculu	640	5	2.1	193	1	H5_AMSAN	P00258	anser anser
568	5	2.1	172	1	IM7B_HUMAN	O60820	homo sapien	641	5	2.1	193	1	MP70_MYCTU	P06513	calrina mos
569	5	2.1	172	1	RUB2_PSEOL	P00272	pseudomonas	642	5	2.1	193	1	H5_CAIMO	O50769	mycobacteri
570	5	2.1	173	1	CRGC_MOUSE	O61597	mus musculu	643	5	2.1	193	1	RHOA_CANFA	P24406	canis famli
571	5	2.1	173	1	CRGD_BOVIN	P08209	bos taurus	644	5	2.1	193	1	RHOA_HUMAN	P06749	homo sapien
572	5	2.1	173	1	CRGD_MOUSE	P04342	mus musculu	645	5	2.1	193	1	RHOA_MOUSE	Q9qu10	mus musculu
573	5	2.1	173	1	CRGD_RAT	P10067	rattus norv	646	5	2.1	193	1	RHOH_HUMAN	P08134	homo sapien
574	5	2.1	173	1	GCSR_BOVIN	P20821	bos taurus	647	5	2.1	193	1	RHOC_MOUSE	O62159	mus musculu
575	5	2.1	174	1	PLU_DROME	P42570	drosophila	648	5	2.1	193	1	VA57_VACCC	P21074	vaccinia vi
576	5	2.1	174	1	POPB_RALSO	O9b51	ralstonia s	649	5	2.1	193	1	VA57_VACCV	O01230	vaccinia vi
577	5	2.1	174	1	Y4TN_RHISN	P55668	rhizobium s	650	5	2.1	193	1	V1N3_BPP4	P13302	bacterioph
578	5	2.1	174	1	Y419_HUMAN	P09002	homo sapien	651	5	2.1	194	1	H1_SALTR	P02824	salmo trutt
579	5	2.1	175	1	CRT2_PANAN	P21668	panoeba ana	652	5	2.1	195	1	AANT_HVSI	P25883	hepatitis d
580	5	2.1	175	1	LPFE_SALTY	P43664	hallothis z	653	5	2.1	195	1	IRX3_HUMAN	P78412	homo sapien
581	5	2.1	175	1	OE56_NPVHZ	O10620	heliothis z	654	5	2.1	196	1	AMEL_MOUSE	P45559	mus musculu
582	5	2.1	175	1	VGG_BPPIX	P03643	bacterioph	655	5	2.1	196	1	RHOI_HUMAN	P01121	homo sapien
583	5	2.1	176	1	VGLI_BPMX	O91x7	bacterioph	656	5	2.1	197	1	CYCL_BACSU	O34577	bacillus su
584	5	2.1	176	1	Y140_MYCTU	O06235	mycobacteri	657	5	2.1	197	1	Y392_PSEAE	P25254	pseudomonas
585	5	2.1	177	1	GPXA_NEIMA	P52036	neisseria m	658	5	2.1	197	1	YU75_ANASP	P58632	anabena sp
586	5	2.1	178	1	HPRT_ECOLI	P36766	eschlerichia	659	5	2.1	198	1	RHOI_CANAL	O42825	candida alb
587	5	2.1	178	1	YE57_HAEIN	O57201	haemophilus	660	5	2.1	198	1	TTK_ECOLI	P06969	eschlerichia
588	5	2.1	180	1	BST2_HUMAN	O10589	homo sapien	661	5	2.1	199	1	CYCY_RHOCA	O05389	rhodobacter
589	5	2.1	180	1	GEHF_HELAN	O23968	heliandus	662	5	2.1	199	1	Y67H_RAT	P16409	rattus norv
590	5	2.1	180	1	NEF_HVNZ	P05860	human immun	663	5	2.1	199	1	Y67H_RAT	P50741	bacillus su
591	5	2.1	181	1	GSPH_ERICH	P24687	erwilia chr	664	5	2.1	200	1	DSBA_VIBCH	P32557	vibrio chol
592	5	2.1	182	1	ARL3_RAT	P07496	rattus norv	665	5	2.1	200	1	RK22_MEDSA	P49163	medicago sa
593	5	2.1	182	1	CASK_HUMAN	P37938	homo sapien	666	5	2.1	200	1	TF21_ARATH	P28167	arabidopsis
594	5	2.1	182	1	FTN_DROME	P35554	drosophila	667	5	2.1	200	1	TF21_MAIZE	P50158	zea mays (m
595	5	2.1	182	1	PTHG_ERWAM	O32521	erwilia amy	668	5	2.1	200	1	TF22_ARATH	P28148	arabidopsis
596	5	2.1	183	1	BTUE_ECOLI	P06610	eschlerichia	669	5	2.1	200	1	TF22_MAIZE	P50159	zea mays (m
597	5	2.1	183	1	H81_NEICO	P07211	neisseria g	670	5	2.1	200	1	TF2D_MESCR	P48511	mesembryant
598	5	2.1	183	1	H8_NEIMA	P57025	neisseria m	671	5	2.1	200	1	TF2D_SOLTU	P26337	solanum tub
599	5	2.1	183	1	H8_NEIMA	P57026	neisseria m	672	5	2.1	200	1	TF2D_SOYBN	O42808	glycine max
600	5	2.1	183	1	H8_NEIMA	P07212	neisseria m	673	5	2.1	200	1	TF2D_TOBAC	P93348	nicotiana t
601	5	2.1	183	1	Y81_ECOLI	P39834	eschlerichia	674	5	2.1	200	1	YORI_COYMY	O19290	comeliina y
602	5	2.1	184	1	VP50_BPAPS	O9t18	bacterioph	675	5	2.1	201	1	TF22_WHEAT	P02820	tritricum ae
603	5	2.1	185	1	AAC6_CITDI	P10051	citrobacter	676	5	2.1	201	1	TRL_PONIE	P05547	pontastacus
604	5	2.1	185	1	SPP2_YEAST	O02521	saccharomyc	677	5	2.1	202	1	RHOI_SCHPO	O09914	schizosacch
605	5	2.1	186	1	MLE1_MUCA	P82159	mugil capit	678	5	2.1	202	1	YE42_MERTJA	O58837	methanococc
606	5	2.1	186	1	VNSC_MEASA	P35977	measles vir	679	5	2.1	203	1	CLP1_MYXXA	O30612	myxococcus
607	5	2.1	186	1	VNSC_MEASE	P03494	measles vir	680	5	2.1	203	1	KGUA_PSEAE	O9ht82	pseudomonas
608	5	2.1	186	1	VNSC_MEASI	P26035	measles vir	681	5	2.1	204	1	RRA2_HUMAN	P17082	homo sapien
609	5	2.1	186	1	VALD_TRYBB	P17962	trypanosoma	682	5	2.1	205	1	KGUA_LACTA	Q9cees3	lactococcus
610	5	2.1	187	1	FMK1_ECOLI	P04740	eschlerichia	683	5	2.1	205	1	NEF_HV104	P24741	human immun
611	5	2.1	188	1	APOM_HUMAN	O95445	homo sapien	684	5	2.1	205	1	Y585_MERTJA	O58005	methanococc
612	5	2.1	188	1	RLI1_LEICH	O94292	leishmania	685	5	2.1	206	1	COX3_BACFI	O04443	bacillus fci
613	5	2.1	188	1	RLI1_LEIMA	P48112	leishmania	686	5	2.1	206	1	DC7M_PARDY	O56337	paracoccus
614	5	2.1	188	1	RNFB_PSEAE	O9hyv9	pseudomonas	687	5	2.1	206	1	HL_ONCMY	P06330	oncorhynch
615	5	2.1	188	1	TRE2_ECOLI	P08322	eschlerichia	688	5	2.1	206	1	RHTB_ECOLI	P27887	eschlerichia
616	5	2.1	188	1	TRE2_ECOLI	P10514	eschlerichia	689	5	2.1	206	1	S3AF_BACSU	P49783	bacillus su
617	5	2.1	189	1	Y006_CHLTR	O84009	chlamydia t	690	5	2.1	207	1	MGMT_HUMAN	P16445	homo sapien

691	5	2.1	207	1	UCRI_CARVI	O31214	chromatium	764	5	2.1	228	1	UL09_HCMVA	P16745	human cytom
692	5	2.1	208	1	BCRB_BACLI	P42333	bacillus 1i	765	5	2.1	228	1	VATE_EWHE	P50518	mus musculus
693	5	2.1	208	1	KTHY_AERPE	O34488	aeropyrum 1i	766	5	2.1	228	1	YTUB_ERMSE	P7826	erwinia her
694	5	2.1	209	1	HIS2_BUCAP	O9zhe0	buchnera ap	767	5	2.1	229	1	CLCB_HUMAN	P09497	homo sapien
695	5	2.1	209	1	PAAD_PSEAE	O9hx08	pseudomonas	768	5	2.1	229	1	SOML_CYCLO	P45640	cyctolpater
696	5	2.1	209	1	RH01_YEAST	P06780	saccharomyc	769	5	2.1	229	1	UNG_CHLMU	G9pj42	chlamydia m
697	5	2.1	209	1	UPE_BACHD	O9k695	bacillus ha	770	5	2.1	229	1	VG14_BP8H8	P14814	bacterioph
698	5	2.1	210	1	COX2_TRYBB	O4372	trypanosoma	771	5	2.1	229	1	Y127_TREPA	P14814	treponema p
699	5	2.1	210	1	SODM_PENCH	O75007	penicillium	772	5	2.1	230	1	COX2_CYPCA	P24987	oncorhynch
700	5	2.1	211	1	RL4_MYCGE	P47398	mycoplasma	773	5	2.1	230	1	COX2_ONCMY	P48117	oncorhynch
701	5	2.1	211	1	TIM3_HUMAN	P35625	homo sapien	774	5	2.1	230	1	COX2_SALSA	O37677	salmo salar
702	5	2.1	211	1	YFB0_YEAST	P43582	saccharomyc	775	5	2.1	230	1	Y4NF_RHITS	P55578	thizobium s
703	5	2.1	212	1	COAT_CIVW	P16486	clover yell	776	5	2.1	230	1	Y636_YEAST	P53274	saccharomyc
704	5	2.1	212	1	IF3_DEIRA	O9sm7	deinococcus	777	5	2.1	230	1	YJ02_MERTH	O27924	methanobact
705	5	2.1	212	1	KAD_STRPY	P82547	streptococc	778	5	2.1	231	1	ATMG_SALTY	P22097	salmonella
706	5	2.1	212	1	KTHY_YERPE	O69169	yersinia pe	779	5	2.1	231	1	SOML_SPAROL	P79894	spartus aura
707	5	2.1	212	1	Y440_CHLPN	O9z8a3	chlamydia p	780	5	2.1	231	1	SOML_PAROL	P20362	paratichthy
708	5	2.1	213	1	KITH_RHOST	O9ziq2	rhodothermu	781	5	2.1	231	1	SOML_SCLOC	O37677	salmo salar
709	5	2.1	213	1	Y851_STRPN	O34916	streptococc	782	5	2.1	231	1	Y236_CAMJE	O39167	scilaenops o
710	5	2.1	214	1	ACH2_LONAC	P23605	lonomita ach	783	5	2.1	231	1	YEDJ_ECOLI	O39168	campylobact
711	5	2.1	214	1	ET3_MOUSE	P48299	mus musculu	784	5	2.1	232	1	6PGL_CAUCR	P46144	escherichia
712	5	2.1	214	1	H11_HUMAN	O02539	homo sapien	785	5	2.1	232	1	HXB9_XENLA	O3661	caulobacter
713	5	2.1	214	1	NADD_MYCLE	O9cbx8	mycobacteri	786	5	2.1	232	1	YFPH_ECOLI	P31272	xenopus lae
714	5	2.1	214	1	RI9A_ARATH	O9str2	arabidopsis	787	5	2.1	233	1	ASH1_RAT	P76561	escherichia
715	5	2.1	214	1	RM06_YEAST	P32904	saccharomyc	788	5	2.1	233	1	BCL2_CHICK	P19359	rattus norv
716	5	2.1	215	1	FLA1_MERVA	P95316	methanococc	789	5	2.1	233	1	Y081_HUMAN	O00709	rattus gall
717	5	2.1	215	1	PTH_DEIRA	O9rrw3	deinococcus	790	5	2.1	234	1	GU38_RAT	O14696	homo sapien
718	5	2.1	216	1	CSGD_ECOLI	P52106	escherichia	791	5	2.1	234	1	MAUM_MERFL	P35897	rattus norv
719	5	2.1	216	1	CSGD_SALTY	O54294	salmonella	792	5	2.1	234	1	POLN_RHDV3	O50443	methyllobact
720	5	2.1	216	1	HYFE_ECOLI	P77524	escherichia	793	5	2.1	234	1	RNH2_XYLF	P27411	rabbit hemo
721	5	2.1	216	1	LEF2_NPYLD	P36869	lymantiria d	794	5	2.1	235	1	H47_STELP	O6pe17	xytelia fas
722	5	2.1	217	1	D1P_HUMAN	O9nyk4	homo sapien	795	5	2.1	235	1	HK29_MOUSE	O41348	stellaria 1
723	5	2.1	217	1	FLA2_MERVA	O58302	methanococc	796	5	2.1	235	1	RS4E_THEVO	O70594	mus musculu
724	5	2.1	217	1	RL6_CAEEL	P47991	caenorhabdi	797	5	2.1	235	1	Y332_MYCPN	O97bw4	thermoplasm
725	5	2.1	217	1	YL02_ARCEU	O28178	archaeoglob	798	5	2.1	235	1	YAEB_ECOLI	P73306	mycoplasma
726	5	2.1	218	1	HLIR_CHICK	P08288	gallus gall	799	5	2.1	236	1	ALDC_LACLA	P56676	escherichia
727	5	2.1	218	1	KTHY_CAEEL	O22018	caenorhabdi	800	5	2.1	236	1	ALDC_LACLC	P77860	lactococcus
728	5	2.1	218	1	RRAS_HUMAN	P10301	homo sapien	801	5	2.1	236	1	PGSA_MYCPL	P77860	lactococcus
729	5	2.1	218	1	RRAS_MOUSE	P10833	mus musculu	802	5	2.1	236	1	PLLI_BOVIN	P97360	mycoplasma
730	5	2.1	218	1	Y364_MYCPN	P75236	mycoplasma	803	5	2.1	236	1	PUL_SHEEP	P09611	bos taurus
731	5	2.1	219	1	ATP6_ARTRF	O37708	artemia san	804	5	2.1	236	1	YIW2_YEAST	P16038	ovis aries
732	5	2.1	219	1	BASP_RAT	O05175	rattus norv	805	5	2.1	237	1	NAPC_PARDT	P40566	saccharomyc
733	5	2.1	219	1	CAV7_PIG	P80015	sus scrofa	806	5	2.1	237	1	RL2_MERVA	O66352	paracoccus
734	5	2.1	219	1	CLD6_MOUSE	O9z262	mus musculu	807	5	2.1	238	1	KE5C_RAT	P21479	methanococc
735	5	2.1	220	1	MPB3_MYCTU	O10790	mycobacteri	808	5	2.1	238	1	NEUM_HUMAN	P56536	rattus norv
736	5	2.1	220	1	VLVS_BPPH6	P07582	bacterioph	809	5	2.1	238	1	TE2D_CHLMU	O31677	homo sapien
737	5	2.1	220	1	VM02_VARY	P34017	variola vir	810	5	2.1	238	1	Y457_CHLTR	P47633	candida alb
738	5	2.1	221	1	EP1B_BOMO	P29522	bombyx mori	811	5	2.1	238	1	Y573_CHLNP	O84463	chlamydia t
739	5	2.1	221	1	NCE3_YEAST	P36615	saccharomyc	812	5	2.1	238	1	Y742_CHLMU	O92770	chlamydia p
740	5	2.1	221	1	RANI_ARATH	P41916	arabidopsis	813	5	2.1	238	1	YIGB_ECOLI	O9pj45	chlamydia m
741	5	2.1	221	1	AMVB_SECC	P30271	secale cere	814	5	2.1	238	1	YRN7_CAEEL	P23306	escherichia
742	5	2.1	223	1	EMBP_MOUSE	O61878	mus musculu	815	5	2.1	239	1	NEUM_BOVIN	O09421	caenorhabdi
743	5	2.1	223	1	GSHU_BRUMA	P35665	brugia mala	816	5	2.1	239	1	TE2D_YEAST	P66836	bos taurus
744	5	2.1	223	1	GSHU_MUCBA	P35666	wuchereria	817	5	2.1	239	1	Y247_MYCPN	P13323	saccharomyc
745	5	2.1	223	1	KCY_BORR	O9rnb6	bordeletia	818	5	2.1	239	1	Y332_MYCGE	P75428	mycoplasma
746	5	2.1	223	1	YB23_PYRHO	O58960	pyrococcus	819	5	2.1	239	1	YG1P_YEAST	P47574	saccharomyc
747	5	2.1	223	1	YB43_YEAST	P38314	saccharomyc	820	5	2.1	240	1	8512_TTCRC	P53223	saccharomyc
748	5	2.1	224	1	Y088_MYCTU	O10885	mycobacteri	821	5	2.1	240	1	CD48_RAT	P18222	trypanosoma
749	5	2.1	224	1	Y364_MYCGE	P47604	mycoplasma	822	5	2.1	240	1	NEF_HV2D2	P10220	rattus norv
750	5	2.1	224	1	YB50_MYCPN	P75036	mycoplasma	823	5	2.1	240	1	T341_ECOLI	P15829	human immun
751	5	2.1	225	1	GDIT_HUMAN	O99819	homo sapien	824	5	2.1	240	1	YDFB_SCHPO	P11257	escherichia
752	5	2.1	226	1	BASP_HUMAN	P80724	bos taurus	825	5	2.1	241	1	MLTE_ECOLI	O10423	schizosacch
753	5	2.1	226	1	BASP_HUMAN	P80723	bos taurus	826	5	2.1	241	1	NEUM_SERCA	P76009	escherichia
754	5	2.1	226	1	I226_ASFB7	P27944	afrian swi	827	5	2.1	242	1	Y956_HELTP	O98967	serlinus can
755	5	2.1	226	1	NEUM_RAT	P07936	rattus norv	828	5	2.1	242	1	Y956_HELTP	O92k5	helicobacte
756	5	2.1	226	1	ND6M_DICDI	O37314	dicrosteali	829	5	2.1	243	1	CYL_EUGER	O25610	helicobacte
757	5	2.1	226	1	VATE_BOVIN	P11019	bos taurus	830	5	2.1	243	1	BRM1_STANU	P20114	euglena gra
758	5	2.1	227	1	COX2_BUDE	P36543	homo sapien	831	5	2.1	243	1	FOL3_HUMAN	P06699	staphylococ
759	5	2.1	227	1	NEUM_MOUSE	P06678	bubalus dep	832	5	2.1	243	1	SUMT_SYNP7	P42451	synechococ
760	5	2.1	227	1	NEUM_MOUSE	P06837	mus musculu	833	5	2.1	244	1	ATP6_BACSP	P12481	baclillus su
761	5	2.1	227	1	Y173_TREPA	O83554	treponema p	834	5	2.1	246	1	ECPD_ECOLI	P33128	escherichia
762	5	2.1	227	1	Y173_TREPA	O83203	treponema p	835	5	2.1	246	1	FLA2_AERPE	O9yan6	aeropyrum p
763	5	2.1	228	1	RPE_RHOCA	P51012	rhodobacter	836	5	2.1	246	1	NEUM_CHICK	P35001	gallus gall

837	5	2.1	246	1	NIFU_RHOSH	001180	rhodobacter	910	5	2.1	269	1	S3AD_SHITFL	P14511	shigella fl
838	5	2.1	246	1	RS2_PSEAE	082850	pseudomonas	911	5	2.1	269	1	TCEI_HUMAN	P36402	homo sapien
839	5	2.1	246	1	TF2D_TFETH	027850	tetrahymena	912	5	2.1	269	1	TRC1_SPRO	P68814	streptomyces
840	5	2.1	246	1	TRVB_RAT	P32832	rattus norv	913	5	2.1	270	1	CATA_RHOOP	P95607	rhodococcus
841	5	2.1	246	1	YEBE_ECOLI	P24237	escherichia	914	5	2.1	270	1	PSA1_ORISA	P52428	oryza sativ
842	5	2.1	246	1	YEBE_HAEIN	P44634	haemophilus	915	5	2.1	270	1	REB_HUMAN	000124	homo sapien
843	5	2.1	247	1	FLAI_THEMA	P57719	thermoplasma	916	5	2.1	270	1	YDHT_ECOLI	P77147	escherichia
844	5	2.1	247	1	SURE_THEMA	P96112	thermotoga	917	5	2.1	271	1	AOP2_HUMAN	P41131	homo sapien
845	5	2.1	247	1	TRV_RAT	P08426	rattus norv	918	5	2.1	271	1	MT04_SPRO	O95305	streptomyces
846	5	2.1	248	1	TRPC_SULSO	006121	sulfolobus	919	5	2.1	271	1	RK2_SPTOL	P06509	spiniacia ol
847	5	2.1	248	1	Y964_PSEAE	051423	pseudomonas	920	5	2.1	272	1	CY1_RHORO	P23153	rhodospirill
848	5	2.1	249	1	RIB7_KLUMA	09P408	kluyveromyc	921	5	2.1	272	1	UL24_HSVEL	P09314	equine herp
849	5	2.1	249	1	RSF2_HUMAN	P28290	homo sapien	922	5	2.1	272	1	UL24_HSVEL	P24432	equine herp
850	5	2.1	250	1	ETV3_HUMAN	P41162	homo sapien	923	5	2.1	272	1	UL24_HSVEL	P28937	equine herp
851	5	2.1	250	1	HXB9_MOUSE	P20615	mus musculu	924	5	2.1	272	1	YTDA_BACSU	P42427	baacillus su
852	5	2.1	250	1	OS35_SOLCO	P50703	solanum com	925	5	2.1	273	1	BAST_MOUSE	P18572	mus musculu
853	5	2.1	250	1	PLSC_BORBU	059188	botreilla bu	926	5	2.1	273	1	DABI_RHTLO	P58210	lactococcus
854	5	2.1	250	1	RS2_ZYMO	09X567	zymomonas m	927	5	2.1	273	1	FPG_LACIC	P42371	gallus gall
855	5	2.1	251	1	CAP7_HUMAN	P20160	homo sapien	928	5	2.1	273	1	PRIO_CHICK	P41096	hordium vul
856	5	2.1	251	1	FGFN_HUMAN	09QZV9	homo sapien	929	5	2.1	273	1	RK2_HORVU	P17788	zea mays (m
857	5	2.1	251	1	TPIS_VIBSA	056738	vibrio sp.	930	5	2.1	273	1	RK2_MAIZE	P17351	oryza sativ
858	5	2.1	252	1	BTE4_HUMAN	09bXK1	homo sapien	931	5	2.1	273	1	RK2_ORISA	P31153	pisum sativ
859	5	2.1	252	1	CEA3_HUMAN	P40198	homo sapien	932	5	2.1	273	1	RK2_PEA	P24618	micromonosp
860	5	2.1	252	1	CRB1_BOVIN	P07318	bos taurus	933	5	2.1	274	1	GRM_MICEC	P24619	micromonosp
861	5	2.1	252	1	RL7_DROME	P32100	drosophila	934	5	2.1	274	1	GRM_MICRO	P56791	arabidopsis
862	5	2.1	252	1	Y455_RICPR	09ZAD8	ricicetisia	935	5	2.1	274	1	RK2_ARATH	P30065	epifagus vl
863	5	2.1	252	1	YCX3_GUTPH	078431	guillardia	936	5	2.1	274	1	RK2_EPTVI	O9MDU0	cenothera h
864	5	2.1	253	1	CYSZ_ECOLI	P12610	escherichia	937	5	2.1	274	1	RK2_OENNO	P27107	sinapis alb
865	5	2.1	253	1	CYSZ_SALTY	P12673	salmonella	938	5	2.1	274	1	RK2_SINHL	P06379	nicotiana t
866	5	2.1	253	1	T2D7_RAT	062860	rattus norv	939	5	2.1	274	1	RK2_TOBAC	P52513	murine cyto
867	5	2.1	253	1	UI170_HUMAN	09HVD2	homo sapien	940	5	2.1	274	1	VGLL_MCNVW	P52513	murine cyto
868	5	2.1	254	1	TPIS_CHLPN	09Z616	chlamydia p	941	5	2.1	274	1	VGLL_MCNVW	P10313	homo sapien
869	5	2.1	254	1	VSPA_SOYBN	P15490	glycine max	942	5	2.1	275	1	IAXX_HUMAN	O91A23	heterodontu
870	5	2.1	254	1	VSPA_SOYBN	P10743	glycine max	943	5	2.1	275	1	HXA5_HERRR	O07942	rhodobacter
871	5	2.1	254	1	WAPA_BACST	P42018	baacillus st	944	5	2.1	275	1	N1H2_RHOCA	P56357	rhodospirill
872	5	2.1	254	1	Y935_MYCPN	P70319	mycoplasma	945	5	2.1	275	1	RK2_CHLVU	P93637	chlorella v
873	5	2.1	254	1	YABI_ECOLI	P30149	escherichia	946	5	2.1	275	1	RK2_NEPOL	O91118	nephrolelm
874	5	2.1	255	1	RS3A_CANAL	P40910	candida alb	947	5	2.1	275	1	RK2_PICAB	O62929	picea abies
875	5	2.1	255	1	P23522_ECOLI	P54461	escherichia	948	5	2.1	275	1	SC65_CANAL	O14415	candida alb
876	5	2.1	256	1	YQEU_BACSU	P54461	baacillus su	949	5	2.1	276	1	OCCF_AGRTU	P31263	nophthalmu
877	5	2.1	257	1	FCEA_HUMAN	P12319	homo sapien	950	5	2.1	276	1	RK2_MESVI	O9MUT9	mesostigma
878	5	2.1	257	1	MOTB_HELPJ	09Z129	helicobacte	951	5	2.1	276	1	RK2_PTINT	O62940	pinus thunb
879	5	2.1	257	1	MOTB_HELPJ	P56427	helicobacte	952	5	2.1	276	1	YBJR_ECOLI	P75820	escherichia
880	5	2.1	258	1	TF2D_ACACA	P26334	acanthamoeb	953	5	2.1	277	1	CLPP_HUMAN	O16740	homo sapien
881	5	2.1	258	1	VT1_SFVKA	P25946	shope fibro	954	5	2.1	277	1	DGK_MOUSE	O9QX60	mus musculu
882	5	2.1	258	1	ZM10_MOUSE	O54692	mus musculu	955	5	2.1	277	1	HXB8_NORVI	P1263	nophthalmu
883	5	2.1	259	1	CTRI_ANOGA	027289	anopheles g	956	5	2.1	277	1	MSMG_STPMU	O00751	streptococc
884	5	2.1	259	1	RUBC_CHIRE	Q42695	chlamydomon	957	5	2.1	277	1	RK2_EUGER	P19185	euglena gra
885	5	2.1	259	1	YGFW_ECOLI	Q46813	escherichia	958	5	2.1	277	1	TRPC_PSEPU	P20578	pseudomonas
886	5	2.1	260	1	AG84_MYCTU	P46816	mycobacteri	959	5	2.1	277	1	Y623_CHLPN	O9Z761	chlamydia p
887	5	2.1	260	1	H11_VOLCA	008864	volvox cart	960	5	2.1	277	1	YDB1_YEAST	P48568	saccharomyc
888	5	2.1	260	1	HA20_HUMAN	P20036	homo sapien	961	5	2.1	278	1	MA32_MOUSE	O35658	mus musculu
889	5	2.1	260	1	NEF_HV2CA	P24103	human immun	962	5	2.1	278	1	MA32_RAT	O35766	rattus norv
890	5	2.1	260	1	VP33_AFICA	Q16943	aplysia cal	963	5	2.1	278	1	RCEL_CHRVI	P31762	chroatiolum
891	5	2.1	261	1	DER3_DERPT	P39675	dermatophag	964	5	2.1	280	1	NUDC_DEIRA	O9V262	delinococcus
892	5	2.1	261	1	TRPC_RHOCA	Q02584	rhodobacter	965	5	2.1	280	1	TRY2_DROME	P24280	drosophila
893	5	2.1	261	1	XPSN_XANCP	P29040	trichomonas	966	5	2.1	280	1	Y747_RICPR	O9ZC73	rickettsia
894	5	2.1	262	1	COR4_WHEAT	P46524	tritricum ae	967	5	2.1	281	1	CEBE_HUMAN	P51574	homo sapien
895	5	2.1	262	1	S3AD_KLEPN	P08881	klebsiella	968	5	2.1	281	1	PANC_XYLPA	O9P948	xylella fas
896	5	2.1	262	1	YCJT_ECOLI	P51993	escherichia	969	5	2.1	282	1	LEPC_CIVACA	O50061	arabidopsis
897	5	2.1	263	1	S3AD_ECOLI	P04826	escherichia	970	5	2.1	282	1	AROK_ARATH	O9H040	halobacteri
898	5	2.1	264	1	HEM4_SYNP7	P42452	synecococc	971	5	2.1	282	1	TAUD_ECOLI	P67368	mus musculu
899	5	2.1	265	1	LEF5_NYPAC	P41658	autographa	972	5	2.1	282	1	YN25_MYCTU	O28918	bos taurus
900	5	2.1	265	1	PYRE_CANRU	09Hf09	candida rug	973	5	2.1	283	1	CGIC_CHICK	O59823	schizosacch
901	5	2.1	265	1	PYRE_ZYGBA	Q9Hf09	candida rug	974	5	2.1	283	1	CGIC_MOUSE	O37355	typanoplas
902	5	2.1	266	1	TF2D_STRPU	P91809	strongyloce	975	5	2.1	283	1	DAPA_MERTH	P21990	treponema p
903	5	2.1	266	1	CD82_RAT	O70332	rattus norv	976	5	2.1	284	1	AROK_HALNI	O40962	phleum prat
904	5	2.1	266	1	RK2_NICDE	P21434	nicotiana d	977	5	2.1	285	1	HXA4_MOUSE		
905	5	2.1	267	1	TRPC_MENJA	O58338	methanococ	978	5	2.1	285	1	STAR_BOVIN		
906	5	2.1	267	1	CGIC_DROME	P25008	drosophila	979	5	2.1	286	1	COX3_TRYBO		
907	5	2.1	268	1	TF2D_EMENI	Q12731	emeritella	980	5	2.1	286	1	FLAI_TREPA		
908	5	2.1	269	1	HXB5_MOUSE	P09079	mus musculu	981	5	2.1	286	1	MP5A_PHLPR		
909	5	2.1	269	1	TOD3_RANCA	P49898	rana catesb	982	5	2.1	286	1			

983	5	2.1	286	1	SYGA_THEMA	Q9wy59
984	5	2.1	287	1	DLX3_HUMAN	O60479
985	5	2.1	287	1	DLX3_MOUSE	O64205
986	5	2.1	287	1	SCF_CHICK	O09108
987	5	2.1	287	1	STXA_CAEEL	P91409
988	5	2.1	287	1	YCAE_BACSU	P40420
989	5	2.1	288	1	BLC3_PSEAE	P37322
990	5	2.1	288	1	BLC4_PSEAE	O51355
991	5	2.1	288	1	BLC6_VIBCH	P31781
992	5	2.1	288	1	BLP1_PSEAE	O03170
993	5	2.1	288	1	BLP4_PSEAE	P16897
994	5	2.1	288	1	EPMO_HUMAN	P32856
995	5	2.1	288	1	PCD1_MOUSE	O02242
996	5	2.1	288	1	PE12_YEAST	P32854
997	5	2.1	288	1	SECF_AQUAE	O67536
998	5	2.1	289	1	SUCD_THERFL	P09143
999	5	2.1	289	1	PTRI_LERTTA	P42556
1000	5	2.1	291	1	DH1L_SATSC	Q29508

## ALIGNMENTS

RESULT 1  
T10C\_HUMAN STANDARD; PRT; 259 AA.

AC 014798; 014755;  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 10C precursor (Decoy receptor 1) (DcR1) (Decoy TRAIL receptor without death domain) (TNF-related apoptosis-inducing ligand receptor 3) (TRAIL receptor 3)  
DE (TRAIL-R3) (TRAIL receptor without an intracellular domain)  
DE (Lymphocyte inhibitor of TRAIL) (Antagonist decoy receptor for TRAIL/Apo-2L)  
GN TNFRSF10C OR DCR1 OR TRAILR3 OR TRID OR LIT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RX MEDLINE=97467318; PubMed=9325248;  
RA MacFarlane M., Ahmed M., Srinivasula S.M., Fernandes-Alnemri T., Cohen G.M., Alnemri E.S.;  
RT "Identification and molecular cloning of two novel receptors for the cytotoxic ligand TRAIL.";  
RL J. Biol. Chem. 272:25417-25420(1997).  
RN [2]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC TISSUE-Foreskin fibroblast;  
RX MEDLINE=97461602; PubMed=9314565;  
RA Degisi-Esposti M.A., Smolak P.J., Malczak H., Waugh J., Huang C.-P., Dubose R.F., Goodwin R.G., Smith C.A.;  
RT "Cloning and characterization of TRAIL-R3, a novel member of the emerging TRAIL receptor family.";  
RL J. Exp. Med. 186:1165-1170(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97390508; PubMed=9242610;  
RA Pan G., Ni J., Wei Y.-F., Yu G.-L., Gentz R., Dixit V.M.;  
RT "An antagonist decoy receptor and a death domain-containing receptor for TRAIL.";  
RL Science 277:815-818(1997).  
RN [4]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF N-TERMINUS.  
RX MEDLINE=97390509; PubMed=9242611;  
RA Sheridan D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I., Goddard A.D., Godowski P., Ashkenazi A.;  
RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy receptors.";

RL Science 277:818-821(1997).  
RN [5]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC TISSUE-Liver, and Spleen;  
RX MEDLINE=98039016; PubMed=9373179;  
RA Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N., Tschopp J.;  
RT "Characterization of two receptors for TRAIL.";  
RL FEBS Lett. 416:329-334(1997).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98211672; PubMed=9551946;  
RA Mongkolsapaya J., Comper A.E., Xu X.-N., Morris G., McMichael A.J., Bell J.I., Sreaton G.R.;  
RT "Lymphocyte inhibitor of TRAIL (TNF-related apoptosis-inducing ligand): a new receptor protecting lymphocytes from the death ligand TRAIL.";  
RL J. Immunol. 160:3-6(1998).  
CC -I- FUNCTION: Receptor for the cytotoxic ligand TRAIL. Lacks a cytoplasmic death domain and hence is not capable of inducing apoptosis. May protect cells against TRAIL mediated apoptosis by competing with TRAIL-R1 and R2 for binding to the ligand.  
CC -I- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. tumor cell lines. Highly expressed in normal tissues than in lymphocytes, spleen, skeletal muscle, placenta, lung and heart.  
CC -I- PTM: N-GLYCOSYLATED AND O-GLYCOSYLATED.  
CC -I- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.  
CC -----  
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CC -----  
DR EMBL: AF020502; AAB71413.1; ALT\_INIT.  
DR EMBL: AF014794; AAC05593.1; ALT\_INIT.  
DR EMBL: AF012629; AAB67110.1; -.  
DR EMBL: AF012536; AAB67104.1; -.  
DR EMBL: AF016267; AAB81181.1; -.  
DR EMBL: AF033854; AAB87506.1; -.  
DR HSSP: P19438; 1EXT.  
DR KIM: 603613; -.  
DR InterPro: IPR001368; TNFR\_c6.  
DR Pfam: PF000020; TNFR\_c6.1.  
DR SMART: SM00208; TNFR\_1.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
KW Receptor; Apoptosis; Glycoprotein; Repeat; GPI-anchor; Signal.  
FT SIGNAL 1 23  
FT CHAIN 24 236  
FT PROPEP 237 259  
FT REPEAT 69 109  
FT REPEAT 110 149  
FT DOMAIN 162 236  
FT REPEAT 162 176  
FT REPEAT 177 191  
FT REPEAT 192 206  
FT REPEAT 207 221  
FT REPEAT 222 236  
FT DISULFID 69 85  
FT DISULFID 88 101  
FT DISULFID 91 109  
FT DISULFID 111 125  
FT DISULFID 128 141  
FT DISULFID 131 149  
FT LIPID 236 236  
FT CARBOHYD 77 77  
FT CARBOHYD 140 140

TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 10C. REMOVED IN MATURE FORM (POTENTIAL). TNFR-CYS 1. TNFR-CYS 2. 5 X 15 AA TANDEM TAPE REPEATS. 1. 2. 3. 4. 5. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. POTENTIAL. GPI-ANCHOR (POTENTIAL). N-LINKED (GLCNAC. . .) (HIGH MANNOSE) (POTENTIAL). N-LINKED (GLCNAC. . .) (HIGH MANNOSE) (POTENTIAL).

FT CARBOHYD 156 156 (POTENTIAL).  
FT N-LINKED (GLCNAC. . .) (HIGH MANNOSE)  
FT (POTENTIAL).  
FT CONFLICT 119 119 E -> V (IN REF. 5).  
FT SEQUENCE 259 AA; 27395 MM; PE3BF7FCEEA5088 CRC64;

Query Match 100.0%; Score 233; DB 1; Length 259;  
Best Local Similarity 100.0%; Pred. No. 4.2e-238;  
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTAQEEVPOQTVAPOQORHSFKSECPAGSHRSEHTGACNCPTEGVDTYNASNNEPSCF 60  
DB 27 TTAQEEVPOQTVAPOQORHSFKSECPAGSHRSEHTGACNCPTEGVDTYNASNNEPSCF 86  
QY 61 PCTVCKSDQKHSSCTMTMDVCOCKEETERNENSPENCRKSCRCPSGEVOVSNCTSDMD 120  
DB 87 PCTVCKSDQKHSSCTMTMDVCOCKEETERNENSPENCRKSCRCPSGEVOVSNCTSDMD 146  
QY 121 IQCVERGANATVETPAEETMNTSPGTPAPAEETMNTSPGTPAPAEETMNTSPGTPA 180  
DB 147 IQCVERGANATVETPAEETMNTSPGTPAPAEETMNTSPGTPAPAEETMNTSPGTPA 206  
QY 181 PAEEETMTTSGTTPAPAEETMTTSPGTPASSHTLCTVIGIIVLIVLIVFV 233  
DB 207 PAEEETMTTSGTTPAPAEETMTTSPGTPASSHTLCTVIGIIVLIVLIVFV 259

RESULT 2  
T10D\_HUMAN STANDARD; PRT; 386 AA.  
ID Q9UBN6; Q9Y6Q4;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 10D precursor (Decoy receptor 2) (Dcr2) (TNF-related apoptosis-inducing ligand receptor 4) (TRAIL receptor-4) (TRAIL-R4) (TRAIL receptor with a truncated death domain).  
GN TNFRSF10D OR DCR2 OR TRAILR4 OR TRUND.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., SEQUENCE OF N-TERMINUS, AND VARIANT.  
RC TISSUE=Fetal lung;  
RX MEDLINE=98044290; PubMed=9382840;  
RA Marsters S.A., Sheridan J.P., Pilti R.M., Huang A., Skubatch M., Baldwin D., Yuan J., Gurney A., Goddard A.D., Godowski P., Ashkenazi A.;  
RT "A novel receptor for Apo2L/TRAIL contains a truncated death domain";  
RL Curr. Biol. 7:1003-1006(1997).  
RN [2]  
RP SEQUENCE FROM N.A., CHARACTERIZATION, AND VARIANTS S-35 AND L-310.  
RC TISSUE=Forebrain fibroblast, and Peripheral blood lymphocytes;  
RX MEDLINE=98090091; PubMed=9430226;  
RA Degli-Esposti M.A., Dougal W.C., Smolak P.J., Maugh J.Y., Smith C.A., Goodwin R.G.;  
RT "The novel receptor TRAIL-R4 induces NF-kappaB and protects against TRAIL-mediated apoptosis, yet retains an incomplete death domain";  
RL Immunity 7:813-820(1997).  
RN [3]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RX MEDLINE=98196860; PubMed=9537512;  
RA Pan G., Ni J., Yu G.-L., Wei Y.-F., Dixit V.M.;  
RT "TRUND, a new member of the TRAIL receptor family that antagonizes TRAIL signaling";  
RL FEBS Lett. 424:41-45(1998).  
CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL. Contains a truncated death domain and hence is not capable of inducing apoptosis but protects against TRAIL-mediated apoptosis. Reports are contradictory with regards to its ability to induce the NF-

CC kappab pathway (According to ref.1 it cannot but according to ref.2 it can induce the NF-kappab pathway).  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- TISSUE SPECIFICITY: Widely expressed, in particular in fetal kidney, lung & liver and in adult testis and liver. Also expressed in peripheral blood leukocytes, colon and small intestine, ovary, prostate, thymus, spleen, pancreas, kidney, lung, placenta and heart.  
CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.  
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN (TRUNCATED).  
CC -----  
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CC -----  
DB EMBL; AF029761; AAD03477.1; -;  
DB EMBL; AF021232; AAC32765.1; -;  
DB EMBL; AF021233; AAC32766.1; -;  
DB EMBL; AF023849; AAC52053.1; -;  
DB HSSP; P19438; INCF.  
DB MIM; 603614; -;  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 2.  
DR SMART; SM00208; TNFR; 2.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE; PS00650; TNFR\_NGFR\_2; 2.  
KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal;  
KW Polymorphism.  
FT SIGNAL 1 55  
FT CHAIN 56 386  
FT TRANSSEM 212 232  
FT DOMAIN 233 386  
FT REPEAT 98 139  
FT REPEAT 140 180  
FT REPEAT 340 366  
FT DOMAIN 225 228  
FT DOMAIN 246 250  
FT DOMAIN 99 115  
FT DISULFID 118 131  
FT DISULFID 121 139  
FT DISULFID 141 155  
FT DISULFID 158 172  
FT CARBOHYD 162 127  
FT CARBOHYD 182 182  
FT CARBOHYD 182 182  
FT VARIANT 35 35  
FT VARIANT 310 310  
FT VARIANT 310 310  
FT SEQUENCE 386 AA; 41823 MM; 77A93577CAAE2632 CRC64;  
SQ

Query Match 6.0%; Score 14; DB 1; Length 386;  
Best Local Similarity 100.0%; Pred. No. 4.8e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 TGACNCPCTEGVDYT 50  
DB 93 TGACNCPCTEGVDYT 106

RESULT 3  
T10B\_HUMAN STANDARD; PRT; 440 AA.  
ID O14763; O15531; O15508; O15517; O14720; Q9BEVO;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)



DT 01-MAR-2002 (Rel. 41, last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 10B precursor (Death  
 DE receptor 5) (TNF-related apoptosis-inducing ligand receptor 2) (TRAIL  
 DE receptor-2) (TRAIL-R2).  
 CN TNFRSF10B OR DR5 OR TRAILR2 OR TRICK2 OR KILLER OR ZTNFR9.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NX NCBI\_TaxID:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (LONG ISOFORM), AND SEQUENCE OF N-TERMINUS.  
 RC TISSUE=ForeSkin; Fldroblast;  
 RX MEDLINE=97459925; PubMed=9311998;  
 RA Walczak H., Degli-Esposti M.A., Johnson R.S., Smolak P.J., Vaugh J.Y.,  
 RA Bolani N., Timour M.S., Gerhart M.J., Schooley K.A., Smith C.A.,  
 RA Goodwin R.G., Rauch C.T.;  
 RT "TRAIL-R2: a novel apoptosis-mediating receptor for TRAIL.";  
 RL EMO J. 16:5386-5397(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS), AND ALTERNATIVE  
 RP SPLICING.  
 RX MEDLINE=97431692; PubMed=9285725;  
 RA Scretion G.R., Mongkolsapaya J., Xu X.-N., Comper A.E.,  
 RA McMichael A.J., Bell J.I.;  
 RT "TRICK2, a new alternatively spliced receptor that transduces the  
 RT cytotoxic signal from TRAIL.";  
 RL Curr. Biol. 7:693-696(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A. (LONG ISOFORM), AND CHARACTERIZATION.  
 RC TISSUE=Liver, and Spleen;  
 RX MEDLINE=98039016; PubMed=9373179;  
 RA Schneider P., Bodmer J.-L., Thome M., Hofmann K., Holler N.,  
 RA Teschopp J.;  
 RT "Characterization of two receptors for TRAIL.";  
 RL FEBS Lett. 416:329-334(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RC TISSUE=Ovary;  
 RX MEDLINE=97467719; PubMed=9326928;  
 RA Wu G.S., Burns T.F., McDonald E.R. III, Jiang W., Meng R.,  
 RA Krantz I.D., Kao G., Gan D.D., Zhou J.Y., Muschel R., Hamilton S.R.,  
 RA Spinner N.B., Markowitz S., Wu G., el-Deiry W.S.;  
 RT "KILLER/DR5 is a DNA damage-inducible p53-regulated death receptor  
 RT gene.";  
 RL Nat. Genet. 17:141-143(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RX MEDLINE=97390508; PubMed=9242610;  
 RA Pan G., Ni J., Wei Y.-F., Yu G.-T., Gentz R., Dixit V.M.;  
 RT "An antagonist decoy receptor and a death domain-containing receptor  
 RT for TRAIL.";  
 RL Science 277:815-818(1997).  
 RN [6]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RX MEDLINE=97467318; PubMed=9325248;  
 RA McFatlaine M., Ahmed M., Srinivasula S.M., Fernandes-Alnemri T.,  
 RA Cohen G.M., Alnemri E.S.;  
 RT "Identification and molecular cloning of two novel receptors for the  
 RT cytotoxic ligand TRAIL.";  
 RL J. Biol. Chem. 272:25417-25420(1997).  
 RN [7]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RX MEDLINE=98090092; PubMed=9430227;  
 RA Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;  
 RT "Death receptor 5, a new member of the TNFR family, and DR4 induce  
 RT FADD-dependent apoptosis and activate the NF-kappaB pathway.";  
 RL Immunity 7:81-83(1997).  
 RN [8]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RX MEDLINE=97390509; PubMed=9242611;  
 RA Sheridan J.P., Masters S.A., Pitti R.M., Gurney A., Skubatch M.,  
 RA Baldwin D., Ramakrishnan L., Gray C.L., Baker K., Wood W.I.,  
 RA Goddard A.D., Godowski P., Ashkenazi A.;

RT "Control of TRAIL-induced apoptosis by a family of signaling and decoy  
 RT receptors.";  
 RL Science 277:818-821(1997).  
 RN [9]  
 RP SEQUENCE FROM N.A. (LONG ISOFORM).  
 RA Arai T., Akiyama Y., Okabe S., Saito K., Iwai T., Yusa Y.;  
 RT "Genomic structure and mutation analyses of the DR5/TRAIL receptor 2  
 RT gene in colorectal carcinoma.";  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [10]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RA Cao X., Zhang W., Wan T.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [11]  
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).  
 RA Farrar T., Vu T., Gilbert T., Cross J., O'Hara P.;  
 RT "Homo sapiens homolog of tumor necrosis factor receptor.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [12]  
 RP SEQUENCE FROM N.A. (LONG ISOFORM).  
 RC TISSUE=Cervix;  
 RA Strausberg R.;  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 54-183.  
 RX MEDLINE=20017054; PubMed=10549288;  
 RA Hymowitz S.G., Christinger H.W., Fuh G., Utsch M., O'Connell M.,  
 RA Kelley R.F., Ashkenazi A., de Vos A.M.;  
 RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a  
 RT complex with death receptor 5.";  
 RL Mol. Cell 4:563-571(1999).  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 69-184.  
 RX PubMed=10542098;  
 RA Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,  
 RA Jones E.Y., Scretion G.R.;  
 RT "Structure of the TRAIL-DR5 complex reveals mechanisms conferring  
 RT specificity in apoptotic initiation.";  
 RL Nat. Struct. Biol. 6:1048-1053(1999).  
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL; mediates  
 CC apoptosis in a caspase-dependent manner. Can trigger the nuclear  
 CC factor kappaB pathway and can bind the cytoplasmic adapter  
 CC molecule FADD/MORT1 which engages initiator caspases such as  
 CC caspase 8 leading to subsequent activation of effector caspases  
 CC that execute apoptotic death of the cell.  
 CC -1- SUBUNIT: Homotrimer (Potential). Can interact with TRADD and RIP.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM/TRICK2B (SHOWN HERE)  
 CC AND A SHORT FORM/TRICK2A; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues;  
 CC very highly expressed in tumor cell lines such as HeLa S3, K562,  
 CC HL-60, SW480, A549 and G361; highly expressed in heart, peripheral  
 CC blood lymphocytes, liver, pancreas, spleen, thymus, prostate,  
 CC ovary, uterus, placenta, testis, esophagus, stomach and throughout  
 CC the intestinal tract; not detectable in brain.  
 CC -1- INDUCTION: TNFRSF10B is regulated by the tumor suppressor p53.  
 CC -1- DISEASE: Defects in TNFRSF10B may be a cause of squamous cell  
 CC carcinoma of the head and neck.  
 CC -1- SIMILARITY: CONTAINS 1 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: AF016849; AAC51778.1; -  
 DR EMBL: AF018657; AAB70577.1; -  
 DR EMBL: AF018658; AAB70578.1; -  
 DR EMBL: AF016266; AAB81180.1; -



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DR EMBL: AF022386; AAB71949.1; -
DR EMBL: AF012628; AAB67109.1; -
DR EMBL: AF020501; AAB71412.1; -
DR EMBL: AF016268; AAC01565.1; -
DR EMBL: AF012535; AAB67103.1; -
DR EMBL: AB014718; BAA33723.1; -
DR EMBL: AB014710; BAA33723.1; JOINED.
DR EMBL: AB014711; BAA33723.1; JOINED.
DR EMBL: AB014712; BAA33723.1; JOINED.
DR EMBL: AB014713; BAA33723.1; JOINED.
DR EMBL: AB014714; BAA33723.1; JOINED.
DR EMBL: AB014715; BAA33723.1; JOINED.
DR EMBL: AB014716; BAA33723.1; JOINED.
DR EMBL: AB014717; BAA33723.1; JOINED.
DR EMBL: AF153687; AAF75587.1; -
DR EMBL: AF192548; AAF07175.1; -
DR EMBL: BC001281; AAO1281.1; -
DR MIM: 603612; -
DR MIM: 601400; -
DR PDB: 1D06; 22-OCT-99.
DR PDB: 1D4V; 01-NOV-99.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death_1.
DR Pfam: PF00020; TNFR_c6; 2.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 2.
DR PROSITE: PS00017; DEATH_DOMAIN; 1.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS00500; TNFR_NGFR_2; 2.
DR Receptor; Apoptosis; Transmembrane; Repeat; Signal;
KW Alternative splicing; 3D-structure.
FT SIGNAL 1 55
FT CHAIN 56 440
FT DOMAIN 56 210 TUMOR NECROSIS FACTOR RECEPTOR
FT TRANSMEM 211 231 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 232 440 POTENTIAL.
FT REPEAT 97 137 CYTOPLASMIC (POTENTIAL).
FT REPEAT 138 178 TNFR-CYS 1.
FT REPEAT 192 206 TNFR-CYS 2.
FT DOMAIN 339 422 TAPE.
FT DOMAIN 250 253 DEATH.
FT DISULEID 81 94 POLY-GLY.
FT DISULEID 97 113
FT DISULEID 116 129
FT DISULEID 119 137
FT DISULEID 139 153
FT DISULEID 156 170
FT DISULEID 160 178

Query Match 3.4%; Score 8; DB 1; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 95 SPEMCRRC 102
Db 149 SPEMCRRC 156

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RP SEQUENCE FROM N.A.
RC STRAIN-MSB8 / DSM 3109;
RX MEDLINE-99287316; PubMed-10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
CC -1- FUNCTION: ASSEMBLES AROUND THE ROD TO FORM THE I-RING AND PROBABLY
CC PROTECTS THE MOTOR/BASAL BODY FROM SHEARING FORCES DURING
CC ROTATION.
CC -1- SUBUNIT: THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE
CC FLAGELLAR ORGANELLE AND CONSISTS OF FOUR RINGS (L,P,S, AND M)
CC MOUNTED ON A CENTRAL ROD (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: OUTER MEMBRANE-ASSOCIATED (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE FLGH FAMILY.
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CC -----
DR EMBL: AE001800; AAD36607.1; -
DR TIGR: TM1540; -
DR InterPro: IPR000527; Flag_Lring.
DR Pfam: PF02107; FLGH; 1.
DR PRINTS: PR01008; FLAGRINGFLGH.
KM Flagella; Outer membrane; Signal; Complete proteome.
FT SIGNAL 1 25
FT CHAIN 26 199
FT SIGNAL 199 POTENTIAL.
FT SEQUENCE 199 AA; 21896 MW; D2A487647F95E22C CRC64;

Query Match 3.0%; Score 7; DB 1; Length 199;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 226 IVLLIVE 232
Db 6 IVLLIVE 12

RESULT 5
ID YJ11.MYCTU STANDARD; PRT; 205 AA.
AC 007722;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 20.2 kDa protein RV1911C.
GN RV1911C OR W11962 OR WTCY180.07.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_Taxid=1773;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RC MEDLINE-98295987; PubMed-9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holtroyd S.,
RA Hornsby T., Jagsels K., Krogh A., Mclean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

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RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence";  
 RL Nature 393:537-544(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayan L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Bishai W., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains.";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE UPF0098 FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: 297193; CAB10030.1; ALT\_INIT.  
 DR EMBL: AE007051; AAK46234.1; -.  
 DR TIGR: MT1962; -.  
 DR Tuberculist: RV1911C; -.  
 DR InterPro: IPR001858; PBP.  
 DR Pfam: PF01161; PBP; 1.  
 KM Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 205 AA; 20243 MW; 6962B69277A2DC3D CRC64;

Query Match 3.0%; Score 7; DB 1; Length 205;  
 Best Local Similarity 100.0%; Pred. No. 6.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 TPAPAE 154  
 Db 52 TPAPAE 58

RESULT 6  
 TF2D\_ARTSF STANDARD; PRT; 275 AA.  
 ID TF2D\_ARTSF  
 AC 017488;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-OCT-2001 (Rel. 40, Last annotation update)  
 DE Transcription initiation factor TFIIID (TATA-box factor) (TATA  
 DE sequence-binding protein) (TBP).  
 OS Artemia salinanciscana (Brine shrimp) (Artemia franciscana).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;  
 OC Artemiidae; Artemia.  
 OX NCBI\_TaxID=6661;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sastre L.;  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: GENERAL FACTOR THAT PLAYS A MAJOR ROLE IN THE ACTIVATION  
 CC OF EUKARYOTIC GENES TRANSCRIBED BY RNA POLYMERASE II. TFIIID BINDS  
 CC SPECIFICALLY TO THE TATA BOX PROMOTER ELEMENT WHICH LIES CLOSE TO  
 CC THE POSITION OF TRANSCRIPTION INITIATION.  
 CC -1- SUBUNIT: BINDS DNA AS A MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: BELONGS TO THE TBP FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: AJ002478; CAA05488.1; -.  
 DR HSSP: P20226; ICDW.  
 DR InterPro: IPR000814; TFIIID.  
 DR Pfam: PF00352; TBP; 2.  
 DR PRINTS: PR00686; TIEFACTORIID.  
 DR PROSITE: PS00351; TFIIID; 2.  
 KM Transcription regulation; DNA-binding; Nuclear protein; Repeat.  
 FT REPEAT 103 179 1.  
 FT REPEAT 193 270 2.  
 SQ SEQUENCE 275 AA; 30605 MW; 1F34F40C0A2EC9E7 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 275;  
 Best Local Similarity 100.0%; Pred. No. 8.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 146 GTPAPA 152  
 Db 80 GTPAPA 86

RESULT 7  
 DRRB\_STRPE STANDARD; PRT; 283 AA.  
 ID DRRB\_STRPE  
 AC P32011;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Daunorubicin resistance transmembrane protein.  
 GN DRRB.  
 OS Streptomyces peucetius  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1950;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 29050;  
 RX MEDLINE=92020891; PubMed=1924314;  
 RA Guillole P.G., Hutchinson C.R.;  
 RT "A bacterial analog of the mdr gene of mammalian tumor cells is  
 RT present in Streptomyces peucetius, the producer of daunorubicin and  
 RT doxorubicin";  
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8553-8557(1991).  
 CC -1- FUNCTION: DRRB AND DRRB MAY ACT JOINTLY TO CONFER DAUNORUBICIN AND  
 CC DOXORUBICIN RESISTANCE BY AN EXPORT MECHANISM.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
 CC (potential).  
 CC -1- SIMILARITY: BELONGS TO THE ABC-2 SUBFAMILY OF INTEGRAL MEMBRANE  
 CC PROTEINS.  
 CC -----  
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 CC -----  
 CC EMBL: M73758; AAA74718.1; -.  
 DR PIR: S27708.  
 DR InterPro: IPR000412; ABC2\_transport.  
 DR PROSITE: PS00890; ABC2\_MEMBRANE; 1.  
 KM Transport; Transmembrane; Inner membrane; Antibiotic resistance.  
 FT TRANSMEM 58 78  
 FT TRANSMEM 85 105 POTENTIAL.  
 FT TRANSMEM 150 170 POTENTIAL.  
 FT TRANSMEM 171 191 POTENTIAL.  
 FT TRANSMEM 198 218 POTENTIAL.  
 FT TRANSMEM 252 272 POTENTIAL.

SQ SEQUENCE 283 AA; 30614 MW; EC42F07A4D15C07A CRC64;  
Query Match 3.0%; Score 7; DB 1; Length 283;  
Best Local Similarity 100.0%; Pred. No. 8.8;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 172 MTSPTGT 178  
|||||||  
DB 1 MTSPTGT 7  
RESULT 8  
YDRL\_SCHPO STANDARD; PRT; 374 AA.  
AC 010354: 09URX5;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE Hypothetical 42.3 kDa protein G22E12.01 in chromosome I.  
GN SPAC22E12.01 OR SPAC890.09.  
OS Schizosaccharomyces pombe (fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE OF 1-258 FROM N.A.  
RC STRAIN=972;  
RA Saunders D., Harris D., McDougall R.C., Rajandream M.A., Barrell B.G.;  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 229-374 FROM N.A.  
RC STRAIN=972;  
RA Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;  
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
RN [1]  
RP SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
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DR EMBL: AL133498; CAB63500.1; -  
DR EMBL: Z70043; CA93888.1; -  
KW Hypothetical protein; Transmembrane.  
FT TRANSMEM 50 70  
FT TRANSMEM 151 171 POTENTIAL.  
FT TRANSMEM 175 195 POTENTIAL.  
FT TRANSMEM 201 221 POTENTIAL.  
FT TRANSMEM 238 258 POTENTIAL.  
FT TRANSMEM 273 293 POTENTIAL.  
FT TRANSMEM 329 349 POTENTIAL.  
SQ SEQUENCE 374 AA; 42300 MW; AE504D822FAF8B12 CRC64;  
Query Match 3.0%; Score 7; DB 1; Length 374;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 222 IIVLIVL 228  
|||||||  
DB 52 IIVLIVL 58  
RESULT 9  
LA\_DROME STANDARD; PRT; 390 AA.  
AC P40796: 02A375: 05YINZ;  
DT 01-FEB-1995 (Rel. 31, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)  
CN LA OR CG10922.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CANTON-S; TISSUE=Ovary;  
RX MEDLINE=94309632; PubMed=8035794;  
RA Bai C., Li Z., Tollas P.P.;  
RT "Developmental characterization of a Drosophila RNA-binding protein  
RT homologous to the human systemic lupus erythematosus-associated  
RT La/5S-B autoantigen."  
RL Mol. Cell. Biol. 14:5123-5129(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94309661; PubMed=8035818;  
RA Yoo C.J., Molin S.L.;  
RT "La proteins from Drosophila melanogaster and Saccharomyces  
RT cerevisiae: a yeast homolog of the La autoantigen is dispensable for  
RT growth."  
RL Mol. Cell. Biol. 14:5412-5424(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA April J.F., Aghayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,  
RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasly E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,  
RA De Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Fostel A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshire A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster."  
RL Science 287:2185-2195(2000).  
CC -1- FUNCTION: MAY BE INVOLVED IN TRANSCRIPTION TERMINATION BY RNA  
CC POLYMERASE III BINDS RNA AND DNA. BINDS TO PRECURSORS OF RNA  
CC POLYMERASE III TRANSCRIPTS. MAY PLAY A SPECIALIZED ROLE DURING FLY  
CC DEVELOPMENT.  
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -1- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT EMBRYONIC, LARVAL,  
CC PUPAL, AND ADULT DEVELOPMENT. EXPRESSION THROUGHOUT THE EMBRYO IS  
CC FOLLOWED BY A RESTRICTED PATTERN OF MESODERMAL EXPRESSION THAT IS  
CC LATER CONFINED TO THE VISCERAL MESODERM, GONADS, GUT, AND SALIVARY  
CC GLANDS.  
CC -1- SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).  
CC -1- SIMILARITY: TO VERTEBRATE PROTEIN LA.  
CC  
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CC  
CC EMBL: U07652; AAA20518.1; -.  
CC EMBL: L32988; AAA21776.1; -.  
CC EMBL: AE003666; AAF53885.1; -.  
CC FLYBASE: FBgn0011638; La.  
CC InterPro: IPR002344; Lupus\_La.  
CC InterPro: IPR000504; RRM.  
CC Pfam: PF00076; rrm; 1.  
CC PRINTS: PR00302; LUPUSLA.  
CC SMART: SM00360; RRM; 1.  
CC PROSITE: PS50102; RRM; 1.  
CC PROSITE: PS00030; RRM\_RNP\_1; 1.  
CC  
CC KM DOMAIN: 149 234 RNA-BINDING (RRM).  
CC FT CONFLICT 169 169 A -> T (IN REF. 1).  
CC FT CONFLICT 182 183 KH -> NS (IN REF. 1).  
CC FT CONFLICT 283 283 A -> R (IN REF. 1).  
CC FT CONFLICT 329 329 K -> N (IN REF. 1).  
CC  
CC SQ SEQUENCE 390 AA; 44884 MW; A8099288B90446A5 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 7; DB 1; Length 390;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 PAPAAEE 155  
Db 36 PAPAAEE 42

RESULT 10  
DCOR\_DATST STANDARD: PRT: 431 AA.  
AC P50134;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Ornithine decarboxylase (EC 4.1.1.17) (ODC).  
OS Datura stramonium (Jimsonweed) (Common Thornapple).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; euasterids I; Solanales; Solanaceae; Datura.  
OX NCBI\_TaxID=4076;  
RN  
RP  
RT  
RA Michael A.J., Furze J.M., Rhodes M.J.C., Burtin D.;  
RX MEDLINE=9615135; PubMed=8660289;  
RT "Molecular cloning and functional identification of a plant ornithine  
RT decarboxylase cDNA.";  
RL Biochem. J. 314:241-248(1996).  
CC -1- CATALYTIC ACTIVITY: L-ornithine = putrescine + CO(2).  
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.  
CC -1- PATHWAY: FIRST STEP AND ALSO THE RATE-LIMITING STEP IN THE PATHWAY  
CC OF POLYAMINE BIOSYNTHESIS.  
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF ORNITHINE, DAP, AND ARGinine  
CC DECARBOXYLASES.

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CC  
CC EMBL: X87847; CAA61121.1; -.  
CC DR HSSP: P00860; 70DC.  
CC DR InterPro: IPR000183; Orn\_DAP\_Arg\_decarboxylase.  
CC Pfam: PF02784; Orn\_Arg\_dec\_N; 1.  
CC Pfam: PF00278; Orn\_DAP\_Arg\_dec; 1.  
CC PRINTS: PR01179; ODACRBXLYSE.  
CC PROSITE: PS00878; ODR\_DC\_2\_1; 1.  
CC PROSITE: PS00879; ODR\_DC\_2\_2; 1.  
CC  
CC KM Lyase; Decarboxylase; Pyridoxal phosphate; Polyamine biosynthesis;  
CC phosphorylation.  
CC FT BINDING 94 94 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
CC FT ACT\_SITE 376 376 BY SIMILARITY.  
CC  
CC SQ SEQUENCE 431 AA; 46659 MW; 8168064D8CC1C9F8 CRC64;

Query Match  
Best Local Similarity 100.0%; Score 7; DB 1; Length 431;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 TPAPAAE 154  
Db 25 TPAPAAE 31

RESULT 11  
BIAR\_MOUSE STANDARD: PRT: 466 AA.  
ID BIAR\_MOUSE  
AC P34971;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Beta-1 adrenergic receptor.  
GN ADRB1 OR ADRB1R.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN  
RP  
RT  
RA Jasper J.R., Link R.E., Chruscinski A.J., Kobilka B.K., Bernstein D.;  
RT "Primary structure of the mouse beta 1-adrenergic receptor gene.";  
RL Biochem. Biophys. Acta 1178:307-309(1993).  
CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-  
CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G  
CC PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH  
CC APPROXIMATELY EQUAL AFFINITY.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS  
CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.  
CC  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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CC  
CC EMBL: L10084; AAA02929.1; -.  
CC DR PIR: S36794; S36794.  
CC DR HSSP: P07700; IDEP.  
CC GCRD: GCR\_0578; -.

DR MGD; MGI:87937; Adrb1.  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G-PROTEIN\_RECIP\_F1\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN\_RECIP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 59  
 FT TRANSMEM 60 83  
 FT DOMAIN 84 96  
 FT TRANSMEM 97 120  
 FT DOMAIN 121 131  
 FT TRANSMEM 132 155  
 FT DOMAIN 156 175  
 FT TRANSMEM 176 199  
 FT DOMAIN 200 221  
 FT TRANSMEM 222 245  
 FT DOMAIN 246 314  
 FT TRANSMEM 315 338  
 FT DOMAIN 339 345  
 FT TRANSMEM 346 369  
 FT DOMAIN 370 466  
 FT CARBOHYD 15 15  
 FT DISULFID 131 209  
 FT LIPID 381 381  
 FT MOD\_RES 296 296  
 FT MOD\_RES 301 301  
 FT MOD\_RES 401 401  
 SQ SEQUENCE 466 AA; 50479 MW; 753CD4C42BC9211 CRC64;

Query Match  
 Best Local Similarity 3.0%; Score 7; DB 1; Length 466;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 225 LIVLIV 231  
 |||||  
 Db 67 LIVLIV 73

RESULT 12  
 ID BLAR\_RAT STANDARD: PRT; 466 AA.  
 AC P18090;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DE 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Beta-1 adrenergic receptor.  
 GN ADRB1 OR ADRB1R.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90330633; PubMed=1695899;  
 RA Machida C.A., Bunzow J.R., Searles R.P., van Tol H.H.M., Tester B.,  
 RA Neve K.A., Teal P., Nipper V., Civelli O.,  
 RT "Molecular cloning and expression of the rat beta 1-adrenergic  
 RT receptor gene."  
 RL J. Biol. Chem. 265:12960-12965(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90356399; PubMed=2167473;  
 RA Shimomura H., Terada A.;  
 RT "Primary structure of the rat beta-1 adrenergic receptor gene."  
 RL Nucleic Acids Res. 18:4591-4591(1990).  
 CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-  
 CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G  
 CC PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH  
 CC APPROXIMATELY EQUAL AFFINITY.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS  
 CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 DR EMBL: J05561; AAA40792.1; -;  
 DR EMBL: D00634; BAA00527.1; -;  
 DR PIR: A36618; A36618.  
 DR PIR: S12591; S12591.  
 DR HSSP: P07700; IDEP.  
 DR GCRDB: GCR\_0126; -;  
 DR GCRDB: GCR\_0127; -;  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G-PROTEIN\_RECIP\_F1\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN\_RECIP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.  
 FT DOMAIN 1 59  
 FT TRANSMEM 60 83  
 FT DOMAIN 84 96  
 FT TRANSMEM 97 120  
 FT DOMAIN 121 131  
 FT TRANSMEM 132 155  
 FT DOMAIN 156 175  
 FT TRANSMEM 176 199  
 FT DOMAIN 200 221  
 FT TRANSMEM 222 245  
 FT DOMAIN 246 314  
 FT TRANSMEM 315 338  
 FT DOMAIN 339 345  
 FT TRANSMEM 346 369  
 FT DOMAIN 370 466  
 FT CARBOHYD 15 15  
 FT DISULFID 131 209  
 FT LIPID 381 381  
 FT MOD\_RES 296 296  
 FT MOD\_RES 301 301  
 FT MOD\_RES 401 401  
 FT CONFLICT 162 162  
 FT CONFLICT 267 267  
 SQ SEQUENCE 466 AA; 50471 MW; 2955CB02494A12B CRC64;

Query Match  
 Best Local Similarity 3.0%; Score 7; DB 1; Length 466;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 225 LIVLIV 231  
 |||||  
 Db 67 LIVLIV 73

RESULT 13  
 ID BLAR\_PIG STANDARD: PRT; 468 AA.  
 AC Q28998; Q46575;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Beta-1 adrenergic receptor.  
 GN ADRB1.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

CC NCBI\_TaxID=9623;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE=98318327; PubMed=9655595;  
 CC Cao H., Bidwell C.A., Williams S.K., Liang W., Mills S.E.;  
 CC "Nucleotide sequence of the coding region for the porcine beta1-  
 CC adrenergic receptor gene.";  
 CC J. Anim. Sci. 76:1720-1721(1998).  
 CC [2]  
 CC SEQUENCE OF 101-468 FROM N.A.  
 CC TISSUE=Heart;  
 CC McNeil R.L., Mersmann H.J.;  
 CC Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-  
 CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G  
 CC PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH  
 CC APPROXIMATELY EQUAL AFFINITY (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS  
 CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY  
 CC SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC -----  
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 CC -----  
 CC EMBL: AF042454; AAB97525.1; -  
 CC EMBL: U56425; AAC06330.1; -  
 CC HSSP: P07700; IDEP.  
 CC InterPro: IPR000276; GPCR\_Rhodpsn.  
 CC Pfam: PF00001; 7tm\_1; 1.  
 CC PRINTS: PR00237; GPCRHHODPSN.  
 CC PROSITE: PS00237; G\_PROTEIN\_RECPEP\_FL\_1; 1.  
 CC PROSITE: PS50262; G\_PROTEIN\_RECPEP\_FL\_2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein;  
 CC Multigene family; Phosphorylation; Lipoprotein; Palmitate.  
 CC DOMAIN 1 59  
 CC TRANSSEM 60 83  
 CC DOMAIN 84 96  
 CC TRANSSEM 97 121  
 CC DOMAIN 122 132  
 CC TRANSSEM 133 153  
 CC DOMAIN 154 176  
 CC TRANSSEM 177 197  
 CC DOMAIN 198 223  
 CC TRANSSEM 224 244  
 CC DOMAIN 245 315  
 CC TRANSSEM 316 336  
 CC DOMAIN 337 347  
 CC TRANSSEM 348 368  
 CC DOMAIN 369 468  
 CC CARBOHYD 15 15  
 CC LIPID 131 208  
 CC CONFLICT 173 173  
 CC CONFLICT 382 382  
 CC CONFLICT 316 316  
 CC CONFLICT 326 328  
 CC CONFLICT 448 448  
 CC CONFLICT 458 458  
 CC CONFLICT 463 464  
 CC SEQUENCE 468 AA; 50098 MM; 93C3AE7BB703225 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 468;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 225 LIVLIV 231

DB 67 LIVLIV 73  
 RESULT 14  
 ID T10A\_HUMAN STANDARD; PRT; 468 AA.  
 AC 000220;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 10A precursor (Death  
 DE receptor-1) (TRAIL-R1).  
 DE TNFRSF10A OR DR4 OR TRAILR1 OR APO2.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 CC NCBI\_TaxID=9606;  
 CC [1]  
 CC SEQUENCE FROM N.A.  
 CC MEDLINE=97238921; PubMed=9082980;  
 CC Pan G., O'Rourke K., Chinaiyan A.M., Gentz R., Edner R., Ni J.,  
 CC Dixit V.M.;  
 CC "The receptor for the cytotoxic ligand TRAIL.";  
 CC Science 276:111-113(1997).  
 CC [2]  
 CC FUNCTION.  
 CC MEDLINE=98090092; PubMed=9430227;  
 CC Chaudhary P.M., Eby M., Jasmin A., Bookwalter A., Murray J., Hood L.;  
 CC "Death receptor 5, a new member of the TNFR family, and DR4 induce  
 CC FADD-dependent apoptosis and activate the NF-kappaB pathway.";  
 CC Immunity 7:821-830(1997).  
 CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL; mediates  
 CC apoptosis in a caspase-dependent manner. Can trigger the nuclear  
 CC factor kappaB-pathway and can bind the cytoplasmic adapter  
 CC molecule FADD/MORT1 which engages initiator caspases such as  
 CC caspase 8 leading to subsequent activation of effector caspases  
 CC that execute apoptotic death of the cell.  
 CC -1- SUBUNIT: Can interact with TRADD and RIP.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: Widely expressed. High levels are found in  
 CC spleen, peripheral blood leukocytes, small intestine and thymus,  
 CC but also in K562 erythroleukemia cells, MCF7 breast carcinoma  
 CC cells and activated T-cells.  
 CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC -----  
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 CC -----  
 CC EMBL: U90875; AAC51226.1; -  
 CC HSSP: P19438; IEXT.  
 CC MIM: 603611; -  
 CC InterPro: IPR000488; Death.  
 CC InterPro: IPR001368; TNFR\_c6.  
 CC Pfam: PF00051; death; 1.  
 CC Pfam: PF00020; TNFR\_c6; 2.  
 CC SMART: SM00005; DEATH; 1.  
 CC SMART: SM00208; TNFR; 2.  
 CC PROSITE: PS00652; TNFR\_NGFR\_1; 1.  
 CC PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 CC PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 CC Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.  
 CC SIGNAL 1 23  
 CC CHAIN 24 468  
 CC DOMAIN 24 239  
 CC SUPPLEMENTARY MEMBER 10A.  
 CC EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 240 262 POTENTIAL.
FT DOMAIN 263 468 CYTOPLASMIC (POTENTIAL).
FT REPEAT 147 188 TNFR-CYS 1.
FT REPEAT 189 229 TNFR-CYS 2.
FT DOMAIN 365 448 DEATH.
FT DOMAIN 29 32 POLY-ALA.
FT DISULFID 132 145 POTENTIAL.
FT DISULFID 148 164 POTENTIAL.
FT DISULFID 167 180 POTENTIAL.
FT DISULFID 170 188 POTENTIAL.
FT DISULFID 190 204 POTENTIAL.
FT DISULFID 207 221 POTENTIAL.
FT DISULFID 211 229 POTENTIAL.
FT CARBOHYD 156 156 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 468 AA; 50025 MW; 1E85DDC2C8760F7 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 468;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 YTNASN 55
|111111|
Db 154 YTNASN 160

RESULT 15
UFO2_MAIZE STANDARD; PRT; 471 AA.
ID UFO2_MAIZE
AC P16165;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (UDP-glucose flavonoid
  3-O-glucosyltransferase) (Bronze-1) (Bz-MC2 allele).
GN BZ1 OR UGT71A1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Furtak D., Schiefelbein J.W., Johnston F., Nelson O.E. Jr.;
RT "Sequence comparisons of 3 wild-type bronze-1 alleles from Zea mays.";
RL Plant Mol. Biol. 11:473-481(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88284304; PubMed=3396861;
RA Raiston E.J., English J.J., Dooner H.K.;
RT "Sequence of three bronze alleles of maize and correlation with the
RT genetic fine structure.";
RL Genetics 119:185-197(1988).
CC -1- FUNCTION: IN THE PRESENCE OF OTHER NECESSARY COLOR FACTORS, THIS
CC GLYCOSYLATION REACTION ALLOWS THE ACCUMULATION OF ANTHOCYANIN
CC PIGMENTS.
CC -1- CATALYTIC ACTIVITY: UDP-glucose + a flavanol = UDP + flavanol
CC 3-O-D-glucoside.
CC -1- PATHWAY: Anthocyanin biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC -----
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CC -----
CC EMBL: X13500; CAA31855.1; -
CC DR EMBL: X07940; CAA30761.1; -
CC PTR: S01052; S01052.
CC PTR: S08324; S08324.

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DR MaizeDB; 13885; -
DR InterPro; IPR002213; UDPGT.
DR Pfam; PF00201; UDPGT; 2.
DR PROSITE; PS00375; UDPGT; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 471 AA; 48769 MW; 6234FD59219AF534 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 471;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 APAEET 156
|111111|
Db 83 APAEET 89

RESULT 16
UFO2_MAIZE STANDARD; PRT; 471 AA.
ID UFO2_MAIZE
AC P16165;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Flavonol 3-O-glucosyltransferase (EC 2.4.1.91) (UDP-glucose flavonoid
  3-O-glucosyltransferase) (Bronze-1) (Bz-MC2 allele).
GN BZ1 OR UGT71A1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Furtak D., Schiefelbein J.W., Johnston F., Nelson O.E. Jr.;
RT "Sequence comparisons of 3 wild-type bronze-1 alleles from Zea mays.";
RL Plant Mol. Biol. 11:473-481(1988).
CC -1- FUNCTION: IN THE PRESENCE OF OTHER NECESSARY COLOR FACTORS, THIS
CC GLYCOSYLATION REACTION ALLOWS THE ACCUMULATION OF ANTHOCYANIN
CC PIGMENTS.
CC -1- CATALYTIC ACTIVITY: UDP-glucose + a flavanol = UDP + flavanol
CC 3-O-D-glucoside.
CC -1- PATHWAY: Anthocyanin biosynthesis.
CC -1- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X13501; CAA31856.1; -
CC DR EMBL: X08325; S08325.
CC DR MaizeDB; 13885; -
CC DR InterPro; IPR002213; UDPGT.
CC DR Pfam; PF00201; UDPGT; 2.
CC DR PROSITE; PS00375; UDPGT; 1.
CC KW Transferase; Glycosyltransferase.
CC SQ SEQUENCE 471 AA; 48621 MW; 81B897410A361299 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 471;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 APAEET 156
|111111|
Db 83 APAEET 89

RESULT 17

```



BLAR\_CANFA STANDARD: PRT: 473 AA.

ID BLAR\_CANFA STANDARD: PRT: 473 AA.

AC P79148;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Beta-1 adrenergic receptor.

GN ADRB1.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OC NCBI\_TaxID=9615;

RN [1]

RX MEDLINE=97364078; PubMed=9220370;

RA Huang R.-R.C., Rapoport D., Schaeffer M.-T., Cascleri M.A.,

RA Fong I.M.,

RT "Molecular cloning of the dog beta 1 and beta 2 adrenergic receptors."

RL J. Recept. Signal Transduct. Res. 17:599-607(1997).

CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH APPROXIMATELY EQUAL AFFINITY.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC -----

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CC -----

DR EMBL: U73207; AAB93648.1; -

DR HSSP: P07700; IDEP.

DR GCRDB: GCR.1183; -

DR InterPro: IPR000276; GPCR\_Rhodopsn.

DR Pfam: PF00001; 7tm\_1; 1.

DR PRINTS: PR00237; GPCR\_Rhodopsn.

DR PROSITE: PS00237; G-PROTEIN\_RECPT\_F1\_1; 1.

DR PROSITE: PS50262; G-PROTEIN\_RECPT\_F1\_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Phosphorylation; Lipoprotein; Palmitate.

KM Multigene family: Phosphorylation; Lipoprotein; Palmitate.

FT DOMAIN 1 59 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 60 83 1 (POTENTIAL).

FT DOMAIN 84 96 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 97 120 2 (POTENTIAL).

FT DOMAIN 121 131 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 132 155 3 (POTENTIAL).

FT DOMAIN 156 175 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 176 199 4 (POTENTIAL).

FT DOMAIN 200 221 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 222 245 5 (POTENTIAL).

FT DOMAIN 246 322 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 323 346 6 (POTENTIAL).

FT DOMAIN 347 353 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 354 377 7 (POTENTIAL).

FT DOMAIN 378 473 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 15 15 N-LINKED (GLCNAc. . .) (PROBABLE).

FT DISULFID 131 209 N-LINKED (GLCNAc. . .) (PROBABLE).

FT MOD\_RES 309 309 PHOSPHORYLATION (BY CAPK) (POTENTIAL).

FT LIPID 389 389 PALMITATE (BY SIMILARITY).

SO SEQUENCE 473 AA; 50060 MW; 361357F7DF9BDB7E CRC64;

OY 225 LIVELIV 231

DB 67 LIVELIV 73

RESULT 18

BLAR\_FELCA STANDARD: PRT: 474 AA.

ID BLAR\_FELCA STANDARD: PRT: 474 AA.

AC O92876;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Beta-1 adrenergic receptor.

GN ADRB1.

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OC NCBI\_TaxID=9685;

RN [1]

RX MEDLINE=97364078; PubMed=9220370;

RA Huang R.-R.C., Rapoport D., Schaeffer M.-T., Cascleri M.A.,

RA Fong I.M.,

RT "Molecular cloning of the dog beta 1 and beta 2 adrenergic receptors."

RL J. Recept. Signal Transduct. Res. 17:599-607(1997).

CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH APPROXIMATELY EQUAL AFFINITY (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC -----

DR EMBL: AF192344; AAF04303.1; -

DR HSSP: P07700; IDEP.

DR GCRDB: GCR.1183; -

DR InterPro: IPR000276; GPCR\_Rhodopsn.

DR Pfam: PF00001; 7tm\_1; 1.

DR PRINTS: PR00237; GPCR\_Rhodopsn.

DR PROSITE: PS00237; G-PROTEIN\_RECPT\_F1\_1; 1.

DR PROSITE: PS50262; G-PROTEIN\_RECPT\_F1\_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Phosphorylation; Lipoprotein; Palmitate.

KM Multigene family: Phosphorylation; Lipoprotein; Palmitate.

FT DOMAIN 1 59 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 60 83 1 (POTENTIAL).

FT DOMAIN 84 96 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 97 120 2 (POTENTIAL).

FT DOMAIN 121 131 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 132 155 3 (POTENTIAL).

FT DOMAIN 156 175 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 176 199 4 (POTENTIAL).

FT DOMAIN 200 221 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 222 245 5 (POTENTIAL).

FT DOMAIN 246 322 CYTOPLASMIC (POTENTIAL).

FT TRANSSEM 323 346 6 (POTENTIAL).

FT DOMAIN 347 353 EXTRACELLULAR (POTENTIAL).

FT TRANSSEM 354 377 7 (POTENTIAL).

FT DOMAIN 378 474 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 15 15 N-LINKED (GLCNAc. . .) (PROBABLE).

FT DISULFID 131 209 N-LINKED (GLCNAc. . .) (PROBABLE).

FT MOD\_RES 309 309 PHOSPHORYLATION (BY CAPK) (POTENTIAL).

FT LIPID 389 389 PALMITATE (BY SIMILARITY).

SO SEQUENCE 474 AA; 50532 MW; 2FC97EDEACFB7C3F CRC64;

Query Match 3.0%; Score 7; DB 1; Length 473;

Best Local Similarity 100.0%; Pred. NO. 14;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Query Match 3.0%; Score 7; DB 1; Length 474;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVILLIV 231  
 |||||  
 Db 67 LIVILLIV 73

RESULT 19

BIAR\_HUMAN STANDARD; PRT; 477 AA.  
 AC P08588; Q90K68; Q90K67;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Beta-1 adrenergic receptor.  
 GN ADRB1 OR ADRB1R OR B1AR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NC NCBL\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RA MEDLINE=88068509; PubMed=2825170;  
 RA Fietelle T., Collins S., Daniel K.W., Caron M.G., Lefkowitz R.J.,  
 RA Koblika B.K.;  
 RT Cloning of the cDNA for the human beta 1-adrenergic receptor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7920-7924(1987).  
 RN [2]  
 RP VARIANT ARG-389.  
 RX MEDLINE=99230291; PubMed=10212248;  
 RA Mason D.A., Moore J.D., Green S.A., Liggett S.B.;  
 RT "A gain-of-function polymorphism in a G-protein coupling domain of the  
 RT human beta1-adrenergic receptor.";  
 RL J. Biol. Chem. 274:12670-12674(1999).  
 RN [3]  
 RP VARIANTS GLY-49 AND ARG-389.  
 RX MEDLINE=99407229; PubMed=10477438;  
 RA Moore J.D., Mason D.A., Green S.A., Hsu J., Liggett S.B.;  
 RT "Racial differences in the frequencies of cardiac beta(1)-adrenergic  
 RT receptor polymorphisms: analysis of c145A>G and c165G>C.";  
 RL Hum. Mutat. 14:271-271(1999).  
 RN [4]  
 RP VARIANT GLY-49.  
 RX MEDLINE=20507547; PubMed=11052857;  
 RA Borjesson M., Magnusson Y., Hjalmarsson A., Andersson B.;  
 RT "A novel polymorphism in the gene coding for the beta(1)-adrenergic  
 RT receptor associated with survival in patients with heart failure.";  
 RL Eur. Heart J. 21:1853-1858(2000).  
 CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-  
 CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G  
 CC PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH  
 CC APPROXIMATIVELY EQUAL AFFINITY.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- PTM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS  
 CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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 CC  
 CC EMBL: J03019; AAA51667.1; -;  
 CC EMBL: AF169006; AAD53696.1; -;  
 CC EMBL: AF169007; AAD53697.1; -;  
 CC DR A39911; A39911.  
 CC HSP; P07700; IDEP.

DR GCRD; GCR\_0048; -;  
 DR MIM; 109630; -;  
 DR InterPro: IPR000276; GPCR\_Rhodopsin.  
 DR Pfam: PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHOOPS.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECPEP\_F1\_1;  
 DR PROSITE; PS50262; G\_PROTEIN\_RECPEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Phosphorylation; Lipoprotein; Palmitate;  
 KW polymorphism.

FT DOMAIN 1 59 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 60 83 1 (POTENTIAL).  
 FT DOMAIN 84 96 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 97 120 2 (POTENTIAL).  
 FT DOMAIN 121 131 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 132 155 3 (POTENTIAL).  
 FT DOMAIN 156 175 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 176 199 4 (POTENTIAL).  
 FT DOMAIN 200 221 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 222 245 5 (POTENTIAL).  
 FT DOMAIN 246 325 CYTOPLASMIC (POTENTIAL).  
 FT TRANSSEM 326 349 6 (POTENTIAL).  
 FT DOMAIN 350 356 EXTRACELLULAR (POTENTIAL).  
 FT TRANSSEM 357 380 7 (POTENTIAL).  
 FT DOMAIN 381 477 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 15 15 N-LINKED (GLCNAC. . .) (PROBABLE).  
 FT DISULFID 131 209 BY SIMILARITY.  
 FT MOD\_RES 312 312 PHOSPHORYLATION (BY CARK) (POTENTIAL).  
 FT MOD\_RES 412 412 PHOSPHORYLATION (BY CAPK) (POTENTIAL).  
 FT LIPID 392 392 PALMITATE (BY SIMILARITY).  
 FT VARIANT 49 49 S -> G.  
 FT /FTID=VAR\_009879.  
 FT VARIANT 389 389 G -> R (ENHANCED BINDING TO G PROTEINS).  
 FT /FTID=VAR\_009880.  
 SQ SEQUENCE 477 AA; 51223 MW; 1D15E6350B564B8 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 477;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVILLIV 231  
 |||||  
 Db 67 LIVILLIV 73

RESULT 20

BIAR\_MACMU STANDARD; PRT; 480 AA.  
 AC P47899;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Beta-1 adrenergic receptor.  
 GN ADRB1.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 NC NCBL\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95078456; PubMed=7987008;  
 RA Seattles R.P., Nipper V.J., Maehla C.A.;  
 RT "The rhesus macaque beta 1-adrenergic receptor gene: structure of the  
 RT gene and comparison of the flanking sequences with the rat beta 1-  
 RT adrenergic receptor gene.";  
 RL DNA Seq. 4:231-241(1994).  
 CC -1- FUNCTION: BETA-ADRENERGIC RECEPTORS MEDIATE THE CATECHOLAMINE-  
 CC INDUCED ACTIVATION OF ADENYLATE CYCLASE THROUGH THE ACTION OF G  
 CC PROTEINS. THIS RECEPTOR BINDS EPINEPHRINE AND NOREPINEPHRINE WITH  
 CC APPROXIMATIVELY EQUAL AFFINITY.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

```

CC -1- PWM: HOMOLOGOUS DESENSITIZATION OF THE RECEPTOR IS MEDIATED BY ITS
CC PHOSPHORYLATION BY BETA-ADRENERGIC RECEPTOR KINASE.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X75540; CA53228.1; -
DR HSSP: P07700; IDEP.
DR GCRDB: GCR_1746; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_FL_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 59
FT TRANSMEM 60 83
FT DOMAIN 84 96
FT TRANSMEM 97 120
FT DOMAIN 121 131
FT TRANSMEM 132 155
FT DOMAIN 156 175
FT TRANSMEM 176 199
FT DOMAIN 200 221
FT TRANSMEM 222 245
FT DOMAIN 246 328
FT TRANSMEM 329 352
FT DOMAIN 353 359
FT TRANSMEM 360 383
FT DOMAIN 384 480
FT CARBOYD 15 15
FT DISULFID 131 209
FT MOD_RES 315 315
FT MOD_RES 415 415
FT LIPID 395 395
SQ SEQUENCE 480 AA; 51608 MW; 25CB18FA03128084 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 480;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVLLIV 231
DB 67 LIVLLIV 73

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RL Proc. Natl. Acad. Sci. U.S.A. 91:9832-9836(1994).
RN [2]
RP REVISIONS TO 69-70.
RA Salir B.H.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP CHARACTERIZATION.
RX MEDLINE-93087514; PubMed-1333606;
RA Subramanian S.V., Salir B.H.;
RT "Carbohydrate cycling in signal transduction: parafusin, a
RT phosphoglycoprotein and possible Ca(2+)-dependent transducer molecule
RT in exocytosis in Paramacium."
RL Proc. Natl. Acad. Sci. U.S.A. 89:11297-11301(1992).
CC -1- FUNCTION: MAY BE INVOLVED IN MEMBRANE FUSION IN EXOCYTOSIS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PWM: PHOSPHORYLATED VIA A CALCIUM-DEPENDENT PROTEIN KINASE.
CC -1- PWM: O-GLYCOSYLATED WITH A SHORT CHAIN OF MANNOSE RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOHEXOSE MUTASES FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L12471; AAB05649.2; -
DR HSSP: P00949; 3PMG.
DR InterPro: IPR001485; PGM_PMM.
DR Pfam: PF00408; PGM_PMM; 1.
DR Pfam: PF02878; PGM_PMM_I; 1.
DR Pfam: PF02879; PGM_PMM_II; 1.
DR Pfam: PF02880; PGM_PMM_III; 1.
DR PRINTS: PR00509; PGM_PMM.
DR PROSITE: PS00710; PGM_PMM; 1.
KW Phosphorylation.
FT ACT_SITE 138
FT ACT_SITE 138
SQ SEQUENCE 584 AA; 65312 MW; D96ED7D815D25A22 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 584;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 TPASSHY 214
DB 112 TPASSHY 118

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RESULT 21
ID PARF_PARTE STANDARD; PRT; 584 AA.
AC P47244;
DT 01-FEB-1996 (Rel. 33, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Parafusin.
OS Paramacium tetraurelia.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Penicillida;
OC Paramacium.
OX NCBI_TaxID=5888;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-STOCK 51;
RX MEDLINE-95024055; PubMed-7937900;
RA Subramanian S.V., Myroba E., Andersen A.P., Salir B.H.;
RT "Cloning and sequencing of parafusin, a calcium-dependent exocytosis-
RT related phosphoglycoprotein."

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RESULT 22
ID CYSJ_ECOLI STANDARD; PRT; 598 AA.
AC P38038; P14782;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sulfite reductase [NADPH] flavoprotein alpha-component (EC 1.8.1.2)
DE (STR-PP).
GN CYSJ OR B2764.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B;
RX MEDLINE-89380164; PubMed-2550423;
RA Ostrowski J., Barber M.J., Rueger D.C., Miller B.E., Siegel L.M.,
RA Kredich N.M.;
RT "Characterization of the flavoprotein moieties of NADPH-sulfite
RT reductase from Salmonella typhimurium and Escherichia coli."

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RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltham T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jajels K., Lacroix C., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrett B.G.;
RT "Massive gene decay in the leprosy bacillus.";
RL Nature 409:1007-1011(2001).
CC -1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
CC RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
CC THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
CC THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
CC + [DNA] (N).
CC -1- SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA
CC CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE
CC DIMERIZATION TO FORM THE POLIIT' COMPLEX. POLIIT' ASSOCIATES WITH
CC THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI,
CC AND CHI) AND WITH THE BETA CHAIN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-C FAMILY. DNAE
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL: AL049478; CAB39586.1; -.
DR EMBL: AL583921; CAC31588.1; -.
DR Leproma; ML1207; -.
DR Interpro: IPR004013; PHP_C.
DR Interpro: IPR003141; PHP_N.
DR Interpro: IPR002309; tRNA-synt_2.
DR Pfam: PF02811; PHP_C; 1.
DR Pfam: PF02231; PHP_N; 1.
DR Pfam: PF01336; tRNA_ant1; 1.
DR SMART: SM00481; POLIITAC; 1.
DR Transferrase: DNA-directed DNA polymerase; DNA replication;
KW Complete proteome.
SQ SEQUENCE 1177 AA; 128971 MW; E53599FE950DDB6B CRC64;

Query Match 3.08; Score 7; DB 1; Length 1177;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 105 CPSEGEVQ 111
Db 154 CPSEGEVQ 160

RESULT 25
DP3A_SPRCO
ID DP3A_STRCO STANDARD; PRT; 1179 AA.
AC Q92618;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA polymerase III alpha subunit (EC 2.7.7.7).
GN DNAB OR SC46.33C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RC SEQUENCE FROM N.A.
RA STRAIN=M145;

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RX MEDLINE=99157597; PubMed=10048037;
RA Flett F., Jungmann-Campello D., Mersinias V., Koh S.L.-M., Godden R.,
RA Smith C.P.;
RT "A 'Gram-negative-type' DNA polymerase III is essential for
RT replication of the linear chromosome of Streptomyces coelicolor
RT A3(2).";
RL Mol. Microbiol. 31:949-958(1999).
RN [2]
RC SEQUENCE FROM N.A.
RA STRAIN=A3(2).
RA Seeger K.J., Harris D., Bentley S.D., Parkhill J., Barrett B.G.,
RA Rajandream M.A.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
CC RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.
CC THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
CC THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
CC + [DNA] (N).
CC -1- SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA
CC CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOW THE CORE
CC DIMERIZATION TO FORM THE POLIIT' COMPLEX. POLIIT' ASSOCIATES WITH
CC THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI,
CC AND CHI) AND WITH THE BETA CHAIN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-C FAMILY. DNAE
CC SUBFAMILY.
CC -----
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CC -----
DR EMBL: AF108191; AADI6978.1; -.
DR EMBL: AL096884; CAB31456.1; -.
DR Interpro: IPR004013; PHP_C.
DR Interpro: IPR003141; PHP_N.
DR Interpro: IPR002309; tRNA-synt_2.
DR Pfam: PF02811; PHP_C; 1.
DR Pfam: PF02231; PHP_N; 1.
DR Pfam: PF01336; tRNA_ant1; 1.
DR SMART: SM00481; POLIITAC; 1.
DR Transferrase: DNA-directed DNA polymerase; DNA replication.
KW VARIANT E->K (IN MUTANT TS-38).
FT VARIANT 802 802 E->K (IN MUTANT TS-38).
SQ SEQUENCE 1179 AA; 130795 MW; 7E4B58675B634CD3 CRC64;

Query Match 3.08; Score 7; DB 1; Length 1179;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 105 CPSEGEVQ 111
Db 154 CPSEGEVQ 160

RESULT 26
DP3A_MYCTU
ID DP3A_MYCTU STANDARD; PRT; 1184 AA.
AC Q10779;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA polymerase III alpha subunit (EC 2.7.7.7).
GN DNAB OR DNAB1 OR RV1547 OR MT1598 OR MYCY48.18C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]

```

RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornby T., Jags K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains.";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTISUBUNIT ENZYME  
 CC RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA.  
 CC THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.  
 CC THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate  
 CC + [DNA](N).  
 CC -1- SUBUNIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THETA  
 CC CHAINS) THAT ASSOCIATES WITH A TAU SUBUNIT WHICH ALLOWS THE CORE,  
 CC DIMERIZATION TO FORM THE POLIIT' COMPLEX. POLIIT' ASSOCIATES WITH  
 CC THE GAMMA COMPLEX (COMPOSED OF CHAINS GAMMA, DELTA, DELTA', PSI,  
 CC AND CHI) AND WITH THE BETA CHAIN (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-C FAMILY. DNAAE  
 CC SUBFAMILY.  
 CC  
 CC -----  
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 CC -----  
 CC EMBL: Z74020; CAA98315.1; -;  
 DR EMBL: AE007026; AAK45865.1; -;  
 DR TIGR: MT1598; -;  
 DR Tuberculist: RV1547; -;  
 DR InterPro: IPR004013; PHP\_C.  
 DR InterPro: IPR003141; PHP\_M.  
 DR InterPro: IPR002309; tRNA-synt\_2.  
 DR Pfam: PF02811; PHP\_C; 1.  
 DR Pfam: PF02231; PHP\_N; 1.  
 DR Pfam: PF01336; tRNA\_anti; 1.  
 DR SMART: SM00481; POLIITac; 1.  
 KW Transferrase; DNA-directed DNA polymerase; DNA replication;  
 KW Complete proteome.  
 SQ SEQUENCE 1184 AA; 129322 MW; A87AB7F0F2E08909 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 1184;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 CPSEGEVQ 111  
 |||||  
 DB 158 CPSEGEVQ 164

RESULT 27  
 MRSP\_STAU STANDARD; PRT; 1637 AA.  
 ID MRSP\_STAU  
 AC P80544; O92F62;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Methicillin-resistant surface protein precursor.  
 GN P1S.  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Staphylococcus.  
 OX NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ISOLATE 1061;  
 RA Savolainen K., Kuusela P., Paulin L., Korhonen T.K.;  
 RT "P1S, a large repeat-rich surface protein of methicillin resistant  
 RT Staphylococcus aureus.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 624-628; 676-682; 938-948; 1156-1168; 1176-1185;  
 RP 1199-1205 AND 1217-1224.  
 RC STRAIN-ISOLATE 1061;  
 RX MEDLINE=96270743; PubMed=8665912;  
 RA Hilden P., Savolainen K., Tyynelae J., Vuento M., Kuusela P.;  
 RT "Purification and characterisation of a plasmin-sensitive surface  
 RT protein of Staphylococcus aureus.";  
 RL Eur. J. Biochem. 236:904-910(1996).  
 CC  
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 CC -----  
 CC EMBL: AF115379; AAD09131.1; -;  
 DR InterPro: IPR001899; Gram\_pos\_anchor.  
 DR Pfam: PF00746; Gram\_pos\_anchor; 1.  
 DR PROSITE: PS00343; GRAM\_POS\_ANCHORING; FALSE\_NEG.  
 KW Cell wall; Transmembrane; Antibiotic resistance; Glycoprotein; Repeat;  
 KW Signal.  
 FT SIGNAL 49 48  
 FT CHAIN 1 1637 POTENTIAL.  
 FT DOMAIN 1301 1582 METHICILLIN-RESISTANT SURFACE PROTEIN.  
 FT DOMAIN 1598 1603 141 X 2 AA TANDEM REPEATS OF D-[SAG].  
 FT CONSERVED IN GRAM-POSITIVE COCCI SURFACE  
 FT PROTEINS.  
 SQ SEQUENCE 1637 AA; 174573 MW; 75BE9ADB469BD309 CRC64;

Query Match 3.0%; Score 7; DB 1; Length 1637;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 APAAEET 156  
 |||||  
 DB 183 APAAEET 189

RESULT 28  
 CCAL\_RAT STANDARD; PRT; 1835 AA.  
 ID CCAL\_RAT  
 AC O92078;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Voltage-dependent T-type calcium channel alpha-1I subunit (CAVT.3).  
 GN CACNA1I.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;  
 RX MEDLINE=99165796; PubMed=10066244;  
 RA Lee J.-H., Daud A.N., Cribbs L.L., Lacerda A.E., Pereverzev A.,  
 RA Kloeckner U., Schneider T., Perez-Reyes E.;  
 RT "Cloning and expression of a novel member of the low voltage-activated  
 RT T-type calcium channel family.";  
 RL J. Neurosci. 19:1912-1921(1999).  
 CC -1- FUNCTION: VOLTAGE-SENSITIVE CALCIUM CHANNELS (VSCC) MEDIANE THE  
 CC ENTRY OF CALCIUM IONS INTO EXCITABLE CELLS AND ARE ALSO INVOLVED  
 CC IN A VARIETY OF CALCIUM-DEPENDENT PROCESSES, INCLUDING MUSCLE  
 CC CONTRACTION, HORMONE OR NEUROTRANSMITTER RELEASE, GENE EXPRESSION,  
 CC CELL MOTILITY, CELL DIVISION AND CELL DEATH. THE ISOFORM ALPHA-11  
 CC GIVES RISE TO T-TYPE CALCIUM CURRENTS. T-TYPE CALCIUM CHANNELS  
 CC BELONG TO THE "LOW-VOLTAGE ACTIVATED (LVA)" GROUP AND ARE STRONGLY  
 CC BLOCKED BY NICKEL AND MIBEFRAZIL. A PARTICULARITY OF THIS TYPE OF  
 CC CHANNELS IS AN OPENING AT QUITE NEGATIVE POTENTIALS, AND A  
 CC VOLTAGE-DEPENDENT INACTIVATION. T-TYPE CHANNELS SERVE PACEMAKING  
 CC FUNCTIONS IN BOTH CENTRAL NEURONS AND CARDIAC NODAL CELLS AND  
 CC SUPPORT CALCIUM SIGNALING IN SECRETORY CELLS AND VASCULAR SMOOTH  
 CC MUSCLE. THEY MAY ALSO BE INVOLVED IN THE MODULATION OF FIRING  
 CC PATTERNS OF NEURONS WHICH IS IMPORTANT FOR INFORMATION PROCESSING  
 CC AS WELL AS IN CELL GROWTH PROCESSES. GATES IN VOLTAGE RANGES  
 CC SIMILAR TO, BUT HIGHER THAN ALPHA 1G OR ALPHA 1H.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: BRAIN.  
 CC -1- DOMAIN: EACH OF THE FOUR INTERNAL REPEATS CONTAINS FIVE  
 CC HYDROPHOBIC TRANSMEMBRANE SEGMENTS (S1, S2, S3, S5, S6) AND ONE  
 CC POSITIVELY CHARGED TRANSMEMBRANE SEGMENT (S4). S4 SEGMENTS  
 CC PROBABLY REPRESENT THE VOLTAGE-SENSOR AND ARE CHARACTERIZED BY A  
 CC SERIES OF POSITIVELY CHARGED AMINO ACIDS AT EVERY THIRD POSITION.  
 CC -1- PTM: IN RESPONSE TO RAISING OF INTRACELLULAR CALCIUM, THE T-TYPE  
 CC CHANNELS ARE ACTIVATED BY CAM-KINASE II (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE CALCIUM CHANNEL ALPHA-1 SUBUNITS  
 CC FAMILY.  
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 CC -----  
 CC EMBL: AF086827; AAD17796.1; -.  
 CC InterPro: IPR002077; Ca\_channel.  
 CC InterPro: IPR002111; Cal\_channel\_Typl.  
 CC InterPro: IPR000636; Calcium\_chan\_non\_11g.  
 CC InterPro: IPR001682; Channel\_pore\_Ca\_Na.  
 CC Pfam: PF00520; Ion\_trans\_4.  
 CC PRINTS: PR00167; CACHANNEL.  
 CC DR Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;  
 CC Calcium channel; Glycoprotein; Repeat; Multigene family;  
 CC Calcium-binding; Phosphorylation.  
 CC KW REPEAT 64 399 I.  
 CC REPEAT 584 823 II.  
 CC REPEAT 1116 1393 III.  
 CC REPEAT 1431 1692 IV.  
 CC FT DOMAIN 1 76  
 CC TRANSMEM 97 97  
 CC DOMAIN 98 115  
 CC TRANSMEM 116 137  
 CC DOMAIN 138 146  
 CC TRANSMEM 147 166  
 CC DOMAIN 167 171  
 CC TRANSMEM 172 189  
 CC DOMAIN 190 209  
 CC TRANSMEM 210 230  
 CC DOMAIN 231 371  
 CC TRANSMEM 372 396  
 CC DOMAIN 397 598  
 CC CYTOPLASMIC (POTENTIAL).  
 CC S1 OF REPEAT I (POTENTIAL).  
 CC EXTRACELLULAR (POTENTIAL).  
 CC S2 OF REPEAT I (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).  
 CC S3 OF REPEAT I (POTENTIAL).  
 CC EXTRACELLULAR (POTENTIAL).  
 CC S4 OF REPEAT I (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).  
 CC S5 OF REPEAT I (POTENTIAL).  
 CC EXTRACELLULAR (POTENTIAL).  
 CC S6 OF REPEAT I (POTENTIAL).  
 CC CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 599 619  
 FT DOMAIN 620 632  
 FT TRANSMEM 633 654  
 FT DOMAIN 655 660  
 FT TRANSMEM 661 679  
 FT DOMAIN 680 687  
 FT TRANSMEM 688 711  
 FT DOMAIN 712 722  
 FT TRANSMEM 723 743  
 FT DOMAIN 744 795  
 FT TRANSMEM 796 820  
 FT DOMAIN 821 1125  
 FT TRANSMEM 1126 1148  
 FT DOMAIN 1149 1166  
 FT TRANSMEM 1167 1187  
 FT DOMAIN 1188 1197  
 FT TRANSMEM 1198 1217  
 FT DOMAIN 1218 1231  
 FT TRANSMEM 1232 1253  
 FT DOMAIN 1254 1263  
 FT TRANSMEM 1264 1287  
 FT DOMAIN 1288 1364  
 FT TRANSMEM 1365 1390  
 FT DOMAIN 1391 1445  
 FT TRANSMEM 1446 1466  
 FT DOMAIN 1467 1480  
 FT TRANSMEM 1481 1502  
 FT DOMAIN 1503 1509  
 FT TRANSMEM 1510 1528  
 FT DOMAIN 1529 1542  
 FT TRANSMEM 1543 1566  
 FT DOMAIN 1567 1580  
 FT TRANSMEM 1581 1601  
 FT DOMAIN 1602 1664  
 FT TRANSMEM 1665 1692  
 FT DOMAIN 1693 1835  
 FT SITE 353 355  
 FT SITE 779 779  
 FT SITE 1339 1339  
 FT SITE 1637 1637  
 FT CARBOHYD 171 171  
 FT CARBOHYD 242 242  
 FT CARBOHYD 309 309  
 FT CARBOHYD 1301 1301  
 FT CARBOHYD 1304 1304  
 SQ SEQUENCE 1835 AA; 205207 MW; 850807A68B82C0BE CRC64;  
 Query Match 3.0%; Score 7; DB 1; Length 1835;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 146 PGTPAPA 152  
 Db 467 PGTPAPA 473  
 RESULT 29  
 MGA\_HUMAN  
 ID MGA\_HUMAN STANDARD; PRT; 1856 AA.  
 AC 043451;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Maltase-glucosylase, intestinal [includes: Maltase (EC 3.2.1.20)  
 DE (Alpha-glucosidase); glucosylase (EC 3.2.1.3) (Glucan 1,4-alpha-  
 DE glucosidase)].  
 GN MGAH OR MGA OR MGAHL.  
 OS Homo sapiens (human).





CC -1- SIMILARITY: BELONGS TO THE S14P FAMILY OF RIBOSOMAL PROTEINS.  
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CC -----  
DR EMBL: AE000795; AAB84518.1; -  
DR InterPro: IPR001209; Ribosomal\_S14.  
DR Pfam: PF00253; Ribosomal\_S14; 1.  
DR PROSITE: PS00527; RIBOSOMAL\_S14; 1.  
KW Ribosomal protein; Complete proteome.  
SQ SEQUENCE 50 AA; 5850 MW; A5B5972652DF2171 CRC64;  
  
Query Match 2.6%; Score 6; DB 1; Length 50;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 100 RKCSRC 105  
Db 13 RKCSRC 18  
  
RESULT 31  
TATA\_RICPR STANDARD; PRT; 54 AA.  
AC Q9ZCJ1;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Sec-Independent protein translocase protein tata/E homolog.  
GN TATA OR Rp749.  
OS Rickettsia prowazekii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiidae; Rickettsia.  
OX NCBI\_TaxID=782;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MADRID E;  
RX MEDLINE=99039499; PubMed=9823893;  
RA Andersson S.G.E., Zomrodipour A., Andersson J.O.,  
RA Sticheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,  
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;  
RT "The genome sequence of Rickettsia prowazekii and the origin of  
RT mitochondria";  
RL Nature 396:133-140(1998).  
CC -1- FUNCTION: REQUIRED FOR CORRECT LOCALIZATION OF PRECURSOR PROTEINS  
CC BEARING SIGNAL PEPTIDES WITH THE TWIN ARGININE CONSERVED MOTIF  
CC S/T-R-X-F-L-K. THIS SEC-INDEPENDENT PATHWAY IS TERMED TAT FOR  
CC TWIN-ARGININE TRANSLLOCATION SYSTEM. THIS SYSTEM MAINLY TRANSPORTS  
CC PROTEINS WITH BOUND COFACTORS THAT REQUIRE FOLDING PRIOR TO EXPORT  
CC (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: MEMBRANE BOUND (PROBABLE).  
CC -1- SIMILARITY: BELONGS TO THE TATA/E FAMILY.  
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CC -----  
DR EMBL: AJ235273; CA115177.1; -  
DR InterPro: IPR003369; MTA\_Hc106.  
DR Pfam: PF02416; MTA\_Hc106; 1.  
KW Transport; Protein transport; Translocation; Transmembrane;  
KW Complete proteome.  
FT TRANSMEM 1 21 POTENTIAL.

SQ SEQUENCE 54 AA; 5884 MW; 607EAE2A977FA3C7 CRC64;  
  
Query Match 2.6%; Score 6; DB 1; Length 54;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 225 LIVLII 230  
Db 9 LIVLII 14  
  
RESULT 32  
Y416\_ARCFU STANDARD; PRT; 62 AA.  
ID Y416\_ARCFU  
AC Q29831;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein AF0416 precursor.  
GN AF0416.  
OS Archaeoglobus fulgidus.  
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;  
OC Archaeoglobus.  
OX NCBI\_TaxID=2234;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
RX MEDLINE=98049343; PubMed=9389475;  
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyriakides N.C.,  
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
RA Kirschner S., Reich C.I., McNeill L.K., McKenney K., Adams M.D., Loftus B.,  
RA Peterson S., Reisch C.I., McNeill L.K., Badger J.H., Glodok A., Zhou L.,  
RA Corton M.D., Spriggs T., Artlach P., Kaine B.P., Sykes S.M.,  
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
RA Venter J.C.;  
RT "The complete genome sequence of the hyperthermophilic, sulphate-  
RT reducing archaeon Archaeoglobus fulgidus";  
RL Nature 390:364-370(1997).  
CC -----  
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CC -----  
DR EMBL: AE001075; AAB90816.1; -  
DR TIGR: AF0416; -  
KW Hypothetical protein; Signal; Complete proteome.  
FT CHAIN 1 22 POTENTIAL.  
FT SIGNAL 23 62  
SQ SEQUENCE 62 AA; 6819 MW; 52BAC837861A8C6 CRC64;  
  
Query Match 2.6%; Score 6; DB 1; Length 62;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 129 ANATVE 134  
Db 27 ANATVE 32  
  
RESULT 33  
IAPP\_FELCA STANDARD; PRT; 89 AA.  
ID IAPP\_FELCA  
AC P12967;



```

DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Islet amyloid polypeptide precursor (Amylin).
GN IAPP.
OS Felis silvestris catus (cat).
OC Eukaryota; Metazoa; Chordata; Cranialata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
ON NCBI_TaxID=9685;
RN [1]
RP MEDLINE=89345542; PubMed=2668946;
RX Nishi M., Chan S.O., Nagamatsu S., Bell G.I., Steiner D.F.;
RT "Conservation of the sequence of islet amyloid polypeptide in five
RL mammals is consistent with its putative role as an islet hormone.";
RN Proc. Natl. Acad. Sci. U.S.A. 86:5738-5742(1989).
RP SEQUENCE OF 34-50.
RX MEDLINE=87231921; PubMed=3035556;
RA Westermarck P., Wernstedt C., Willander E., Hayden D.W., O'Brien T.D.,
RA Johnson K.H.;
RT "Amyloid fibrils in human insulinoma and islets of Langerhans of the
RT diabetic cat are derived from a neuropeptide-like protein also
RT present in normal islet cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:3881-3885(1987).
CC -1- FUNCTION: SELECTIVELY INHIBITS INSULIN-STIMULATED GLUCOSE
CC UTILIZATION AND GLYCOGEN DEPOSITION IN MUSCLE, WHILE NOT AFFECTING
CC ADIPOCYTE GLUCOSE METABOLISM.
CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.
CC -----
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CC -----
DR EMBL; M25388; AAA30813.1; -
DR PIR; A33542; A33542.
DR PIR; B26619; B26619.
DR InterPro; IPR001693; Calc_CGRP_IAPP.
DR Pfam; PF00214; Calc_CGRP_1.
DR PRINTS; PR00818; ISLETAMYLOID.
DR SMART; SM00113; CALCITONIN; 1.
DR PROSITE; PS00258; CALCITONIN; 1.
KW Hormone; Cleavage on pair of basic residues; Amidation; Amyloid;
KW Signal.
FT SIGNAL. 1 22 POTENTIAL.
FT PEPTIDE 34 70 ISLET AMYLOID POLYPEPTIDE.
FT DISULFID 35 40 BY SIMILARITY.
FT MOD RES 70 70 AMIDATION (G-71 PROVIDE AMIDE GROUP).
SQ SEQUENCE 89 AA; 9831 MW; 0834D783DEAD72A8 CRC64;

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Query Match 2.6%; Score 6; DB 1; Length 89;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 224 VLIVL 229
    |||||
Db 9 VLIVL 14

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RESULT 34
RL25_BUCAT STANDARD; PRT; 95 AA.
AC P57238;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L25.

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GN RPL25 OR BUI138.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
ON NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TOKYO 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS.";
RN Nature 407:81-86(2000).
CC -1- SIMILARITY: BELONGS TO THE L25P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL; AP001118; BAB12856.1; -
DR InterPro; IPR001021; Ribosomal_L25p.
DR Pfam; PF01386; Ribosomal_L25p; 1.
DR ProDom; PD012503; Ribosomal_L25p; 1.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 95 AA; 11336 MW; C234CE06D0F7A84C CRC64;

```

```

Query Match 2.6%; Score 6; DB 1; Length 95;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 18 QRHSFK 23
    |||||
Db 78 QRHSFK 83

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RESULT 35
RLAL_ALTRAL STANDARD; PRT; 110 AA.
ID RLAL_ALTRAL
AC P49148;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE 60S acidic ribosomal protein P1 (Allergen Alt a 12) (Alt a XII).
GN ALTA12.
OS Alternaria alternata.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria.
ON NCBI_TaxID=5599;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=08-0203-BERLIN;
RX MEDLINE=95206305; PubMed=7898496;
RA Achatz G., Oberkofler H., Lechner E., Simon B., Unger A.,
RA Kandler D., Ebner C., Prillinger H., Kraft D., Breitenbach M.;
RT "Molecular cloning of major and minor allergens of Alternaria
RT alternata and Cladosporium herbarum.";
RL Mol. Immunol. 32:213-227(1995).
CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP OF
CC PROTEIN SYNTHESIS.
CC -1- SUBUNIT: P1 AND P2 EXIST AS DIMERS AT THE LARGE RIBOSOMAL
CC SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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 CC -----  
 DR EMBL; X84216; CAA58989.1; -  
 DR InterPro; IPR001813; 60s\_ribosomal.  
 DR Pfam; PF00428; 60s\_ribosomal.2.  
 KW Ribosomal protein; Phosphorylation; Allergen.  
 SQ SEQUENCE 110 AA; 11736 MW; F06A23B67C3259F CRC64;

Query Match 2.6%; Score 6; DB 1; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 APAEE 155  
 |||||  
 DB 86 APAEE 91

RESULT 36  
 RL2\_SCHPO STANDARD; PRT; 110 AA.  
 AC P08094;  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 60S acidic ribosomal protein P2-alpha (A2) (L40C) (L12ET).  
 GN RPP2A OR RPP2A OR SPBP87.06.  
 OS Schizosaccharomyces pombe (Fission Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetaceae; Schizosaccharomycetaceae;  
 OC Schizosaccharomyces.  
 ON NCBI\_TaxID=4896;  
 RX MEDLINE=90220620; PubMed=2325655;  
 RA Beltrame M., Bianchi M.E.;  
 RT "Sequence of the cDNA for one acidic ribosomal protein of  
 RT Schizosaccharomyces pombe.";  
 RL Nucleic Acids Res. 15:9089-9089(1987).  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90220620; PubMed=2325655;  
 RA Beltrame M., Bianchi M.E.;  
 RT "A gene family for acidic ribosomal proteins in Schizosaccharomyces  
 RT pombe: two essential and two nonessential genes.";  
 RL Mol. Cell. Biol. 10:2341-2348(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RA Beck A., Reinhardt R., Lyne M., Rajandream M.A., Barrell B.G.;  
 RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 1-40.  
 RX MEDLINE=84038947; PubMed=6355773;  
 RA Otake E., Higo K.-H., Itoh T.;  
 RT "Yeast ribosomal proteins: VII. Cytoplasmic ribosomal proteins from  
 RT Schizosaccharomyces pombe.";  
 RL Mol. Genet. 191:519-524(1983).  
 CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP OF  
 CC PROTEIN SYNTHESIS.  
 CC -1- SUBUNIT: P1 AND P2 EXIST AS DIMERS AT THE LARGE RIBOSOMAL  
 CC SUBUNIT.  
 CC -1- PTM: PHOSPHORYLATED (BY SIMILARITY).  
 CC -1- MISCELLANEOUS: YEASTS CONTAIN 4 INDIVIDUAL SMALL RIBOSOMAL A  
 CC PROTEINS (RPA) WHICH CAN BE CLASSIFIED INTO TWO COUPLES OF SIMILAR  
 CC BUT NOT IDENTICAL SEQUENCES. EACH COUPLE IS DISTINCTLY RELATED TO  
 CC ONE OF THE TWO A PROTEINS PRESENT IN MULTICELLULAR ORGANISMS.  
 CC -1- MISCELLANEOUS: RPA3 AND RPA4 ARE ESSENTIAL FOR CELL SURVIVAL,  
 CC WHEREAS RPA1 AND RPA2 ARE NOT.  
 CC -1- SIMILARITY: ALL FOUR RPA SHOW 35% IDENTITY. RPA4 IS HIGHLY RELATED  
 CC TO RPA2.  
 CC -1- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.

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 CC -----  
 DR EMBL; Y00466; CAA68528.1; -  
 DR EMBL; M3138; AA35335.1; -  
 DR EMBL; AL032684; CAN21791.1; -  
 DR PIR; B34715; R6BY22.  
 DR InterPro; IPR001813; 60s\_ribosomal.  
 DR Pfam; PF00428; 60s\_ribosomal.1.  
 KW Ribosomal protein; Phosphorylation; Multigene family.  
 SQ SEQUENCE 110 AA; 11158 MW; 2B45A4E51606FE CRC64;

Query Match 2.6%; Score 6; DB 1; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 APAEE 155  
 |||||  
 DB 83 APAEE 88

RESULT 37  
 RL12\_AERPE STANDARD; PRT; 111 AA.  
 AC Q9Y9W9;  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 50S ribosomal protein L12p.  
 GN RL12P OR AEP2170.  
 OS Aeropyrum pernix.  
 OC Archaea; Crenarchaeota; Desulfurococcaceae; Desulfurococcaceae;  
 OC Aeropyrum.  
 ON NCBI\_TaxID=56636;  
 RX MEDLINE=99310339; PubMed=10382966;  
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Hatakeyama Y.,  
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankei A., Kosugi H.,  
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,  
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,  
 RA Yamazaki J., Kushida N., Ogunchi A., Aoki K.-I., Kubota K.,  
 RT "Complete genome sequence of an aerobic hyper-thermophilic  
 RT crenarchaeon, Aeropyrum pernix K1.";  
 RL DNA Res. 6:83-101(1999)  
 CC -1- FUNCTION: SEEMS TO BE THE BINDING SITE FOR SEVERAL OF THE FACTORS  
 CC INVOLVED IN PROTEIN SYNTHESIS AND APPEARS TO BE ESSENTIAL FOR  
 CC ACCURATE TRANSLATION (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----  
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 CC -----  
 DR EMBL; AP000063; BAA81181.1; -  
 DR InterPro; IPR001813; 60s\_ribosomal.  
 DR Pfam; PF00428; 60s\_ribosomal.1.  
 KW Ribosomal protein; Complete proteome.  
 SQ SEQUENCE 111 AA; 11794 MW; 2330740B03C6412A CRC64;

Query Match - 2.6%; Score 6; DB 1; Length 111;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 APAEE 155  
 Db 77 APAEE 82

RESULT 38  
 RLAA2\_BRAFL STANDARD; PRT; 116 AA.

AC 001725;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE 60S acidic ribosomal protein p2.  
 OS Branchiostoma floridae (Florida lancelet) (Amphioxus).  
 OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;  
 CC Branchiostoma.  
 CC NCBI\_TaxID=7739;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tweedie S., Charlton J., Clark V., Bird A.;  
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP OF  
 CC PROTEIN SYNTHESIS  
 CC -1- SUBUNIT: P1 AND P2 EXIST AS DIMERS. AT THE LARGE RIBOSOMAL  
 CC SUBUNIT.  
 CC -1- PTM: PHOSPHORYLATED (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.

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DR EMBL: Z63263; CAB05855.1; -  
 DR InterPro: IPR001813; 60S\_rribosomal.  
 DR Pfam: PF00428; 60S\_rribosomal; 1.  
 KM Ribosomal protein: Phosphorylation.  
 SQ SEQUENCE 116 AA; 11557 MW; 39C1654F10DC00C CRC64;

Query Match 2.6%; Score 6; DB 1; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 45;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 APAEE 155  
 Db 88 APAEE 93

RESULT 39  
 HYL1B\_HUMAN STANDARD; PRT; 117 AA.

AC P01743;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig heavy chain V-I region H63 precursor.

OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 CC NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83144028; Pubmed=6298778;  
 RA Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;

RT "Evolutionary aspects of immunoglobulin heavy chain variable region  
 RT (VH) gene subgroups.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).

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DR EMBL: J00240; AAA52988.1; -  
 DR PIR: A02024; HVHUG;  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 1.  
 DR SMART: SM00406; IgV; 1.  
 KM Immunoglobulin V region: Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION H63.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match 2.6%; Score 6; DB 1; Length 117;  
 Best Local Similarity 100.0%; Pred. No. 45;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 76 TMTSDT 81  
 Db 88 TMTSDT 93

RESULT 40  
 ID MUTT\_BUCAI STANDARD; PRT; 124 AA.

AC P57298;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Mutator mult protein (7,8-dihydro-8-oxoguanine-triphosphatase)  
 DE (8-oxo-dcnpase) (EC 3.6.1.-) (dcnp pyrophosphohydrolase).  
 GN MUTT OR BU202.  
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum  
 OS symbiotic bacterium).  
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.  
 CC NCBI\_TaxID=118099;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RP STRAIN-TOKYO 1998;  
 RX MEDLINE=20445173; Pubmed=10993077;  
 RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;  
 RT "Genome sequence of the endocellular bacterial symbiont of aphids  
 RT Buchnera sp. APS.";  
 RL Nature 407:81-86(2000).

CC -1- FUNCTION: INVOLVED IN THE GO SYSTEM RESPONSIBLE FOR REMOVING AN  
 CC OXIDATIVELY DAMAGED FORM OF GUANINE (7,8-DIHYDRO-8-OXOGUANINE)  
 CC FROM DNA AND THE NUCLEOTIDE POOL. 8-OXO-DGTP IS INSERTED OPPOSITE  
 CC DA AND DC RESIDUES OF TEMPLATE DNA WITH ALMOST EQUAL EFFICIENCY  
 CC THUS LEADING TO A.T TO G.C TRANSVERSIONS. MUTT SPECIFICALLY  
 CC DEGRADES 8-OXO-DGTP TO THE MONOPHOSPHATE (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: 8-OXO-DGMP + H(2)O = 8-OXO-DGMP +  
 CC PYROPHOSPHATE.

CC -1- COFACTOR: REQUIRES MAGNESIUM (BY SIMILARITY).  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE NODIX HYDROLASE FAMILY.

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DR EMBL: AP001118; BAB12919.1; -  
DR InterPro: IPR000086; NUDIX\_hydrolase.  
DR Pfam: PF00293; NUDIX.1.  
DR PRINTS: PR00502; NUDIXFAMILY.  
DR PROSITE: PS00893; NUDIX.1.  
KW Mutator protein; DNA replication; DNA repair; Hydrolase; Magnesium;  
KW Complete proteome.  
FT DOMAIN 26 47 NUDIX BOX.  
SQ SEQUENCE 124 AA; 15061 MW; E1120D460C70801F CRC64;

Query Match 2.6%; Score 6; DB 1; Length 124;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 220 VGIIVL 225  
|||||  
DB 46 VGIIVL 51

RESULT 41  
Y192\_RICPR STANDARD; PRT; 128 AA.  
AC O9ZDX2;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein RPI92.  
GN RPI92.  
OS Rickettsia prowazekii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxId=782;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MADRID E;  
RX MEDLINE=99039499; PubMed=9823893;  
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,  
RA Sichevitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naestlund A.K.,  
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;  
RT "The genome sequence of Rickettsia prowazekii and the origin of  
RT mitochondria."  
RL Nature 396:133-140(1998).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -----  
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DR EMBL: AJ235270; CAA14658.1; -  
KW Hypothetical protein; Transmembrane; Complete proteome.  
FT TRANSMEM 30 50 POTENTIAL.  
FT TRANSMEM 65 85 POTENTIAL.  
FT TRANSMEM 93 113 POTENTIAL.  
SQ SEQUENCE 128 AA; 13943 MW; 6C12DCD7EE348223 CRC64;

Query Match 2.6%; Score 6; DB 1; Length 128;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 220 VGIIVL 225  
|||||  
DB 77 VGIIVL 82

RESULT 42  
TYRT\_STRGA STANDARD; PRT; 134 AA.  
ID TYRT\_STRGA  
AC P55047;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Tyrosinase co-factor (URF402).  
DE MELC1.  
OS Streptomyces glaucescens.  
GN Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxId=1907;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 13032 / ETH 22794 / GLA.0;  
RX MEDLINE=88040431; PubMed=3118334;  
RA Huber M., Huettler R., Lerch K.;  
RT "The promoter of the Streptomyces glaucescens mel operon."  
RL Nucleic Acids Res. 15:8106-8106(1987).  
CC -1- FUNCTION: THIS PROTEIN MAY FUNCTION TO DELIVER COPPER TO  
CC TYROSINASE.  
CC -----  
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DR EMBL: Y00457; CAA68512.1; -  
KW Melanin biosynthesis; Copper.  
SQ SEQUENCE 134 AA; 13593 MW; 1E874145A7D1B9AE CRC64;

Query Match 2.6%; Score 6; DB 1; Length 134;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 206 PGT PAS 211  
|||||  
DB 48 PGT PAS 53

RESULT 43  
PSAD\_ODOST STANDARD; PRT; 139 AA.  
ID PSAD\_ODOST  
AC P49481;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE Photosystem I reaction center subunit II (Photosystem I 16 kDa  
DE polypeptide) (Pst-D).  
GN PSAD.  
OS Odontella sinensis.  
ON Chloroplast.  
OC Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;  
OC Biddulphiophycidae; Eupodiscates; Eupodiscaceae; Odontella.  
OX NCBI\_TaxId=2839;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kowalik K.V., Stoebe B., Schafran I., Kroth-Pancic P., Freier U.;  
RT "The chloroplast genome of a chlorophyll a+c-containing alga,  
RT Odontella sinensis."  
RL Plant Mol. Biol. Rep. 13:336-342(1995).  
CC -1- FUNCTION: PSAD CAN FORM COMPLEXES WITH FERREDOXIN AND FERREDOXIN-  
CC OXIDOREDUCTASE IN PHOTOSYSTEM I (PS I) REACTION CENTRE.  
CC -1- SIMILARITY: BELONGS TO THE PSAD FAMILY.  
CC -----  
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 CC -----  
 DR EMBL: Z67753; CAA91679.1; -  
 DR Mendel: 13229; ODO81; Psad.1.  
 DR InterPro: IPR003685; Psad.  
 DR Pfam: PF02531; Psad.1.  
 KM Photosynthesis; Photosystem I; Chloroplast; Thylakoid; Membrane.  
 SQ SEQUENCE 139 AA; 15515 MW; 25F63D31CDDCAE8C CRC64;

Query Match 2.6%; Score 6; DB 1; Length 139;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 106 PSGEVQ 111  
 111111  
 Db 88 PSGEVQ 93

RESULT 44  
 PSAD\_SKECO STANDARD; PRT: 139 AA.  
 AC 096800;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Photosystem I reaction center subunit II (Photosystem I 16 kDa  
 DE polypeptide) (PSI-D).  
 GN PSAD.  
 OS Skeletonema costatum.  
 OC Chloroplast.  
 OC Eukaryota; Stramenopiles; Bacillariophyta; Coscinodiscophyceae;  
 OC Thalassiosirophycidae; Thalassiosirales; Skeletonemataceae;  
 OC Skeletonema.  
 OX NCBI\_Taxid=2843;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NIES-323;  
 RA Tada N., Otsuka S., Oyaizu H., Matsumoto S.;  
 RT "Plastid DNA sequences of Skeletonema costatum NIES 323.";  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: PSAD CAN FORM COMPLEXES WITH FERREDOXIN AND FERREDOXIN-  
 CC OXIDOREDUCTASE IN PHOTOSYSTEM I (PS I) REACTION CENTRE.  
 CC -1- SIMILARITY: BELONGS TO THE PSAD FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AJ132263; CAA10621.1; -  
 DR InterPro: IPR003685; Psad.  
 DR Pfam: PF02531; Psad.1.  
 KM Photosynthesis; Photosystem I; Chloroplast; Thylakoid; Membrane.  
 SQ SEQUENCE 139 AA; 15504 MW; AFD7319C87EBC265 CRC64;

Query Match 2.6%; Score 6; DB 1; Length 139;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 106 PSGEVQ 111  
 111111  
 Db 88 PSGEVQ 93  
 RESULT 45

PSAD\_SYNY3 STANDARD; PRT: 140 AA.  
 AC P19569;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Photosystem I reaction center subunit II (Photosystem I 16 kDa  
 DE polypeptide) (PSI-D).  
 GN PSAD OR SLR0737.  
 OS Synechocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 OX NCBI\_Taxid=1148;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=89034300; Pubmed=3141423.  
 RA Reilly P., Holmes J.D., Pan Y.-C.E., Nelson N.;  
 RA "Molecular cloning and sequencing of the psad gene encoding subunit  
 RA II of photosystem I from the cyanobacterium, Synechocystis sp. PCC  
 RA 6803.";  
 RL J. Biol. Chem. 263:17658-17662(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; Pubmed=8905231;  
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 RA Miyajima N., Hiroseawa M., Sugliura M., Sasamoto S., Kimura T.,  
 RA Osunouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,  
 RA Okamura S., Shimo S., Takeuchi C., Wada T., Watanabe A.,  
 RA Yamada M., Yasuda M., Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 RT entire genome and assignment of potential protein-coding regions.";  
 RL DNA Res. 3:109-136(1996).  
 CC -1- FUNCTION: PSAD CAN FORM COMPLEXES WITH FERREDOXIN AND FERREDOXIN-  
 CC OXIDOREDUCTASE IN PHOTOSYSTEM I (PS I) REACTION CENTRE.  
 CC -1- SUBUNIT: PS I FROM SYNECHOCYSTIS SP. CONTAINS SEVEN DIFFERENT  
 CC POLYPEPTIDES. THE POLYPEPTIDE CORRESPONDING TO SUBUNIT II FROM  
 CC HIGHER PLANTS IS MISSING.  
 CC -1- SIMILARITY: BELONGS TO THE PSAD FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: J04195; AAA8625.1; -  
 DR EMBL: D90899; BAA16688.1; -  
 DR PIR: A32124; A32124.  
 DR InterPro: IPR003685; Psad.  
 DR Pfam: PF02531; Psad.1.  
 KM Photosynthesis; Photosystem I; Complete proteome.  
 FT INT\_MET 0  
 FT INT\_MET 0  
 SQ SEQUENCE 140 AA; 15513 MW; 263C35D5B47B9F8E CRC64;

Query Match 2.6%; Score 6; DB 1; Length 140;  
 Best Local Similarity 100.0%; Pred. No. 53;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 106 PSGEVQ 111  
 111111  
 Db 89 PSGEVQ 94  
 RESULT 46  
 PSAD\_GUITH STANDARD; PRT: 141 AA.  
 AC 078502;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Photosystem I reaction center subunit II (Photosystem I 16 kDa polypeptide) (PSI-D).

GN PSAD.

OS Guillardia theta (Cryptomonas phi).

CG Chloroplast.

OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.

ON NCBI\_Taxid=35529;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9912821; PubMed=9929392;

RA Douglas S.E., Penny S.L.;

RT "The plastid genome of the cryptophyte alga, Guillardia theta: complete sequence and conserved synteny groups confirm its common ancestry with red algae."

RL J. Mol. Evol. 48:236-244(1999).

CC -1- FUNCTION: PSAD CAN FORM COMPLEXES WITH FERREDOXIN AND FERREDOXIN-OXIDOREDUCTASE IN PHOTOSYSTEM I (PS I) REACTION CENTRE.

CC -1- SIMILARITY: BELONGS TO THE PSAD FAMILY.

CC -----

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CC -----

DR EMBL: AF041468; AAC35693.1; -.

DR InterPro: IPR003685; Psad.

DR Pfam: PF02531; Psad. 1

KM Photosynthesis; Photosystem I; Chloroplast; Thylakoid; Membrane.

SO SEQUENCE 141 AA; 15687 MW; 5ADE5DB37DBC89E CRC64;

Query Match 2.6%; Score 6; DB 1; Length 141;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 106 PSEVQ 111

Db 91 PSEVQ 96

|||||

RESULT 47

EXBD\_NEIGO STANDARD; PRT; 144 AA.

ID EXBD\_NEIGO

AC 006434;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DE Biopolymer transport exbd protein.

GN EXBD.

OS Neisseria gonorrhoeae.

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI\_Taxid=485;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FA19;

RX MEDLINE=97285757; PubMed=9140974;

RA Biswas G.D., Anderson J.E., Sparling P.F.;

RT "Cloning and functional characterization of Neisseria gonorrhoeae tonb, exbd and exbd genes."

RL Mol. Microbiol. 24:169-179(1997).

CC -1- FUNCTION: INVOLVED IN THE TONB-DEPENDENT ENERGY-DEPENDENT TRANSPORT OF VARIOUS RECEPTOR-BOUND SUBSTRATES (BY SIMILARITY).

CC -1- SUBUNIT: THE ACCESSORY PROTEINS EXBD AND EXBD SEEM TO FORM A COMPLEX WITH TONB (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane (Probable).

CC -1- SIMILARITY: BELONGS TO THE EXBD / TOLR FAMILY.

CC -----

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CC -----

DR EMBL: U79563; AAC45288.1; -.

DR InterPro: IPR003400; Exbd.

DR Pfam: PF02472; Exbd. 1.

KW Transport; Protein transport; Transmembrane; Inner membrane.

FT DOMAIN 1 18 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 19 39 POTENTIAL.

FT DOMAIN 40 144 PERIPLASMIC (POTENTIAL).

SO SEQUENCE 144 AA; 15514 MW; 4819D6B5138E9339 CRC64;

Query Match 2.6%; Score 6; DB 1; Length 144;

Best Local Similarity 100.0%; Pred. No. 55;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 227 VLLIVF 232

Db 28 VLLIVF 33

|||||

RESULT 48

EXBD\_NEIMA STANDARD; PRT; 144 AA.

ID EXBD\_NEIMA

AC P95376;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Biopolymer transport exbd protein.

GN EXBD OR NMA1983 OR NMA1728.

OS Neisseria meningitidis (serogroup A).

OS Neisseria meningitidis (serogroup B), and

OS Neisseria meningitidis (serogroup C).

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI\_Taxid=65699, 491, 135720;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=8013.6 / SEROGROUP C;

RX MEDLINE=97158676; PubMed=9006036;

RA Stojiljkovic I., Srinivasan N.;

RT "Neisseria meningitidis tonb, exbd, and exbd genes: Ton-dependent utilization of protein-bound iron in Neisseriae."

RL J. Bacteriol. 179:805-812(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;

RX MEDLINE=20222556; PubMed=10761919;

RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltham T., Hamlin N., Holroyd S., Jagers K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrett B.G.;

RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491."

RL Nature 404:502-506(2000).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=MC58 / SEROGROUP B;

RX MEDLINE=20175755; PubMed=10710307;

RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwyn M.L., Debay R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Citron H., Clark E.B., Cotton M.D., Utecherack T.R., Khouli H., Qin H., Yamathayan J., Gill J., Scarlato V., Maignani V., Piza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappunli R., Venter J.C.;

RT "Complete genome sequence of Neisseria meningitidis serogroup B strain

```

RT MC58.":
RL Science 287:1809-1815(2000).
CC -1- FUNCTION: INVOLVED IN THE TONB-DEPENDENT ENERGY-DEPENDENT
CC TRANSPORT OF VARIOUS RECEPTOR-BOUND SUBSTRATES (BY SIMILARITY).
CC -1- SUBUNIT: THE ACCESSORY PROTEIN EXB AND EXD SEEM TO FORM A
CC COMPLEX WITH TONB (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane
CC (Probable).
CC -1- SIMILARITY: BELONGS TO THE EXB / TOLR FAMILY.
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-----
CC EMBL: U77738; AAC44836.1; -.
DR EMBL: AL162757; CAB85203.1; -.
DR EMBL: AE002523; AAF42073.1; -.
DR TIGR: NMB1728; -.
DR InterPro: IPR003400; Exbd.
DR Pfam: PF02472; Exbd; 1.
KW Transport; Protein transport; Transmembrane; Inner membrane;
KW Complete proteome.
FT DOMAIN 1 18 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 19 39 POTENTIAL.
FT DOMAIN 40 144 PERIPLASMIC (POTENTIAL).
FT SEQUENCE 144 AA; 15514 MW; 96DCD7A142DAC370 CRC64;

Query Match
Best Local Similarity 2.6%; Score 6; DB 1; Length 144;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 YLVIVF 232
DB 28 YLVIVF 33

RESULT 49
SMG_BUCAI STANDARD; PRT; 157 AA.
AC P57562;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Smg protein homolog.
GN SMG OR BU495.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OC symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=OKYO 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT Genome sequence of the endocellular bacterial symbiont of aphids
BU Buchnera sp. APS.
RL Nature 407:81-86(2000).
CC -1- SIMILARITY: TO E.COLI SMG.
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-----
CC EMBL: AP001119; BAB13188.1; -.

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KW Complete proteome.
SQ SEQUENCE 157 AA; 18662 MW; 9958D9CACA47CFEE0 CRC64;

Query Match
Best Local Similarity 2.6%; Score 6; DB 1; Length 157;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 223 YLVIVL 228
DB 126 YLVIVL 131

RESULT 50
WH16_STRCO
ID WH16_STRCO STANDARD; PRT; 157 AA.
AC P23157;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 16.7 kDa protein in white locus (White ORF II).
GN SC6G9.14.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=91171868; PubMed=2077356;
RA Davis N.K., Chater K.F., Bruton C.J.;
RT "Spore colour in Streptomyces coelicolor A3(2) involves the
RT developmentally regulated synthesis of a compound biosynthetically
RT related to polyketide antibiotics.";
RL Mol. Microbiol. 4:1679-1691(1990).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D., James K.D., Parkhill J., Barrell B.G.,
RA Rajandream M.A.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SCHB/CURC FAMILY.
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-----
CC EMBL: X55942; CA39407.1; -.
DR EMBL: AL079356; CAB45605.1; -.
DR PIR: S11973; S11973.
SQ SEQUENCE 157 AA; 16669 MW; 2E650E3BED9F0CBD CRC64;

Query Match
Best Local Similarity 2.6%; Score 6; DB 1; Length 157;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 PAPAAE 154
DB 149 PAPAAE 154

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Search completed: August 13, 2002, 08:41:32  
Job time: 211 sec





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OM protein - protein search, using sw model

Run on: August 13, 2002, 08:38:22 ; Search time 26.68 Seconds  
(without alignments)  
1510.788 Million cell updates/sec

Title: US-09-826-212-2\_COPY\_27\_259  
Perfect score: 233  
Sequence: 1 TTARQEEVPOQTAPQ000RH.....YLCTGIVLIIVLIVFV 233

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 17294929 residues

Word size : 5

Total number of hits satisfying chosen parameters: 14653

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP\_mhc:\*  
8: SP\_organelle:\*  
9: SP\_phage:\*  
10: SP\_plant:\*  
11: SP\_rodent:\*  
12: SP\_virus:\*  
13: SP Vertebrate:\*  
14: SP Unclassified:\*  
15: SP\_virus:\*  
16: SP\_bacteriap:\*  
17: SP\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	3.4	109	5	Q9WZB6
2	8	3.4	217	4	Q9HA66
3	8	3.4	464	16	Q9Z7U4
4	8	3.4	468	4	Q9EB62
5	8	3.4	494	16	Q9ZDD2
6	8	3.4	685	16	Q9JWP0
7	8	3.4	801	5	Q23635
8	7	3.0	100	5	Q9V5T2
9	7	3.0	106	17	Q9HL72
10	7	3.0	144	2	O69204
11	7	3.0	151	15	O56349
12	7	3.0	155	10	Q39133
13	7	3.0	158	10	Q9FNT2
14	7	3.0	165	5	Q19762
15	7	3.0	184	17	Q9TWN5
16	7	3.0	219	16	Q9RW97

17	7	3.0	231	4	Q96EX2	Q96EX2 homo sapien
18	7	3.0	241	10	Q9FT78	Q9FT78 arabidopsis
19	7	3.0	249	16	Q9BEG1	Q9BEG1 rhizobium l
20	7	3.0	255	10	Q9SBT8	Q9SBT8 hordeum vul
21	7	3.0	255	10	Q9SP44	Q9SP44 hordeum vul
22	7	3.0	255	10	Q43488	Q43488 hordeum vul
23	7	3.0	256	5	Q9VW71	Q9VW71 drosophila
24	7	3.0	256	16	Q9PD13	Q9PD13 xyella fas
25	7	3.0	256	16	Q9PCV1	Q9PCV1 xyella fas
26	7	3.0	256	16	Q9PV65	Q9PV65 xyella fas
27	7	3.0	259	10	P93608	P93608 triticum ae
28	7	3.0	262	10	O81288	O81288 arabidopsis
29	7	3.0	263	5	Q17806	Q17806 caenorhabd1
30	7	3.0	266	2	Q9ZEF0	Q9ZEF0 rhodobacter
31	7	3.0	268	10	P93607	P93607 triticum ae
32	7	3.0	272	16	Q988Y8	Q988Y8 rhizobium l
33	7	3.0	295	2	Q32850	Q32850 mycobacteri
34	7	3.0	299	2	Q93D93	Q93D93 streptococc
35	7	3.0	313	2	O50268	O50268 agrobacteri
36	7	3.0	326	4	Q9BVC4	Q9BVC4 homo sapien
37	7	3.0	330	4	Q96SU5	Q96SU5 homo sapien
38	7	3.0	346	13	Q98TD7	Q98TD7 paratichthy
39	7	3.0	365	16	Q9YF60	Q9YF60 neisseria m
40	7	3.0	365	16	Q9JY44	Q9JY44 neisseria m
41	7	3.0	366	10	O80413	O80413 zea mays (m
42	7	3.0	380	8	Q79658	Q79658 pueraria ma
43	7	3.0	390	2	Q9RK28	Q9RK28 streptomyce
44	7	3.0	397	17	O58434	O58434 pyrococcus
45	7	3.0	401	5	Q9BWM3	Q9BWM3 onchocerca
46	7	3.0	405	11	Q9CRR2	Q9CRR2 mus musculu
47	7	3.0	419	10	Q9FNT4	Q9FNT4 arabidopsis
48	7	3.0	450	5	O17854	O17854 caenorhabd1
49	7	3.0	452	4	Q9H7M8	Q9H7M8 homo sapien
50	7	3.0	458	10	Q9AY47	Q9AY47 oryza sativ
51	7	3.0	465	16	Q98CE4	Q98CE4 rhizobium l
52	7	3.0	471	10	Q9ATX0	Q9ATX0 zea mays (m
53	7	3.0	485	2	Q93DB1	Q93DB1 streptococc
54	7	3.0	485	16	Q97N19	Q97N19 streptococc
55	7	3.0	494	10	Q93V55	Q93V55 arabidopsis
56	7	3.0	497	4	Q9H6L5	Q9H6L5 homo sapien
57	7	3.0	526	2	Q9R3F9	Q9R3F9 streptomyce
58	7	3.0	526	12	Q90899	Q90899 spodoptera
59	7	3.0	532	12	Q9DYA7	Q9DYA7 avian pneum
60	7	3.0	532	12	Q9DYA5	Q9DYA5 avian pneum
61	7	3.0	532	12	Q9DYA4	Q9DYA4 avian pneum
62	7	3.0	532	12	Q9DYA3	Q9DYA3 avian pneum
63	7	3.0	532	12	Q9DYA2	Q9DYA2 avian pneum
64	7	3.0	532	12	Q9DYA1	Q9DYA1 avian pneum
65	7	3.0	532	12	Q9DYA0	Q9DYA0 avian pneum
66	7	3.0	532	12	O91S36	O91S36 avian pneum
67	7	3.0	534	12	Q9DYP9	Q9DYP9 avian pneum
68	7	3.0	537	12	Q9WR13	Q9WR13 avian pneum
69	7	3.0	537	12	Q9QD13	Q9QD13 avian pneum
70	7	3.0	537	12	Q9QD12	Q9QD12 avian pneum
71	7	3.0	537	12	Q9QD11	Q9QD11 avian pneum
72	7	3.0	540	10	Q9FNT2	Q9FNT2 arabidopsis
73	7	3.0	542	5	Q9GUY4	Q9GUY4 penaeus jap
74	7	3.0	548	16	O06404	O06404 mycobacteri
75	7	3.0	548	17	Q97UB8	Q97UB8 sulfolobus
76	7	3.0	551	4	Q9Y613	Q9Y613 homo sapien
77	7	3.0	556	2	Q9ZFS8	Q9ZFS8 streptomyce
78	7	3.0	556	2	Q9S2C0	Q9S2C0 streptomyce
79	7	3.0	572	5	O02605	O02605 paramyxi
80	7	3.0	572	5	O02606	O02606 paramyxi
81	7	3.0	575	11	O88339	O88339 rattus norv
82	7	3.0	576	4	Q9HA18	Q9HA18 homo sapien
83	7	3.0	589	16	Q9HVT0	Q9HVT0 pseudomonas
84	7	3.0	596	10	Q9FNT3	Q9FNT3 arabidopsis
85	7	3.0	599	2	Q9F8V2	Q9F8V2 streptomyce
86	7	3.0	612	2	Q9Z614	Q9Z614 streptomyce
87	7	3.0	640	8	Q9GEM6	Q9GEM6 aegiceras c
88	7	3.0	640	8	Q9GET9	Q9GET9 solanella
89	7	3.0	657	8	Q9GDV8	Q9GDV8 trileptis l

90	7	3.0	660	8	Q9GDV9	Q9gdv9 tricyrtis a	163	6	2.6	80	12	Q9WN64	Q9wn64 hepatitis c
91	7	3.0	669	10	Q9MIG3	Q9mig3 arabidopsis	164	6	2.6	80	12	Q9WN63	Q9wn63 hepatitis c
92	7	3.0	670	8	Q9BAQ4	Q9baq4 buxus citrl	165	6	2.6	80	12	Q9WN62	Q9wn62 hepatitis c
93	7	3.0	677	5	Q9VBK7	Q9vbk7 drosophila	166	6	2.6	80	12	Q9WN61	Q9wn61 hepatitis c
94	7	3.0	694	8	Q32008	Q32008 clerodendru	167	6	2.6	80	12	Q9WN60	Q9wn60 hepatitis c
95	7	3.0	695	8	Q9MUA4	Q9mua4 solanum nit	168	6	2.6	80	12	Q9WN59	Q9wn59 hepatitis c
96	7	3.0	697	8	Q9TLC9	Q9tlc9 lampocapro	169	6	2.6	80	12	Q9WN58	Q9wn58 hepatitis c
97	7	3.0	702	6	Q9SUT0	Q9suto macaca fasc	170	6	2.6	80	12	Q9WN57	Q9wn57 hepatitis c
98	7	3.0	717	4	Q9NXL0	Q9nxl0 homo sapien	171	6	2.6	80	12	Q9WN56	Q9wn56 hepatitis c
99	7	3.0	734	8	Q9LUT3	Q9lut3 guettarda u	172	6	2.6	80	12	Q9WN55	Q9wn55 hepatitis c
100	7	3.0	744	8	Q32737	Q32737 onoseris hy	173	6	2.6	80	12	Q9WN54	Q9wn54 hepatitis c
101	7	3.0	761	8	Q9LILL	Q9lill streptomyc	174	6	2.6	80	12	Q9WN53	Q9wn53 hepatitis c
102	7	3.0	780	5	Q9SYK4	Q9syk4 clona savig	175	6	2.6	80	12	Q9WN52	Q9wn52 hepatitis c
103	7	3.0	837	5	P90666	P90666 antiochdarl	176	6	2.6	80	12	Q9WN50	Q9wn50 hepatitis c
104	7	3.0	838	5	Q27422	Q27422 caenorhabd1	177	6	2.6	80	12	Q9WN48	Q9wn48 hepatitis c
105	7	3.0	838	5	Q18761	Q18761 caenorhabd1	178	6	2.6	82	12	Q9X524	Q9x524 thlobacillu
106	7	3.0	970	16	Q92KJ8	Q92kj8 rhizobium m	179	6	2.6	82	12	Q9G303	Q9g303 hepatitis c
107	7	3.0	1058	16	Q97TJ9	Q97tj9 clostridium	180	6	2.6	82	16	Q97NXL	Q97nxl streptococ
108	7	3.0	1110	13	Q9J255	Q9j255 petromyzon	181	6	2.6	83	5	Q23304	Q23304 caenorhabd1
109	7	3.0	1247	5	Q9VX80	Q9vx80 drosophila	182	6	2.6	84	2	Q9ZHY7	Q9zhy7 thlobacillu
110	7	3.0	1318	5	Q19733	Q19733 caenorhabd1	183	6	2.6	85	10	Q9FW74	Q9fw74 oryza sativ
111	7	3.0	1461	5	Q9GYB7	Q9gyb7 leishmania	184	6	2.6	86	5	Q21699	Q21699 caenorhabd1
112	7	3.0	1698	2	Q9LCO0	Q9lco0 staphylococ	185	6	2.6	87	5	Q20368	Q20368 caenorhabd1
113	7	3.0	1742	16	Q55583	Q55583 synechocyst	186	6	2.6	90	5	Q9XVX2	Q9xvx2 caenorhabd1
114	7	3.0	1834	11	Q9EQS9	Q9eqs9 ratcus norv	187	6	2.6	90	12	Q99CY8	Q99cy8 bovine herp
115	7	3.0	2026	2	Q9JPU4	Q9jpu4 neisseria m	188	6	2.6	93	4	Q9H5A9	Q9h5a9 homo sapien
116	7	3.0	2938	11	Q61769	Q61769 mus musculu	189	6	2.6	93	8	Q36903	Q36903 hansenua w
117	7	3.0	3739	2	Q92G14	Q92g14 streptomyc	190	6	2.6	94	10	Q9FEW0	Q9few0 oryza sativ
118	7	3.0	4685	2	Q93HJ2	Q93hj2 streptomyc	191	6	2.6	94	16	Q99VS9	Q99vs9 staphylococ
119	6	2.6	22	1	Q9V2S4	Q9v2s4 halobacteri	192	6	2.6	101	11	Q9D7U2	Q9d7u2 mus musculu
120	6	2.6	36	16	Q97S76	Q97s76 streptococ	193	6	2.6	104	16	Q92D67	Q92d67 listeria in
121	6	2.6	37	16	Q97OP3	Q97op3 streptococ	194	6	2.6	104	16	Q92D67	Q92d67 listeria in
122	6	2.6	44	16	Q9KLB9	Q9klb9 vibrio chol	195	6	2.6	104	17	Q9GWS7	Q9gws7 sulfoloba
123	6	2.6	45	12	Q68613	Q68613 hepatitis c	196	6	2.6	105	5	Q91706	Q91706 drosophila
124	6	2.6	45	12	Q68614	Q68614 hepatitis c	197	6	2.6	105	5	P92201	P92201 drosophila
125	6	2.6	45	12	Q68617	Q68617 hepatitis c	198	6	2.6	106	16	Q9A2W3	Q9a2w3 caulobacter
126	6	2.6	45	12	Q68618	Q68618 hepatitis c	199	6	2.6	109	4	Q95724	Q95724 homo sapien
127	6	2.6	45	12	Q68619	Q68619 hepatitis c	200	6	2.6	109	5	O61467	O61467 caenorhabd1
128	6	2.6	45	12	Q68620	Q68620 hepatitis c	201	6	2.6	109	11	Q92155	Q92155 mus musculu
129	6	2.6	45	12	Q68625	Q68625 hepatitis c	202	6	2.6	109	11	Q92157	Q92157 mus dunni (
130	6	2.6	53	16	Q92G33	Q92g33 rickettsia	203	6	2.6	109	11	Q92156	Q92156 mus famulus
131	6	2.6	55	5	P90700	P90700 brugia mala	204	6	2.6	110	3	O41317	O41317 schizosacch
132	6	2.6	59	9	Q92XK2	Q92xk2 enococcus	205	6	2.6	110	5	O21156	O21156 caenorhabd1
133	6	2.6	59	13	Q9T859	Q9t859 fuqu rubrip	206	6	2.6	111	3	Q9H6U9	Q9h6u9 aspergillus
134	6	2.6	59	16	Q9K411	Q9k411 bacillus ha	207	6	2.6	112	5	Q9NA97	Q9na97 caenorhabd1
135	6	2.6	62	16	Q92GE4	Q92ge4 rickettsia	208	6	2.6	112	10	Q9NMA5	Q9nma5 arabidopsis
136	6	2.6	73	12	P90335	P90335 panicum mos	209	6	2.6	113	5	Q9N923	Q9n923 trypanosoma
137	6	2.6	74	12	Q91F76	Q91f76 chilo iride	210	6	2.6	113	10	Q9FRT9	Q9ftr9 arabidopsis
138	6	2.6	75	16	Q99245	Q99245 streptococ	211	6	2.6	114	12	Q91PM8	Q91pm8 hepatitis c
139	6	2.6	76	12	Q68496	Q68496 hepatitis c	212	6	2.6	114	12	Q91PM7	Q91pm7 hepatitis c
140	6	2.6	76	12	Q68497	Q68497 hepatitis c	213	6	2.6	114	12	Q91PM6	Q91pm6 hepatitis c
141	6	2.6	76	12	Q68498	Q68498 hepatitis c	214	6	2.6	114	12	Q91PM5	Q91pm5 hepatitis c
142	6	2.6	76	12	Q68499	Q68499 hepatitis c	215	6	2.6	114	12	Q91PM4	Q91pm4 hepatitis c
143	6	2.6	77	16	Q99VK3	Q99vk3 staphylococ	216	6	2.6	114	12	Q91PM3	Q91pm3 hepatitis c
144	6	2.6	80	12	Q9W8C0	Q9w8c0 hepatitis c	217	6	2.6	114	12	Q91PM1	Q91pm1 hepatitis c
145	6	2.6	80	12	Q9W447	Q9w447 hepatitis c	218	6	2.6	114	12	Q91PL9	Q91pl9 hepatitis c
146	6	2.6	80	12	Q9WA15	Q9wa15 hepatitis c	219	6	2.6	114	12	Q91PL8	Q91pl8 hepatitis c
147	6	2.6	80	12	Q9W9W8	Q9w9w8 hepatitis c	220	6	2.6	114	12	Q91PL7	Q91pl7 hepatitis c
148	6	2.6	80	12	Q9W9B4	Q9w9b4 hepatitis c	221	6	2.6	114	12	Q91PL4	Q91pl4 hepatitis c
149	6	2.6	80	12	Q9W903	Q9w903 hepatitis c	222	6	2.6	114	12	Q91PL3	Q91pl3 hepatitis c
150	6	2.6	80	12	Q9W852	Q9w852 hepatitis c	223	6	2.6	114	12	Q91PL2	Q91pl2 hepatitis c
151	6	2.6	80	12	Q9W9M3	Q9w9m3 hepatitis c	224	6	2.6	114	12	Q91PL1	Q91pl1 hepatitis c
152	6	2.6	80	12	Q9W9K3	Q9w9k3 hepatitis c	225	6	2.6	114	12	Q91PL0	Q91pl0 hepatitis c
153	6	2.6	80	12	Q9WN77	Q9wn77 hepatitis c	226	6	2.6	114	12	Q91PK9	Q91pk9 hepatitis c
154	6	2.6	80	12	Q9WN76	Q9wn76 hepatitis c	227	6	2.6	114	12	Q91PK8	Q91pk8 hepatitis c
155	6	2.6	80	12	Q9WN75	Q9wn75 hepatitis c	228	6	2.6	114	12	Q91PK7	Q91pk7 hepatitis c
156	6	2.6	80	12	Q9WN74	Q9wn74 hepatitis c	229	6	2.6	114	12	Q91PK6	Q91pk6 hepatitis c
157	6	2.6	80	12	Q9WN73	Q9wn73 hepatitis c	230	6	2.6	114	12	Q91PK5	Q91pk5 hepatitis c
158	6	2.6	80	12	Q9WN72	Q9wn72 hepatitis c	231	6	2.6	114	12	Q91PK4	Q91pk4 hepatitis c
159	6	2.6	80	12	Q9WN70	Q9wn70 hepatitis c	232	6	2.6	114	12	Q91PK3	Q91pk3 hepatitis c
160	6	2.6	80	12	Q9WN69	Q9wn69 hepatitis c	233	6	2.6	114	12	Q91PK2	Q91pk2 hepatitis c
161	6	2.6	80	12	Q9WN68	Q9wn68 hepatitis c	234	6	2.6	114	12	Q91PK1	Q91pk1 hepatitis c
162	6	2.6	80	12	Q9WN67	Q9wn67 hepatitis c	235	6	2.6	114	12	Q91PK0	Q91pk0 hepatitis c

236	6	2.6	114	12	Q9JPF9	Q9JPF9 hepatitis c	309	6	2.6	149	5	Q9VAI6	Q9VAI6 drosophila
237	6	2.6	115	4	Q9BTD1	Q9BTD1 homo sapien	310	6	2.6	149	16	Q9K7Y0	Q9K7Y0 bacillus ha
238	6	2.6	115	13	Q90YW9	Q90YW9 ictalurus p	311	6	2.6	150	10	Q9SUN5	Q9SUN5 arabidopsis
239	6	2.6	118	17	Q9YET0	Q9YET0 aeryprum p	312	6	2.6	150	11	Q9CQW4	Q9CQW4 mus musculi
240	6	2.6	119	10	Q43548	Q43548 malus domes	313	6	2.6	151	5	Q9S267	Q9S267 osterlaga
241	6	2.6	119	16	Q92J28	Q92J28 rickettsia	314	6	2.6	151	15	Q9S356	Q9S356 human immun
242	6	2.6	120	17	Q9EXJ2	Q9EXJ2 klebsiella	315	6	2.6	152	11	Q9D0D8	Q9D0D8 mus musculi
243	6	2.6	120	17	Q97AD9	Q97AD9 thermoplasma	316	6	2.6	153	7	Q9XR14	Q9XR14 xanthomonas
244	6	2.6	121	12	Q72213	Q72213 hepatitis c	317	6	2.6	153	7	Q9XR14	Q9XR14 equus asinu
245	6	2.6	121	17	Q58660	Q58660 pyrococcus	318	6	2.6	154	10	Q9LUR6	Q9LUR6 arabidopsis
246	6	2.6	124	4	Q9UL92	Q9UL92 homo sapien	319	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
247	6	2.6	125	4	Q9UL95	Q9UL95 homo sapien	320	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
248	6	2.6	125	16	Q51048	Q51048 borrelia bu	321	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
249	6	2.6	130	5	Q9VWK6	Q9VWK6 drosophila	322	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
250	6	2.6	131	5	Q27236	Q27236 schistosoma	323	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
251	6	2.6	132	12	P89035	P89035 pantum mos	324	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
252	6	2.6	133	5	Q9V508	Q9V508 bacillus sp	325	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
253	6	2.6	133	5	Q9V107	Q9V107 rickettsia	326	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
254	6	2.6	133	16	Q92JL7	Q92JL7 drosophila	327	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
255	6	2.6	133	17	Q9XG03	Q9XG03 aeryprum p	328	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
256	6	2.6	135	5	Q17016	Q17016 anopheles g	329	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
257	6	2.6	135	5	Q68188	Q68188 hepatitis c	330	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
258	6	2.6	135	16	Q9XU67	Q9XU67 vibrio chol	331	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
259	6	2.6	136	2	Q93D35	Q93D35 uncultured	332	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
260	6	2.6	136	11	Q9CRJ5	Q9CRJ5 mus musculi	333	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
261	6	2.6	136	16	Q9P1U9	Q9P1U9 campylobact	334	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
262	6	2.6	136	16	Q92EM0	Q92EM0 listeria in	335	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
263	6	2.6	137	12	Q911I1	Q911I1 hepatitis c	336	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
264	6	2.6	137	12	Q911I0	Q911I0 hepatitis c	337	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
265	6	2.6	137	12	Q911I9	Q911I9 hepatitis c	338	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
266	6	2.6	137	12	Q911H8	Q911H8 hepatitis c	339	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
267	6	2.6	137	12	Q911H7	Q911H7 hepatitis c	340	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
268	6	2.6	137	12	Q911H6	Q911H6 hepatitis c	341	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
269	6	2.6	137	12	Q911H5	Q911H5 hepatitis c	342	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
270	6	2.6	137	12	Q911H4	Q911H4 hepatitis c	343	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
271	6	2.6	137	12	Q911H3	Q911H3 hepatitis c	344	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
272	6	2.6	137	12	Q911H2	Q911H2 hepatitis c	345	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
273	6	2.6	137	12	Q911H1	Q911H1 hepatitis c	346	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
274	6	2.6	137	12	Q911H0	Q911H0 hepatitis c	347	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
275	6	2.6	137	12	Q911G9	Q911G9 hepatitis c	348	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
276	6	2.6	137	12	Q911G8	Q911G8 hepatitis c	349	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
277	6	2.6	137	12	Q911G7	Q911G7 hepatitis c	350	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
278	6	2.6	137	12	Q911G6	Q911G6 hepatitis c	351	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
279	6	2.6	137	12	Q911G5	Q911G5 hepatitis c	352	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
280	6	2.6	137	12	Q911G4	Q911G4 hepatitis c	353	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
281	6	2.6	137	12	Q911G3	Q911G3 hepatitis c	354	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
282	6	2.6	137	12	Q911G2	Q911G2 hepatitis c	355	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
283	6	2.6	137	12	Q911G1	Q911G1 hepatitis c	356	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
284	6	2.6	137	12	Q911G0	Q911G0 hepatitis c	357	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
285	6	2.6	137	12	Q911F9	Q911F9 hepatitis c	358	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
286	6	2.6	137	12	Q911F8	Q911F8 hepatitis c	359	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
287	6	2.6	137	12	Q911F6	Q911F6 hepatitis c	360	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
288	6	2.6	137	12	Q911F5	Q911F5 hepatitis c	361	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
289	6	2.6	137	12	Q911F4	Q911F4 hepatitis c	362	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
290	6	2.6	137	12	Q911F3	Q911F3 hepatitis c	363	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
291	6	2.6	137	12	Q911F2	Q911F2 hepatitis c	364	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
292	6	2.6	137	12	Q911F1	Q911F1 hepatitis c	365	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
293	6	2.6	137	12	Q911F0	Q911F0 hepatitis c	366	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
294	6	2.6	137	12	Q911E9	Q911E9 hepatitis c	367	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
295	6	2.6	137	12	Q911E8	Q911E8 hepatitis c	368	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
296	6	2.6	137	12	Q911E7	Q911E7 hepatitis c	369	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
297	6	2.6	137	12	Q911E6	Q911E6 hepatitis c	370	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
298	6	2.6	137	12	Q911E5	Q911E5 hepatitis c	371	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
299	6	2.6	137	12	Q911E4	Q911E4 hepatitis c	372	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
300	6	2.6	139	2	Q9AKS1	Q9AKS1 pseudomonas	373	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
301	6	2.6	139	2	Q53856	Q53856 spiropilasma	374	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
302	6	2.6	139	6	Q96TL4	Q96TL4 oplostoma	375	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
303	6	2.6	139	6	Q9SK12	Q9SK12 macaca fasc	376	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
304	6	2.6	139	16	Q9UR37	Q9UR37 neisseria m	377	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
305	6	2.6	141	16	Q9US31	Q9US31 pseudomonas	378	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
306	6	2.6	144	10	Q9SMD6	Q9SMD6 lamnaria d	379	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
307	6	2.6	144	16	Q51117	Q51117 borrelia bu	380	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c
308	6	2.6	148	8	Q09353	Q09353 lycopodium	381	6	2.6	154	12	Q9LUR6	Q9LUR6 hepatitis c

382	6	2.6	186	12	091YX9	091YX9 hepatitis c	455	6	2.6	212	10	09FTK1	09ftk1 oryza sativ
383	6	2.6	186	12	091YX8	091YX8 hepatitis c	456	6	2.6	213	13	09YH82	09yhb2 gallus gall
384	6	2.6	186	12	091YX7	091YX7 hepatitis c	457	6	2.6	213	13	09PPR9	09ppr9 gallus gall
385	6	2.6	186	12	091YX6	091YX6 hepatitis c	458	6	2.6	214	16	092710	092710 listeria in
386	6	2.6	186	12	091YX5	091YX5 hepatitis c	459	6	2.6	215	2	09XA90	09xa90 streptomyce
387	6	2.6	186	12	091Y12	091Y12 hepatitis c	460	6	2.6	215	5	09YXS1	09yxs1 leishmania
388	6	2.6	186	12	091Y11	091Y11 hepatitis c	461	6	2.6	218	5	09V6P3	09v6p3 drosophila
389	6	2.6	186	12	091Y10	091Y10 hepatitis c	462	6	2.6	218	16	09K790	09k790 bacillus ha
390	6	2.6	186	12	091YK9	091YK9 hepatitis c	463	6	2.6	219	17	09HNX8	09hnx8 halobacteri
391	6	2.6	186	12	091YK8	091YK8 hepatitis c	464	6	2.6	219	5	09VAF1	09vaf1 drosophila
392	6	2.6	186	12	091YK5	091YK5 hepatitis c	465	6	2.6	220	4	096S11	096s11 homo sapien
393	6	2.6	186	12	091YK5	091YK5 hepatitis c	466	6	2.6	220	8	09T4W8	09t4w8 cyanophora
394	6	2.6	186	12	091YK4	091YK4 hepatitis c	467	6	2.6	221	15	091019	091019 human immun
395	6	2.6	186	12	091YK3	091YK3 hepatitis c	468	6	2.6	222	4	09H532	09h532 homo sapien
396	6	2.6	186	12	091YK2	091YK2 hepatitis c	469	6	2.6	222	10	093VG5	093vg5 streptomyce
397	6	2.6	186	12	091YK0	091YK1 hepatitis c	470	6	2.6	223	12	010691	010691 cymbidium m
398	6	2.6	186	12	091YK0	091YK0 hepatitis c	471	6	2.6	223	16	09A0K2	09a0k2 streptococ
399	6	2.6	186	12	091YJ9	091YJ9 hepatitis c	472	6	2.6	224	3	003322	003322 saccharomyc
400	6	2.6	186	12	091YJ8	091YJ8 hepatitis c	473	6	2.6	224	16	025350	025350 helicobacte
401	6	2.6	186	12	091YJ7	091YJ7 hepatitis c	474	6	2.6	226	2	086726	086726 streptomyce
402	6	2.6	186	12	091YJ6	091YJ6 hepatitis c	475	6	2.6	226	10	09LN67	09ln67 arabidopsis
403	6	2.6	186	12	091YJ5	091YJ5 hepatitis c	476	6	2.6	226	15	087114	087114 chimpanzee
404	6	2.6	186	12	091YJ4	091YJ4 hepatitis c	477	6	2.6	227	16	09CD41	09cd41 mycobacteri
405	6	2.6	186	12	091YJ3	091YJ3 hepatitis c	478	6	2.6	228	12	092454	092454 bombyx mori
406	6	2.6	186	12	091YJ0	091YJ1 hepatitis c	479	6	2.6	229	16	09CK96	09ck96 pasteurella
407	6	2.6	186	12	091YJ0	091YJ0 hepatitis c	480	6	2.6	230	5	061518	061518 caenorhabdi
408	6	2.6	186	12	091YI9	091YI9 hepatitis c	481	6	2.6	230	10	09F1S1	09f1s1 arabidopsis
409	6	2.6	186	12	091YI8	091YI8 hepatitis c	482	6	2.6	230	10	09ATN6	09atb6 zea mays
410	6	2.6	186	12	091YI7	091YI7 hepatitis c	483	6	2.6	231	2	P77975	P77975 shewanella
411	6	2.6	186	12	091YI6	091YI6 hepatitis c	484	6	2.6	231	7	008613	008613 cyphotilapia
412	6	2.6	186	12	091YI5	091YI5 hepatitis c	485	6	2.6	232	5	09VYGA	09vyga drosophila
413	6	2.6	186	12	091YI4	091YI4 hepatitis c	486	6	2.6	232	10	049910	049910 nicotiana t
414	6	2.6	187	2	052564	052564 pseudomonas	487	6	2.6	232	10	09MAJ3	09maj3 nicotiana t
415	6	2.6	188	4	096T59	096T59 homo sapien	488	6	2.6	236	12	085028	085028 pseudorhabd
416	6	2.6	188	5	096T7M7	096T7M7 chaetastus	489	6	2.6	236	17	09AHV1	09ahv1 halobacteri
417	6	2.6	189	2	09L0W6	09L0W6 streptomyce	490	6	2.6	238	2	09XB10	09xb10 manduca sex
418	6	2.6	190	2	09ALK4	09ALK4 escherichia	491	6	2.6	239	5	09NB10	09nb10 manduca sex
419	6	2.6	190	15	09DVI6	09dvi6 human immun	492	6	2.6	239	10	023889	023889 oryza sativ
420	6	2.6	192	12	081414	081414 hepatitis c	493	6	2.6	241	5	09GPI3	09gpi3 drosophila
421	6	2.6	192	12	081432	081432 hepatitis c	494	6	2.6	241	5	095UN3	095un3 drosophila
422	6	2.6	192	12	081435	081435 hepatitis c	495	6	2.6	241	5	095NK2	095nk2 drosophila
423	6	2.6	192	12	081397	081397 hepatitis c	496	6	2.6	241	5	095NM6	095nm6 drosophila
424	6	2.6	194	4	09UG17	09ug17 homo sapien	497	6	2.6	247	5	09XVS9	09xvs9 caenorhabdi
425	6	2.6	194	12	068581	068581 hepatitis c	498	6	2.6	247	16	092K30	092k30 helicobacte
426	6	2.6	194	16	097D08	097d08 clostridium	499	6	2.6	248	2	P71465	P71465 lacticobacill
427	6	2.6	195	2	09R5Y6	09r5y6 azotobacter	500	6	2.6	248	16	092CQ9	092c99 listeria in
428	6	2.6	195	5	016759	016759 caenorhabdi	501	6	2.6	249	3	074385	074385 schistosach
429	6	2.6	196	5	026864	026864 trypanosoma	502	6	2.6	250	4	09NV53	09nv53 homo sapien
430	6	2.6	196	16	P95270	P95270 mycobacteri	503	6	2.6	250	4	096G66	096g66 homo sapien
431	6	2.6	197	9	038147	038147 bacterioph	504	6	2.6	250	11	09CR18	09cr18 mus musculu
432	6	2.6	197	12	083114	083114 mastadenovi	505	6	2.6	251	2	09S2R7	09s2r7 streptomyce
433	6	2.6	198	12	069020	069020 human herpe	506	6	2.6	251	16	092YR4	092yr4 rhizobium m
434	6	2.6	198	16	09KFE3	09kfe3 bacillus ha	507	6	2.6	253	16	098B17	098b17 rhizobium l
435	6	2.6	199	16	092R09	092r09 rhizobium m	508	6	2.6	254	2	09K316	09k316 streptomyce
436	6	2.6	200	16	09K570	09k570 mycobacteri	509	6	2.6	254	10	043422	043422 cucumis sat
437	6	2.6	201	2	09K523	09k523 mycobacteri	510	6	2.6	254	10	09S8K2	09s8k2 cucumis sat
438	6	2.6	201	5	09VUS1	09vus1 drosophila	511	6	2.6	254	16	09A4Y5	09a4y5 caulobacter
439	6	2.6	203	7	09XRNO	09xrno rhinoceros	512	6	2.6	256	8	0940R4	0940r4 pleurotus o
440	6	2.6	204	5	019022	019022 caenorhabdi	513	6	2.6	257	4	09PIV9	09pi99 homo sapien
441	6	2.6	204	11	0922V3	0922v3 mus musculu	514	6	2.6	257	10	004233	004233 victoria faba
442	6	2.6	204	16	092T45	092t45 rhizobium m	515	6	2.6	258	5	09N4P4	09n4p4 caenorhabdi
443	6	2.6	205	5	045937	045937 caenorhabdi	516	6	2.6	260	10	09S0B4	09s0b4 arabidopsis
444	6	2.6	207	5	076756	076756 apis mellif	517	6	2.6	260	10	09AS67	09as67 oryza sativ
445	6	2.6	207	15	091028	091028 human immun	518	6	2.6	263	2	005370	005370 actinobacill
446	6	2.6	208	13	090YR6	090yr6 ictalurus p	519	6	2.6	265	17	097AN5	097an5 thermoplaem
447	6	2.6	208	15	091026	091026 human immun	520	6	2.6	267	6	002764	002764 oryctolagus
448	6	2.6	208	16	09ABR4	09abr4 caulobacter	521	6	2.6	268	10	P93654	P93654 arabidopsis
449	6	2.6	209	3	093915	093915 schizophy11	522	6	2.6	269	5	092B38	092b38 listeria in
450	6	2.6	209	13	09PSN8	09psn8 trimeresuru	523	6	2.6	269	5	09R9E2	09r9e2 bacillus su
451	6	2.6	209	15	0906Y5	0906y5 human immun	524	6	2.6	270	11	09XV58	09xv58 caenorhabdi
452	6	2.6	209	15	091043	091043 human immun	525	6	2.6	270	11	099K19	099k19 mus musculu
453	6	2.6	211	13	09PWP2	09pwp2 gallus gall	526	6	2.6	270	16	09A3H3	09a3h3 caulobacter
454	6	2.6	212	5	09VYI4	09vyi4 drosophila	527	6	2.6	270	16	098BP8	098bp8 mycoplasma

528	6	2.6	272	2	Q93Q65	Q93q65 klebsiella	601	6	2.6	325	10	Q9SWA2	Q9swa2 acetabulari
529	6	2.6	272	5	O17311	O17311 drosophila	602	6	2.6	326	5	Q9VLE9	Q9vle9 drosophila
530	6	2.6	272	5	O17312	O17312 drosophila	603	6	2.6	326	16	P73753	P73753 synechocyst
531	6	2.6	272	5	Q9VUJ1	Q9vuj1 drosophila	604	6	2.6	327	2	Q9RPD1	Q9rpd1 rhodobacter
532	6	2.6	273	2	Q9FCH8	Q9fch8 streptomyce	605	6	2.6	327	2	Q54790	Q54790 rhodobacter
533	6	2.6	273	17	O57735	O57735 pyrococcus	606	6	2.6	327	11	Q9CYU4	Q9cyu4 mus musculi
534	6	2.6	274	5	O16860	O16860 drosophila	607	6	2.6	328	5	Q9V5B6	Q9v5b6 drosophila
535	6	2.6	274	5	Q9VAD9	Q9vad9 drosophila	608	6	2.6	328	17	Q9VCB9	Q9vcb9 thermoplas
536	6	2.6	274	5	Q964T5	Q964t5 porcillo s	609	6	2.6	329	12	O09798	O09798 human herpe
537	6	2.6	274	5	Q95RR6	Q95rr6 drosophila	610	6	2.6	329	16	Q9PC8	Q9pc8 ureaplasma
538	6	2.6	274	9	O64041	O64041 bacterioph	611	6	2.6	329	16	Q9CKZ3	Q9ckz3 pasteurella
539	6	2.6	274	12	Q91B76	Q91b76 adoxophyes	612	6	2.6	330	2	Q9RK26	Q9rk26 streptomyce
540	6	2.6	274	16	O31981	O31981 bacillus su	613	6	2.6	330	16	Q92XE3	Q92xe3 rhizobium m
541	6	2.6	275	16	O34437	O34437 bacillus su	614	6	2.6	330	17	Q97AR5	Q97ar5 thermoplas
542	6	2.6	275	16	Q97FS8	Q97fs8 clostridium	615	6	2.6	331	3	Q9UWZ0	Q9uwz0 candida alb
543	6	2.6	277	4	Q961D9	Q961d9 homo sapien	616	6	2.6	332	2	O68170	O68170 lactococcus
544	6	2.6	280	17	Q9V2J1	Q9v2j1 pyrococcus	617	6	2.6	332	12	Q9PVL8	Q9pvl8 xestia c-nl
545	6	2.6	281	4	Q9BZ90	Q9bz90 homo sapien	618	6	2.6	333	4	Q9BVH1	Q9bvh1 homo sapien
546	6	2.6	281	10	Q9XE15	Q9xe15 oryza sativ	619	6	2.6	334	4	Q96FE7	Q96fe7 homo sapien
547	6	2.6	281	12	P89133	P89133 simian hemo	620	6	2.6	335	16	Q99VY7	Q99vy7 staphylococ
548	6	2.6	281	17	Q9HPJ3	Q9hpi3 halobacteri	621	6	2.6	335	16	Q93ZFO	Q93zf0 staphylococ
549	6	2.6	283	10	Q9SJB6	Q9sjb6 arabidopsis	622	6	2.6	337	5	Q9GV75	Q9gv75 trypanosoma
550	6	2.6	284	3	O42914	O42914 schizosacch	623	6	2.6	337	16	Q92VV7	Q92vv7 rhizobium m
551	6	2.6	284	16	Q9WVW7	Q9wvw7 thermotoga	624	6	2.6	339	16	Q910Z1	Q910z1 pseudomonas
552	6	2.6	284	16	Q98GL4	Q98gl4 rhizobium l	625	6	2.6	340	11	Q9DBT3	Q9dbt3 mus musculu
553	6	2.6	286	5	Q9VBE0	Q9vbe0 drosophila	626	6	2.6	340	13	Q9YHY2	Q9yhy2 lampetra fl
554	6	2.6	286	16	Q9CKX6	Q9ckx6 pasteurella	627	6	2.6	341	5	O19550	O19550 caenorhabdi
555	6	2.6	289	4	Q96N10	Q96n10 homo sapien	628	6	2.6	342	2	O68130	O68130 neisseria
556	6	2.6	294	2	Q9XAM3	Q9xam3 lactobacill	629	6	2.6	342	2	O68332	O68332 neisseria e
557	6	2.6	294	5	Q9VVE2	Q9vve2 drosophila	630	6	2.6	342	2	Q9R3R1	Q9r3r1 neisseria l
558	6	2.6	294	10	Q9LE53	Q9le53 oryza sativ	631	6	2.6	342	2	Q9R3R0	Q9r3r0 neisseria c
559	6	2.6	294	16	O07242	O07242 mycobacteri	632	6	2.6	342	2	Q9R3A4	Q9r3a4 neisseria p
560	6	2.6	296	12	O69118	O69118 human herpe	633	6	2.6	342	2	Q9R3A3	Q9r3a3 neisseria m
561	6	2.6	296	16	O87127	O87127 pseudomonas	634	6	2.6	342	2	Q9R3R3	Q9r3r3 neisseria p
562	6	2.6	297	9	Q38373	Q38373 lactococcus	635	6	2.6	342	2	O86406	O86406 neisseria p
563	6	2.6	297	16	Q9CEW6	Q9cew6 lactococcus	636	6	2.6	342	2	O86379	O86379 neisseria c
564	6	2.6	298	2	Q91067	Q91067 streptomyce	637	6	2.6	342	2	O86413	O86413 neisseria s
565	6	2.6	299	4	Q9Y4N1	Q9y4n1 homo sapien	638	6	2.6	342	2	O86386	O86386 neisseria f
566	6	2.6	299	16	Q98GB2	Q98gb2 rhizobium l	639	6	2.6	342	2	O86416	O86416 neisseria s
567	6	2.6	300	16	Q929B2	Q929b2 listeria in	640	6	2.6	342	2	O86400	O86400 neisseria m
568	6	2.6	301	16	Q947Y9	Q947y9 caulobacter	641	6	2.6	342	2	O86407	O86407 neisseria p
569	6	2.6	302	10	Q9ATN1	Q9atn1 zea mays (m	642	6	2.6	342	2	O86336	O86336 neisseria p
570	6	2.6	303	2	Q9Z9P7	Q9z9p7 bacillus ha	643	6	2.6	342	2	Q9R807	Q9r807 neisseria m
571	6	2.6	304	6	Q9N120	Q9n120 oryctolagus	644	6	2.6	342	2	Q9R808	Q9r808 neisseria m
572	6	2.6	305	5	Q9NSW0	Q9nsw0 caenorhabdi	645	6	2.6	342	2	O86409	O86409 neisseria p
573	6	2.6	308	4	Q9UFU3	Q9ufu3 homo sapien	646	6	2.6	342	2	O86401	O86401 neisseria p
574	6	2.6	309	11	Q9EQA6	Q9eqa6 mus musculu	647	6	2.6	342	2	O86387	O86387 neisseria f
575	6	2.6	309	11	Q9EQA4	Q9eqa4 mus musculu	648	6	2.6	342	2	O86377	O86377 neisseria f
576	6	2.6	310	2	Q9ZAL1	Q9zal1 escherichia	649	6	2.6	342	2	O86410	O86410 neisseria p
577	6	2.6	310	16	Q910X5	Q910x5 pseudomonas	650	6	2.6	342	2	Q9R806	Q9r806 neisseria p
578	6	2.6	311	17	O26780	O26780 methanococ	651	6	2.6	342	2	O86390	O86390 neisseria p
579	6	2.6	312	16	Q9P1X5	Q9p1x5 campylobact	652	6	2.6	343	3	Q9P866	Q9p866 candida alb
580	6	2.6	312	17	Q97U31	Q97u31 sulfolobus	653	6	2.6	343	3	Q9P7S8	Q9p7s8 schizosacch
581	6	2.6	313	2	O05094	O05094 bacillus su	654	6	2.6	343	10	Q91VW5	Q91vw5 arabidopsis
582	6	2.6	313	16	P94529	P94529 mus musculu	655	6	2.6	344	2	O82858	O82858 acetobacter
583	6	2.6	314	11	Q9EQA5	Q9eqa5 mus musculu	656	6	2.6	344	10	Q91LY4	Q91ly4 brassica na
584	6	2.6	315	4	Q9UHJ9	Q9uhj9 homo sapien	657	6	2.6	345	5	Q9U3J7	Q9u3j7 caenorhabdi
585	6	2.6	315	4	Q9UF01	Q9uf01 homo sapien	658	6	2.6	345	5	Q95VP7	Q95vp7 leishmania
586	6	2.6	315	10	Q9SWA1	Q9swa1 acetabulari	659	6	2.6	345	16	Q98RH7	Q98rh7 mycoplasma
587	6	2.6	315	10	Q9SWA0	Q9swa0 acetabulari	660	6	2.6	347	2	Q59797	Q59797 neisseria g
588	6	2.6	315	11	O62943	O62943 rattus norv	661	6	2.6	347	16	Q9RXM2	Q9rxm2 delinococcus
589	6	2.6	315	12	Q98UL4	Q98ul4 hepatitis c	662	6	2.6	348	2	Q9ZBJ3	Q9zbj3 streptomyce
590	6	2.6	315	12	Q98UL3	Q98ul3 hepatitis c	663	6	2.6	348	10	Q9AAT9	Q9aat9 pennisetum
591	6	2.6	315	12	Q9WMZ7	Q9wmz7 nanovirus-1	664	6	2.6	349	2	Q9EY91	Q9ey91 clostridium
592	6	2.6	317	5	Q18947	Q18947 caenorhabdi	665	6	2.6	349	16	Q97K00	Q97k00 clostridium
593	6	2.6	317	10	Q94HA7	Q94ha7 oryza sativ	666	6	2.6	350	16	Q9PPI2	Q9ppi2 xylella fas
594	6	2.6	317	13	Q919B8	Q919b8 gallus gall	667	6	2.6	351	17	Q971V4	Q971v4 sulfolobus
595	6	2.6	318	16	Q92XE4	Q92xe4 rhizobium m	668	6	2.6	352	4	Q9BYE7	Q9bye7 homo sapien
596	6	2.6	318	16	Q92EP4	Q92ef4 listeria in	669	6	2.6	352	16	Q9A0B4	Q9a0b4 streptococ
597	6	2.6	320	16	Q9PBQ4	Q9pbq4 candida alb	670	6	2.6	353	7	Q9VPD8	Q9vpd8 drosophila
598	6	2.6	320	16	Q92SG2	Q92sg2 rhizobium m	671	6	2.6	353	7	Q9TNZ2	Q9tnz2 sus scrofa
599	6	2.6	322	2	O32511	O32511 delinococcus	672	6	2.6	353	16	Q9RSX8	Q9rsx8 delinococcus
600	6	2.6	325	10	O80682	O80682 arabidopsis	673	6	2.6	353	17	Q9UXV8	Q9uxv8 pyrococcus

674	2.6	354	4	Q9H254	Q9H2s4 homo sapien	747	6	400	16	Q988C1	Q988c1 rhizobium 1
675	2.6	354	10	Q94LH4	Q94Lh4 oryza sativ	748	6	401	16	Q07563	Q07563 bacillus su
676	2.6	355	2	Q93IP2	Q93IP2 burkholderi	749	6	402	5	Q9VDQ4	Q9VDq4 drosophila
677	2.6	355	10	Q81748	Q81748 arabdiposis	750	6	402	2	Q07675	Q07675 haemophilus
678	2.6	356	2	Q9L340	Q9L340 sphingomonas	751	6	406	12	Q11374	Q11374 molluscum c
679	2.6	357	16	Q91256	Q91256 pseudomonas	752	6	407	10	Q9SXD7	Q9Sxd7 arabdiposis
680	2.6	357	16	Q9CHR2	Q9chr2 lactococcus	753	6	409	10	Q9SBM1	Q9sbm1 volvox cart
681	2.6	359	16	Q9CHR9	Q9chr9 lactococcus	754	6	410	11	Q9JRD2	Q9jrd2 rattus norv
682	2.6	361	6	Q19075	Q19075 sus scrofa	755	6	410	11	Q9JRD1	Q9jrd1 rattus norv
683	2.6	361	7	Q19242	Q19242 sus scrofa	756	6	410	11	Q9JRD2	Q9jrd2 mus musculu
684	2.6	361	7	Q19244	Q19244 sus scrofa	757	6	411	13	Q9JRD1	Q9jrd1 mus musculu
685	2.6	361	7	Q19244	Q19244 sus scrofa	757	6	411	13	Q9JRD1	Q9jrd1 mus musculu
686	2.6	362	16	Q92K12	Q92K12 rhizobium m	758	6	413	2	Q9PA21	Q9PA21 xylella me
687	2.6	363	7	Q30870	Q30870 papio hamad	759	6	413	5	Q937R4	Q937r4 brucella me
688	2.6	363	7	Q9BCZ0	Q9bcz0 papio cynoc	760	6	413	5	Q9VM09	Q9vm09 drosophila
689	2.6	363	7	Q31067	Q31067 sus scrofa	761	6	414	2	Q32383	Q32383 streptomyce
690	2.6	364	6	Q9TSW2	Q9TSW2 sus scrofa	762	6	414	10	Q9ART0	Q9ART0 oryza sativ
691	2.6	364	7	Q19243	Q19243 sus scrofa	763	6	414	16	Q53279	Q53279 mycobacteri
692	2.6	364	7	Q19245	Q19245 sus scrofa	764	6	414	16	Q92RKO	Q92Rk0 rhizobium m
693	2.6	364	7	Q31068	Q31068 sus scrofa	765	6	415	11	Q9WTO3	Q9Wtq3 rattus norv
694	2.6	364	10	P93070	P93070 betula verr	766	6	415	11	Q9EPW2	Q9EPw2 mus musculu
695	2.6	364	16	Q92R39	Q92r39 rhizobium m	767	6	417	5	Q15828	Q15828 leishmania
696	2.6	365	2	Q9XD39	Q9xd39 bacteroides	768	6	417	16	Q92RGO	Q92Rg0 rhizobium m
697	2.6	365	5	Q9U220	Q9u220 caenorhabdi	769	6	418	16	Q98DY8	Q98dy8 rhizobium l
698	2.6	366	2	Q9KZ00	Q9Kz00 streptomyc	770	6	419	16	Q55115	Q55115 synchocyst
699	2.6	366	4	Q96PM9	Q96pm9 homo sapien	771	6	419	16	Q9PJ00	Q9pj00 chlamydia m
700	2.6	366	7	Q31069	Q31069 sus scrofa	772	6	419	16	Q9K013	Q9K013 neisseria m
701	2.6	367	17	Q96X16	Q96x16 sulfolobus	773	6	419	16	Q9JVT6	Q9jvt6 neisseria m
702	2.6	368	2	Q86984	Q86984 thermomono	774	6	419	16	Q9HMY1	Q9hmv1 pseudomonas
703	2.6	369	2	Q52807	Q52807 amycolatops	775	6	420	2	P97011	P97011 streptomyce
704	2.6	369	10	Q65663	Q65663 arabdiposis	776	6	420	2	Q9ZAG7	Q9Zag7 actinobacil
705	2.6	370	16	Q9RTU4	Q9rtu4 delnococcus	777	6	420	4	Q9H255	Q9h255 homo sapien
706	2.6	371	5	Q46052	Q46052 drosophila	778	6	420	4	Q96QB5	Q96qb5 homo sapien
707	2.6	371	10	Q9C914	Q9C914 arabdiposis	779	6	420	16	Q9CUR2	Q9Csr2 pasteurella
708	2.6	372	3	Q12121	Q12121 saccharomyc	780	6	421	2	Q9X782	Q9X782 streptomyce
709	2.6	372	10	Q9C913	Q9c913 arabdiposis	781	6	421	5	Q9BIC9	Q9bic9 trichinella
710	2.6	372	16	Q9KRG6	Q9Krg6 bacillus ha	782	6	421	16	Q92RKO	Q92Rk0 rhizobium m
711	2.6	374	13	Q9W6F8	Q9W6f8 xenopus lae	783	6	422	5	Q45786	Q45786 caenorhabdi
712	2.6	375	16	Q9RW21	Q9RW21 delnococcus	784	6	423	2	Q9ZH30	Q9zh30 listeria mo
713	2.6	376	5	Q9W566	Q9W566 drosophila	785	6	423	2	Q93Q15	Q93q15 listeria mo
714	2.6	378	11	P89002	P89002 praomys nat	786	6	423	16	Q9K6E8	Q9K6E8 bacillus ha
715	2.6	378	17	Q97YU3	Q97yus3 sulfolobus	787	6	423	16	Q927U2	Q927u2 listeria in
716	2.6	379	2	Q87181	Q87181 streptococc	788	6	424	10	Q94DK9	Q94dk9 oryza sativ
717	2.6	379	2	Q9AQJ1	Q9aqj1 streptococc	789	6	425	3	Q9F7M3	Q9f7m3 uncultured
718	2.6	380	5	Q93878	Q93878 caenorhabdi	790	6	425	3	Q9C007	Q9c007 neurospora
719	2.6	381	3	Q43031	Q43031 schizosacch	791	6	425	10	Q9LDO2	Q9Ldo2 nicotiana t
720	2.6	381	10	Q9CAC3	Q9cac3 arabdiposis	792	6	426	3	Q96M33	Q96m33 podospora a
721	2.6	382	5	Q22541	Q22541 caenorhabdi	793	6	427	2	Q99PX1	Q99px1 vibrio algi
722	2.6	383	2	Q9Z3A8	Q9z3a8 burkholderi	794	6	427	2	P95326	P95326 myxococcus
723	2.6	383	5	Q9VD25	Q9vd25 drosophila	795	6	427	5	Q9VG80	Q9vg80 drosophila
724	2.6	384	4	Q96GN1	Q96gn1 homo sapien	796	6	428	2	Q32417	Q32417 mycoplasma
725	2.6	384	5	Q9V612	Q9V612 drosophila	797	6	428	2	Q9R3N6	Q9r3n6 mycoplasma
726	2.6	384	16	Q986H2	Q986h2 rhizobium 1	798	6	428	2	Q9RCX7	Q9rcx7 mycoplasma
727	2.6	385	11	Q91YH1	Q91yhl cricetus	799	6	428	2	Q9RCX5	Q9rcx5 mycoplasma
728	2.6	386	5	Q966D5	Q966d5 caenorhabdi	800	6	428	2	Q9RCX3	Q9rcx3 mycoplasma
729	2.6	386	10	Q9FNV1	Q9fnv1 dactylis gl	801	6	429	2	Q9RGX6	Q9rgx6 mycoplasma
730	2.6	388	4	Q96H72	Q96h72 homo sapien	802	6	429	2	Q9RGX4	Q9rgx4 mycoplasma
731	2.6	391	11	Q9D9N3	Q9d9n3 mus musculu	803	6	429	4	Q96B82	Q96b82 homo sapien
732	2.6	391	16	Q98A00	Q98a00 rhizobium 1	804	6	430	12	Q39780	Q39780 equine herp
733	2.6	391	17	Q9HOK2	Q9hok2 halobacteri	805	6	431	16	Q9KSH6	Q9Ksh6 vibrio chol
734	2.6	392	6	Q9BDQ4	Q9bdq4 canis famli	806	6	432	5	Q9W216	Q9W216 drosophila
735	2.6	392	10	Q9M9C3	Q9m9c3 arabdiposis	807	6	433	2	Q9X8V6	Q9x8v6 streptomyce
736	2.6	392	17	Q9U228	Q9u228 pyrococcus	808	6	433	3	Q74763	Q74763 schizosacch
737	2.6	393	2	Q9EMC4	Q9emc4 streptomyce	809	6	439	2	Q53589	Q53589 staphylococ
738	2.6	394	5	Q9AWM1	Q9awm1 caenorhabdi	810	6	439	4	Q9H2V8	Q9h2v8 homo sapien
739	2.6	396	5	Q9XXC7	Q9xxc7 caenorhabdi	811	6	440	16	Q922L9	Q922l9 rickettsia
740	2.6	397	5	Q9GR07	Q9grq7 leishmania	812	6	442	16	Q05507	Q05507 bacillus su
741	2.6	397	11	Q70348	Q70348 mus musculu	813	6	442	16	Q909C7	Q909c7 caenorhabdi
742	2.6	397	11	Q99K08	Q99k08 mus musculu	814	6	444	16	Q34545	Q34545 bacillus su
743	2.6	399	5	Q43935	Q43935 trichomonas	815	6	445	16	Q94304	Q94304 caenorhabdi
744	2.6	399	6	Q9TSM1	Q9tsm1 sus scrofa	816	6	448	5	Q960U7	Q960u7 drosophila
745	2.6	400	2	Q938T4	Q938t4 streptococc	817	6	448	16	Q31428	Q31428 bacillus su
746	2.6	400	16	Q9A0M2	Q9a0m2 streptococc	819	6	449	11	Q9CYK8	Q9cyk8 mus musculu

820	6	2.6	450	16	083238	08338	treponema p	893	6	2.6	510	5	024425	024425 drosophila
821	6	2.6	451	11	035254	035254	rattus norv	894	6	2.6	510	10	042875	042875 lycopersico
822	6	2.6	452	2	091176	091176	streptomyces	895	6	2.6	516	1	09c4m3	09c4m3 halobacteri
823	6	2.6	452	3	09HEB4	09HEB4	neurospora	896	6	2.6	516	16	0970P4	0970P4 streptococc
824	6	2.6	453	2	094BV5	094BV5	arabidopsis	897	6	2.6	516	17	097AB0	097AB0 thermoplasma
825	6	2.6	453	2	093S03	093S03	pseudomonas	898	6	2.6	518	10	095VG8	095VG8 arabidopsis
826	6	2.6	453	2	093S01	093S01	pseudomonas	899	6	2.6	523	3	094CQ1	094CQ1 oryza sativ
827	6	2.6	453	16	09K8Q5	09K8Q5	bacillus ha	900	6	2.6	525	10	09VUC9	09VUC9 drosophila
828	6	2.6	454	4	09BR11	09BR11	homo sapien	901	6	2.6	526	3	060097	060097 schizosacch
829	6	2.6	458	16	092HL2	092HL2	ricketsia	902	6	2.6	526	5	09Y110	09Y110 trichomonas
830	6	2.6	459	5	095R06	095R06	drosophila	903	6	2.6	526	11	054887	054887 mus musculu
831	6	2.6	460	17	09HKK1	09HKK1	thermoplasma	904	6	2.6	526	12	085027	085027 pseudocorale
832	6	2.6	464	16	084498	084498	chlamydia t	905	6	2.6	526	16	09RUB1	09RUB1 streptococc
833	6	2.6	466	2	09AQ17	09AQ17	streptococc	906	6	2.6	528	5	0960B6	0960B6 drosophila
834	6	2.6	466	2	09AFH1	09AFH1	streptococc	907	6	2.6	529	12	085213	085213 pity virus
835	6	2.6	466	2	093T13	093T13	streptococc	908	6	2.6	531	17	09HKH9	09HKH9 thermoplasma
836	6	2.6	466	15	09DSK6	09DSK6	human immun	909	6	2.6	532	5	095R30	095R30 drosophila
837	6	2.6	467	12	P89433	P89433	hepates slimp	910	6	2.6	534	2	09RPV9	09RPV9 bacillus me
838	6	2.6	468	4	09N2L2	09N2L2	homo sapien	911	6	2.6	534	5	018515	018515 hydra atten
839	6	2.6	468	17	028528	028528	archaeoglob	912	6	2.6	535	2	052716	052716 klebsiella
840	6	2.6	469	10	09FV71	09FV71	arabidopsis	913	6	2.6	535	2	076919	076919 drosophila
841	6	2.6	469	10	09FNV1	09FNV1	arabidopsis	914	6	2.6	536	12	09WRT5	09WRT5 macaca mulla
842	6	2.6	470	10	09SUI6	09SUI6	arabidopsis	915	6	2.6	536	12	09J2L9	09J2L9 macaca mulla
843	6	2.6	471	8	095B76	095B76	cycas taiwa	916	6	2.6	537	5	09V8K8	09V8K8 drosophila
844	6	2.6	471	8	095B75	095B75	cycas taiwa	917	6	2.6	539	16	09RMQ4	09RMQ4 delnococtus
845	6	2.6	472	10	09FTH7	09FTH7	oryza sativ	918	6	2.6	540	5	09NA46	09NA46 caenorhabdi
846	6	2.6	473	10	049868	049868	hordeum vul	919	6	2.6	540	6	095K25	095K25 macaca fasc
847	6	2.6	473	11	099K48	099K48	mus musculu	920	6	2.6	541	10	048583	048583 arabidopsis
848	6	2.6	473	11	063887	063887	mus sp. non	921	6	2.6	542	16	098P11	098P11 mycoplasma
849	6	2.6	474	5	061472	061472	aplysia cal	922	6	2.6	543	16	098102	098102 rhizobium l
850	6	2.6	474	16	09CR21	09CR21	delnococtus	923	6	2.6	543	16	092XV7	092XV7 rhizobium m
851	6	2.6	476	11	09RCU34	09RCU34	mus musculu	924	6	2.6	545	5	09VMI4	09VMI4 drosophila
852	6	2.6	476	15	09A990	09A990	caulobacter	925	6	2.6	545	6	09MY00	09MY00 bos taurus
853	6	2.6	477	15	09QF42	09QF42	human immun	926	6	2.6	546	16	09CE14	09CE14 lactococcus
854	6	2.6	478	5	09UXF4	09UXF4	caenorhabdi	927	6	2.6	547	2	059117	059117 artirobacte
855	6	2.6	478	15	09QF41	09QF41	human immun	928	6	2.6	547	4	096MS8	096MS8 homo sapien
856	6	2.6	480	5	09BHF5	09BHF5	leishmania	929	6	2.6	551	16	09H0D4	09H0D4 pseudomonas
857	6	2.6	480	16	09RYX7	09RYX7	caulobacter	930	6	2.6	552	4	096NM5	096NM5 homo sapien
858	6	2.6	481	16	09A211	09A211	delnococtus	931	6	2.6	556	2	0918K4	0918K4 mycobacteri
859	6	2.6	484	2	09KH18	09KH18	lactobacill	932	6	2.6	556	10	09FM25	09FM25 arabidopsis
860	6	2.6	484	5	0965H9	0965H9	caenorhabdi	933	6	2.6	557	10	09LXV3	09LXV3 arabidopsis
861	6	2.6	484	16	083499	083499	treponema p	934	6	2.6	559	2	030349	030349 burkholderi
862	6	2.6	487	10	09SYL8	09SYL8	arabidopsis	935	6	2.6	559	11	063135	063135 rattus norv
863	6	2.6	491	16	09CFH8	09CFH8	lactococcus	936	6	2.6	559	16	092R30	092R30 rhizobium m
864	6	2.6	491	16	0984W7	0984W7	rhizobium l	937	6	2.6	561	2	09X9P8	09X9P8 streptomyces
865	6	2.6	492	16	09KSG1	09KSG1	vibrio chol	938	6	2.6	561	10	09T014	09T014 arabidopsis
866	6	2.6	494	11	09ER20	09ER20	mus musculu	939	6	2.6	563	2	069070	069070 streptococc
867	6	2.6	494	11	091X69	091X69	mus musculu	940	6	2.6	567	5	096156	096156 plasmodium
868	6	2.6	494	16	09RWF6	09RWF6	delnococtus	941	6	2.6	567	16	09A4P0	09A4P0 caulobacter
869	6	2.6	495	2	09V9J2	09V9J2	pseudomonas	942	6	2.6	568	4	096P21	096P21 homo sapien
870	6	2.6	496	5	09V9J2	09V9J2	drosophila	943	6	2.6	570	10	09SNE7	09SNE7 oryza sativ
871	6	2.6	497	11	063612	063612	rattus norv	944	6	2.6	573	16	09KMD7	09KMD7 vibrio chol
872	6	2.6	497	16	09PEX2	09PEX2	xylella fas	945	6	2.6	573	16	09CTP6	09CTP6 lactococcus
873	6	2.6	498	16	097JG4	097JG4	clostridium	946	6	2.6	575	2	09APR6	09APR6 uncultured
874	6	2.6	499	5	094996	094996	tetrahymena	947	6	2.6	575	2	09RJQ2	09RJQ2 streptomyces
875	6	2.6	500	2	09RAU2	09RAU2	lactococcus	948	6	2.6	575	3	09Y7A8	09Y7A8 neurospora
876	6	2.6	500	2	093MY8	093MY8	lactococcus	949	6	2.6	575	16	09APE98	09APE98 drosophila
877	6	2.6	500	16	09CER8	09CER8	lactococcus	950	6	2.6	578	10	09LTI6	09LTI6 rhizobium l
878	6	2.6	502	5	018672	018672	caenorhabdi	951	6	2.6	578	10	09XGNO	09XGNO arabidopsis
879	6	2.6	502	12	088621	088621	beet necrot	952	6	2.6	579	2	09REN3	09REN3 zymomonas m
880	6	2.6	502	12	086971	086971	drosofila	953	6	2.6	580	5	09GUB3	09GUB3 dictyostel
881	6	2.6	503	5	09VUL4	09VUL4	equine hept	954	6	2.6	583	3	09P768	09P768 schizosacch
882	6	2.6	503	12	039779	039779	equine hept	955	6	2.6	583	5	09BHA5	09BHA5 plasmodium
883	6	2.6	504	16	089481	089481	hantaan vir	956	6	2.6	583	5	09BHR3	09BHR3 plasmodium
884	6	2.6	504	16	09KBB9	09KBB9	procamburus	957	6	2.6	585	3	P78978	P78978 yarrowia li
885	6	2.6	505	5	090913	090913	vibrio chol	958	6	2.6	585	10	048713	048713 arabidopsis
886	6	2.6	505	16	09KLU9	09KLU9	caenorhabdi	959	6	2.6	585	4	09LMT7	09LMT7 oryza sativ
887	6	2.6	506	5	09V789	09V789	caenorhabdi	960	6	2.6	586	4	09UHT3	09UHT3 homo sapien
888	6	2.6	507	5	045182	045182	caenorhabdi	961	6	2.6	588	5	09VKV9	09VKV9 drosophila
889	6	2.6	508	5	021897	021897	bacteroides	962	6	2.6	588	9	09BOD1	09BOD1 staphylococ
890	6	2.6	509	2	09RCK3	09RCK3	mus musculu	963	6	2.6	592	5	09XV50	09XV50 caenorhabdi
891	6	2.6	509	11	09D0Q2	09D0Q2	candida alb	964	6	2.6	592	8	0957Q7	0957Q7 dogania sub
892	6	2.6	510	3	093992	093992	candida alb	965	6	2.6	593	15	09DSK7	09DSK7 human immun

966	6	2	6	594	4	09C0A9	09C09	homo sapien
967	6	2	6	594	4	09C0A9	09C0A1	homo sapien
968	6	2	6	595	8	09M199	09M19	lymphx mori
969	6	2	6	596	10	09A4H63	09M139	typhlonecte
970	6	2	6	598	3	09P6X0	09A163	oryza sativ
971	6	2	6	599	5	0246529	09P6K0	neutrospora
972	6	2	6	601	8	09XP86	0246529	drosophila
973	6	2	6	603	16	09PEP4	09XP6	chelonilla
974	6	2	6	603	16	09PEP4	09PEP4	chelonilla
975	6	2	6	605	8	098D88	09PEP4	chelonilla
976	6	2	6	605	8	09XP84	09PEP4	chelonilla
977	6	2	6	606	5	09NC26	09PEP4	chelonilla
978	6	2	6	608	2	045398	09NC26	chelonilla
979	6	2	6	608	16	09ABG0	045398	caulobacter
980	6	2	6	610	5	096659	09ABG0	caulobacter
981	6	2	6	611	4	0966N2	096659	hirudo medi
982	6	2	6	612	8	094SM4	0966N2	homo sapien
983	6	2	6	613	5	09VLA2	094SM4	exocoetus v
984	6	2	6	613	15	09DSJ2	09VLA2	drosophila
985	6	2	6	614	11	088561	09DSJ2	human immun
986	6	2	6	615	4	09P1Z0	088561	mus musculu
987	6	2	6	616	16	09PCM5	09P1Z0	homo sapien
988	6	2	6	619	4	094917	09PCM5	xyella fas
989	6	2	6	619	5	09VA04	094917	homo sapien
990	6	2	6	622	16	092EP2	09VA04	drosophila
991	6	2	6	622	3	09Y7A5	092EP2	chloobium m
992	6	2	6	632	3	09Y7A6	09Y7A5	coprinus c1
993	6	2	6	635	5	09YU7K7	09Y7A6	coprinus c1
994	6	2	6	635	12	0693087	09YU7K7	drosophila
995	6	2	6	638	2	092389	0693087	human herpe
996	6	2	6	638	11	09D3P1	092389	streptomyce
997	6	2	6	642	12	098310	09D3P1	mus musculu
998	6	2	6	643	4	09NMVL6	098310	molluscum c
999	6	2	6	652	2	09F5N2	09NMVL6	homo sapien
1000	6	2	6	652	5	09VCK9	09F5N2	thizobium m
							09VCK9	drosophila

## ALIGNMENTS

RESULT 1			
ID	Q9W2B6	PRELIMINARY:	PRT: 109 AA.
AC	Q9W2B6:		
DT	01-MAY-2000 (TREMBlrel. 13, Created)		
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)		
DT	01-DEC-2001 (TREMBlrel. 19, Last annotation update)		
DE	CG13494 PROTEIN.		
GN	CG13494.		
OS	Drosophila melanogaster (Fruit Fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_taxid=7227;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BERKELEY.		
EX	MEDLINE-20196006; PubMed-10731132;		
RA	Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutton G.G., Wotman J.R., Yendell M.D., Zhang Q., Chen L.X.,		
RA	Stratton R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,		
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos C.L.G.,		
RA	Abail J.F., Agbayanti A., An H.-U., Andrews-Pfankuch C., Baldwin D.,		
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu T., Beasley E.M.,		
RA	Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,		
RA	Burtis K.C., Bussey D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA	Cherry J.M., Casley S., Dahlke C., Davenport L.B., Davies P.,		
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	Dodon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Dunham K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,		

RA Foster C., Gabriellian A.E., Garg N.S., Gelbhart W.M., Glasser K.,  
RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,  
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kraevitz S., Kulp D., Lai Z.,  
RA Lako P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Mostrel A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,  
RA Palazzolo M., Peltman G.S., Pan S., Pollard J., Putil V., Reese M.G.,  
RA Reinett K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Slden-Klamos I., Stimpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stepleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasserman D.A., Welstock G.M., Weltschbach J.,  
RA Williams S.M., Woodgate T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,"  
RT "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
DR EMBL: AE003455; AAFA6776.1; -.  
DR HSSP: P01180; INPO.  
DR FlyBase: FBgn0034671; CG13494.  
SQ SEQUENCE 109 AA; 10413 MW; 84EDA6C087990895 CRC64;

```
Query Match      3.48; Score 8; DB 5; Length 109;
Best Local Similarity 100.08; Pred. No. 2.1;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	220	VGIIVLIV	22
Db	27	VGIIVLIV	34

RESULT	2		
Q9HAA6			
Q9HAA6	PRELIMINARY;	PRF:	217 AA.
AC	Q9HAA6;		
DT	01-MAR-2001 (Tremblrel. 16, Created)		
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)		
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)		
DE	CNDA FLJ12165 FIS. CLONE MAMMA1000612, MODERATELY SIMILAR TO HOMO		
DE	SAPIENS G PROTEIN BETA SUBUNIT MNNA.		
OS	Homo sapiens (Human)		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
CC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=MAMMARY GLAND;		
RA	Isoegl T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,		
RA	Nishikawa T., Nagai K., Sato H., Sugano S., Shiratori A., Sudo H.		
RA	Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara		
RA	Takanashi S., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi		
RA	Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.		
RA	Yamanoto J., Ikeyanaka T., Nakamura Y., Nagahari K., Masuno Y.,		
RA	Ninomiya K., Iwakatsu T.;		
RT	"NEDO human cDNA sequencing project.;"		
RL	Submitted (AUG-2000) to the EMBL/GenBank/DBD databases.		
CC	-1- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).		
CC	EMBL; AK022227; BABI1990.1. -		
DR	InterPro; IPR001680; WD40.1.		
DR	Pfam; PF00400; WD40.4.		
DR	PRINTS; PRO00320; GPROTEINBPT.		
DR	SMART; SM00320; WD40.4.		
DR	PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.		
DR	PROSITE; PS50082; WD_REPEATS_2; 2.		
DR	PROSITE; PS50294; WD_REPEATS_REGION; 1.		
FM	Repeat; WD repeat.		



SQ SEQUENCE 217 AA; 23817 MW; 31600C65FBE99DA3 CRC64;

Query Match 3.4%; Score 8; DB 4; Length 217;  
Best Local Similarity 100.0%; Pred. No. 3.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 141 TMNTSPT 148  
Db 19 TMNTSPT 26

RESULT 3  
092704 PRELIMINARY; PRT; 464 AA.  
AC 092704;  
DT 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE TRANSCRIPTION TERMINATION FACTOR.  
GN RHO OR CPN0610 OR CP0137.  
OS Chlamydia pneumoniae (Chlamydia pneumoniae).  
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.  
OX NCBI\_TaxID=83558;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CML029;  
RX MEDLINE=99206606; PubMed=10192388;  
RA Kaiman S., Mitchell W., Marathe R., Lamme C., Fan J., Hyman R.W.,  
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;  
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";  
RL Nat. Genet. 21:385-389(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AR39;  
RX MEDLINE=20150255; PubMed=10684935;  
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,  
RA White O., Hickey E.K., Peterson J., Uterback T., Berry K., Baas S.,  
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,  
RA Gelin M., Nelson W., Deboy R., Kolonay J., McClarty G., Salzberg S.L.,  
RA Eisen J., Fraser C.M.;  
RT "Genome sequences of Chlamydia trachomatis Mobn and Chlamydia  
RT pneumoniae AR39.";  
RL Nucleic Acids Res. 28:1397-1406(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=J138;  
RX MEDLINE=20330349; PubMed=10871362;  
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,  
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;  
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138  
RT from Japan and CML029 from USA.";  
RL Nucleic Acids Res. 28:2311-2314(2000).  
CC -1- SIMILARITY: TO ATPASE ALPHA/BETA CHAINS FAMILY.  
DR EMBL: AE001645; AAD18749.1; -;  
DR EMBL: AE002175; AAF38020.1; -;  
DR EMBL: AP002547; BAA98817.1; -;  
DR HSSP: P03002; 1A8Y; -;  
DR PHCI-2DPAGE: Q92704; -;  
DR TIGR: CP0137; -;  
DR InterPro: IPR000194; ATPase\_alpha\_beta.  
DR InterPro: IPR002059; Cold\_shock.  
DR Pfam: PF00006; ATP-synt\_ab; 1.  
DR SMART: SM00357; CSP; 1.  
KW Complete proteome; Hydrogen ion transport; Hydrolyase.  
SQ SEQUENCE 464 AA; 51818 MW; D00F6001AB6BC18 CRC64;

Query Match 3.4%; Score 8; DB 16; Length 464;  
Best Local Similarity 100.0%; Pred. No. 7.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 223 IVLIVLLI 230

Db 248 IVLIVLLI 255

RESULT 4  
096E62 PRELIMINARY; PRT; 468 AA.  
AC 096E62;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE SIMILAR TO TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER  
DE 10A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=OVARY, AND ADENOCARCINOMA;  
RA Strausberg R.;  
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC012866; AAH12866.1; -;  
KW Receptor.  
SQ SEQUENCE 468 AA; 50061 MW; 7E9661859A550CD4 CRC64;

Query Match 3.4%; Score 8; DB 4; Length 468;  
Best Local Similarity 100.0%; Pred. No. 7.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 97 EMCRCR 104  
Db 202 EMCRCR 209

RESULT 5  
092DD2 PRELIMINARY; PRT; 494 AA.  
AC 092DD2;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE LIN0882 PROTEIN.  
GN LIN0882.  
OS Listeria innocua.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Listeria.  
OX NCBI\_TaxID=1642;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CLIP 11262 / SEROVAR 6A;  
RX PubMed=11679659;  
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,  
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,  
RA Charbit A., Chelouani F., Couve E., de Darvar A., Dehoux P.,  
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,  
RA Entian K.-D., Fehli H., Garcia-del Portillo F., Garrido P.,  
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,  
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst J., Kutupat G.,  
RA Madueno E., Maitounam A., Mata Vicente J., Ng E., Nedjari H.,  
RA Nordstedt G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,  
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,  
RA Vazquez-Holand J.-A., Voss H., Wehland J., Cossart P.;  
RT "Comparative genomics of Listeria species.";  
RL Science 294:849-852(2001).  
DR EMBL: AL596166; CAC96114.1; -;  
DR ListList; LIN00882; -;  
KW Complete proteome.  
SQ SEQUENCE 494 AA; 56324 MW; 90CFE64DE83B0A00 CRC64;

Query Match 3.4%; Score 8; DB 16; Length 494;

Best Local Similarity 100.0%; Pred. No. 7.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 221 GIIVLIVL 228  
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Db 231 GIIVLIVL 238

## RESULT 6

O9JWP0  
ID O9JWP0 PRELIMINARY; PRT; 685 AA.  
AC O9JWP0;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10).  
GN MEG OR NMA0275.  
OS Neisseria meningitidis (serogroup A).  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=65699;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;  
RX MEDLINE-2022556; PubMed-10761919;  
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,  
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,  
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,  
RA Jagsels K., Leather S., Moule S., Mungall K., Quail M.A.,  
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,  
RA Whitehead S., Spratt B.G., Barrall B.G.;  
RT "Complete DNA sequence of a serogroup A strain of Neisseria  
RT meningitidis 22491."  
RL Nature 404:502-506(2000).  
DR EMBL; AL162752; CAB83583.1; .  
DR HSSP; P00959; 1MEA.  
DR InterPro: IPR001412; tRNA-synt\_1.  
DR InterPro: IPR002304; tRNA-synt\_met.  
DR InterPro: IPR002547; tRNA\_bind.  
DR Pfam; PF01588; tRNA\_bind; 1.  
DR PRINTS; PRO1041; TRNASYNTHET.  
DR POSITIVE; PS00178; AA\_TRNA\_LIGASE\_I; 1.  
KW Aminocyl-tRNA synthetase; Ligase; Complete proteome.  
SQ SEQUENCE 685 AA; 76984 MW; 07FDA5915ED3BEF3 CRC64;

Query Match 3.4%; Score 8; DB 16; Length 685;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 148 TPAPAE 155  
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Db 561 TPAPAE 568

## RESULT 7

ID O23635 PRELIMINARY; PRT; 801 AA.  
AC O23635;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE 2K84.1 PROTEIN.  
GN 2K84.1.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Pelodermidae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RX MEDLINE-94150718; PubMed-7906398;  
RA Wilson R., Alnough R., Anderson K., Baynes C., Berks M.,  
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,  
RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,  
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
RA Watson A., Weinstock L., Wilkinson-Spratt J., Woldman P.,  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans".  
RL Nature 368:32-38(1994).

RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA Kirsten J.;  
RT "The sequence of C. elegans cosmid 2K84."  
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U23181; AAC48204.1; .  
SQ SEQUENCE 801 AA; 77123 MW; 070D8F085A71EF28 CRC64;

Query Match 3.4%; Score 8; DB 5; Length 801;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAEET 156  
|||||  
Db 267 PAPAEET 274

## RESULT 8

O9V5T2  
ID O9V5T2 PRELIMINARY; PRT; 100 AA.  
AC O9V5T2;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
DE CG13231 PROTEIN.  
GN CG13231.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BERKELEY;  
RX MEDLINE-20196006; PubMed-10731132;  
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang O., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,  
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Adil J.F., Agbayani A., An H.-J., Andrews-Plannoch C., Baldwin D.,  
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RT "The genome sequence of *Drosophila melanogaster*."  
RL Science 287:2185-2195(2000).  
DR EMBL: AEO03827; AAF58716.1; -.  
DR FlyBase: FBgn0033580; CG13231.  
SQ SEQUENCE 100 AA; 10738 MW; A273705DC9F72137 CRC64;

Query Match 3.0%; Score 7; DB 5; Length 100;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAEE 155  
DB 19 PAPAEE 25

RESULT 9  
ID 09HL72 PRELIMINARY; PRT; 106 AA.  
AC 09HL72;  
DT 01-MAR-2001 (TReMBLrel. 16, Created)  
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
DE PROBABLE 50S RIBOSOMAL PROTEIN L12.  
GN TA0358.  
OS Thermoplasma acidophilum.  
OC Archaea; Euryarchaeota; Thermoplasmatales; Thermoplasmaceae;  
OC Thermoplasma.  
OX NCBI\_TaxID=2303;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSM 1728;  
RX MEDLINE=20479972; PubMed=11029001;  
RA Reupp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,  
RA Mewes H.-W., Flisman D., Stocker S., Lupas A.N., Baumeister W.,  
RT "The genome sequence of the thermophilic scavenger *Thermoplasma*  
RT *acidophilum*."  
RL Nature 407:508-513(2000).  
DR EMBL: AL445064; CAC11502.1; -.  
DR InterPro: IPR001813; 60s\_ribosomal.  
DR Pfam: PF00428; 60s\_ribosomal; 1.  
KW Ribosomal protein; Complete proteome.  
SQ SEQUENCE 106 AA; 11677 MW; DFB2EC1137DF478C CRC64;

Query Match 3.0%; Score 7; DB 17; Length 106;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 149 PAPAEE 155  
DB 66 PAPAEE 72

RESULT 10  
ID 069204 PRELIMINARY; PRT; 144 AA.  
AC 069204;  
DT 01-AUG-1998 (TReMBLrel. 07, Created)  
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 15.4 KDA PROTEIN.

OS Actinosynema pretiosum (subsp. auranticum).  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Pseudonocardineae; Actinosynnemataceae;  
OC Actinosynema.  
OX NCBI\_TaxID=42198;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC31565;  
RX MEDLINE=98174059; PubMed=9512878;  
RA August P.R., Tang L., Yoon Y.J., Ning S., Mueller R., Yu T.W.,  
RA Taylor M., Hoffmann D., Kim C.G., Zhang X., Hutchinson C.R.,  
RA Floss H.G.,  
RT "Biosynthesis of the ansamycin antibiotic rifamycin: deductions from  
RT the molecular analysis of the rif biosynthetic gene cluster of  
RT *Amycolatopsis mediterranei* s699."  
RL Chem. Biol. 5:69-79(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC31565;  
RX MEDLINE=98165773; PubMed=9497318;  
RA Kim C.G., Yu T.W., Fryhle C.B., Handa S., Floss H.G.,  
RT "3-Amino-5-hydroxybenzoic acid synthase, the terminal enzyme in the  
RT formation of the precursor of mc7N units in rifamycin and related  
RT antibiotics."  
RL J. Biol. Chem. 273:6030-6040(1998).  
DR EMBL: U33059; AAC13999.1; -.  
DR InterPro: IPR003594; HATPase\_c.  
DR InterPro: IPR004359; HIS\_KIN\_sig.  
DR Pfam: PF02518; HATPase\_c; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 144 AA; 15360 MW; 3CF9D1669D3B4DC6 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 144;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 146 PGTPAPA 152  
DB 15 PGTPAPA 21

RESULT 11  
ID 056349 PRELIMINARY; PRT; 151 AA.  
AC 056349;  
DT 01-JUN-1998 (TReMBLrel. 06, Created)  
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE GP41 (FRAGMENT).  
GN ENV.  
OS Human immunodeficiency virus type 2.  
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11709;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=POL;  
RX Heredia A.,  
RT "Phylogenetic analysis of circulating HIV-2 strains in Portugal."  
RL AIDS Res. Hum. Retroviruses 0:0-0(1998).  
DR EMBL: AF039490; AAB99979.1; -.  
DR InterPro: IPR000328; Env\_GP41.  
DR Pfam: PF00517; GP41; 1.  
KW Transmembrane.

FT NON\_TER 1 1  
 RT NON\_TER 151 151  
 SQ SEQUENCE 151 AA; 18112 MW; 8B42239D646B974B CRC64;

## Query Match

Best Local Similarity 3.0%; Score 7; DB 15; Length 151;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 IVGIIVL 225  
 |||||  
 Db 129 IVGIIVL 135

## RESULT 12

039133 PRELIMINARY; PRT; 155 AA.  
 AC 039133;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE MAJOR LATEX PROTEIN TYPE3 (MAJOR LATEX-LIKE PROTEIN).  
 GN MLP3.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_Taxid=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COL 0;  
 RA Grellier F., Cooke R., Laudie M., Raynal M., Delseny M.;  
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COL 0;  
 RA Muller S., Klimek S., Hauser M.T.;  
 RT "Molecular and phylogenetic analysis of a gene family in Arabidopsis  
 thaliana with similarities to major latex, pathogenesis-related and  
 ripening-induced proteins.";  
 RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: X91961; CAA63027.1; -;  
 DR EMBL: AJ306138; CAC83602.1; -;  
 SQ SEQUENCE 155 AA; 17879 MW; 61DC38712D035CFE CRC64;

## Query Match

Best Local Similarity 3.0%; Score 7; DB 10; Length 155;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 91 RNEENSPE 97  
 |||||  
 Db 123 RNEENSPE 129

## RESULT 13

09FNT2 PRELIMINARY; PRT; 158 AA.  
 AC 09FNT2;  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE RS2 PROTEIN.  
 GN RS2.  
 OS Beta vulgaris (Sugar beet).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.  
 OX NCBI\_Taxid=3555;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV, REGINA; TISSUE-STORAGE ORGAN;  
 RA Fowler M.R., Gartland J., Norton W., Slater A., Elliott M.C.,

RA Scott N.W.;  
 RT "Rs2: a sugar beet gene related to the latex-allergen family.";  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ278989; CAC18641.1; -;  
 SQ SEQUENCE 158 AA; 16099 MW; 12DFB67F1AF439A0 CRC64;

## Query Match

Best Local Similarity 3.0%; Score 7; DB 10; Length 158;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 APAEET 156  
 |||||  
 Db 42 APAEET 48

## RESULT 14

019762 PRELIMINARY; PRT; 165 AA.  
 AC 019762;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE F23H12.3 PROTEIN.  
 GN F23H12.3.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderiinae; Caenorhabditis.  
 OX NCBI\_Taxid=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kershaw J.K.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA none;  
 RT "Genome sequence of the nematode C. elegans: A platform for  
 RT investigating biology.";  
 RL Science 282:2012-2018(1998).  
 DR EMBL: Z74472; CAA98941.1; -;  
 SQ SEQUENCE 165 AA; 18513 MW; 1E2C7A2653179E12 CRC64;

## Query Match

Best Local Similarity 3.0%; Score 7; DB 5; Length 165;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 221 GIIVLIV 227  
 |||||  
 Db 89 GIIVLIV 95

## RESULT 15

097WN5 PRELIMINARY; PRT; 184 AA.  
 AC 097WN5;  
 DT 01-OCT-2001 (TREMblrel. 18, Created)  
 DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TREMblrel. 18, Last annotation update)  
 DE HYPOTHETICAL PROTEIN SS02176.  
 GN SS02176.  
 OS Sulfolobus solfataricus.  
 OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.  
 OX NCBI\_Taxid=2287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 35092 / DSM 1617 / P2;  
 RX MEDLINE=21332296; PubMed=11427726;  
 RA She O., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,  
 Rayner M.J., Chan-Welner C.C.-Y., Clausen I.G., Curtis B.A.,  
 De Moors A., Trauso G., Fletcher C., Gordon P.M.K.,  
 Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,  
 RA Charlebois R.L., Doilittle W.F., Duguet M., Gaasterland T.,  
 RA Garrett R.A., Ragan M.A., Sengen C.W., Van der Oost J.:  
 RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2."  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).  
 DR EMBL: AE006823; AAK42351.1; -.  
 KW Hypothetical protein; Complete proteome.  
 SO SEQUENCE 184 AA; 21050 MW; 555DF2EED2172D7 CRC64;

Query Match 3.0%; Score 7; DB 17; Length 184;  
 Best Local Similarity 100.0%; Pred. No. 36;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 225 LIVLLIV 231  
 |||||  
 Db 164 LIVLLIV 170

RESULT 16  
 Q9RM97 PRELIMINARY; PRT; 219 AA.  
 AC Q9RM97;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE HYPOTHETICAL 22.6 KDA PROTEIN.  
 GN DR0772.  
 OS Deinococcus radiodurans.  
 OC Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.  
 NC NCBI\_TaxID=1299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RI;  
 RX MEDLINE=20036896; PubMed=10567266;  
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,  
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,  
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,  
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,  
 RA Fraser C.M.;  
 RT "Genome sequence of the radioresistant bacterium Deinococcus  
 RT radiodurans RI."  
 RL Science 286:1571-1577(1999).  
 DR EMBL: AE001932; AAF10355.1; -.  
 DR TIGR: DR0772; -.  
 KW Hypothetical protein; Complete proteome.  
 SO SEQUENCE 219 AA; 22631 MW; 72AD261C8B37AB2F CRC64;

Query Match 3.0%; Score 7; DB 16; Length 219;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 GTPAPAA 153  
 |||||  
 Db 205 GTPAPAA 211

RESULT 17  
 Q96EX2 PRELIMINARY; PRT; 231 AA.  
 AC Q96EX2;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE SIMILAR TO HYPOTHETICAL PROTEIN FLJ14627.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NC NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=MUSCLE, AND RHABDOMYOSARCOMA;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC011878; AAH1878.1; -.  
 SO SEQUENCE 231 AA; 25722 MW; B4D36B0360D3C57C CRC64;

Query Match 3.0%; Score 7; DB 4; Length 231;  
 Best Local Similarity 100.0%; Pred. No. 44;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 146 GTPAPAA 152  
 |||||  
 Db 56 GTPAPAA 62

RESULT 18  
 Q9FT78 PRELIMINARY; PRT; 241 AA.  
 AC Q9FT78;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE P23 CO-CHAPERONE.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NC NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bowra S.;  
 RT "A plant p23: the missing link suggesting glucocorticoid receptors  
 RT exist in plants."  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ297951; CAC16575.1; -.  
 SO SEQUENCE 241 AA; 25455 MW; 90989FE950BDC3D CRC64;

Query Match 3.0%; Score 7; DB 10; Length 241;  
 Best Local Similarity 100.0%; Pred. No. 46;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 150 APAABET 156  
 |||||  
 Db 228 APAABET 234

RESULT 19  
 Q98EG1 PRELIMINARY; PRT; 249 AA.  
 AC Q98EG1;  
 DT 01-OCT-2001 (TREMBlrel. 18, Created)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
 DE M14259 PROTEIN.  
 GN M14259.  
 OS Rhizobium loti (Mesorhizobium loti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 NC NCBI\_TaxID=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAFF303099;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 Mesorhizobium loti.";

RL DNA Res. 7:331-338(2000).  
 DR EMBL: AP003003; BAB50958.1; -.  
 KM Complete Proteome.  
 SQ SEQUENCE 249 AA; 27855 MW; D780EDB3298A2A40 CRC64;

Query Match  
 Best Local Similarity 3.0%; Score 7; DB 16; Length 249;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 PAPAEE 155  
 |||||||  
 Db 176 PAPAEE 182

RESULT 20  
 Q9SB18 PRELIMINARY; PRT; 255 AA.  
 AC Q9SB18;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE DEHYDRIN 8.  
 GN DHN8.  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_Taxid=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. DICKTOO;  
 RA Choi D.-W., Zhu B., Close T.J.;  
 RT "The barley (Hordeum vulgare L.) dehydrin multigene family: sequences,  
 RT chromosome assignments, and expression characteristics of 11 dhn genes  
 RT of cv. Dicktoo.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF043093; AAD02259.1; -.  
 DR InterPro: IPR000167; Dehydrin.  
 DR Pfam: PF00257; dehydrin; 2.  
 DR PROSITE: PS00823; DEHYDRIN\_2; 2.  
 SQ SEQUENCE 255 AA; 27726 MW; 08D7FAFF7F811AAF CRC64;

Query Match  
 Best Local Similarity 3.0%; Score 7; DB 10; Length 255;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 PAPAEE 155  
 |||||||  
 Db 206 PAPAEE 212

RESULT 21  
 Q9SP4 PRELIMINARY; PRT; 255 AA.  
 AC Q9SP4;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE DEHYDRIN.  
 GN DHN8.  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_Taxid=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. MOREX;  
 RA Choi D.-W., Close T.J.;  
 RT "Morex barley (Hordeum vulgare L. cv. Morex) dehydrin multigene  
 RT family.";

RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF181458; AAF01696.1; -.  
 DR InterPro: IPR000167; Dehydrin.  
 DR Pfam: PF00257; dehydrin; 2.  
 DR PROSITE: PS00823; DEHYDRIN\_2; 2.  
 SQ SEQUENCE 255 AA; 27670 MW; 5289E18CB420BF3B CRC64;

Query Match  
 Best Local Similarity 3.0%; Score 7; DB 10; Length 255;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 PAPAEE 155  
 |||||||  
 Db 206 PAPAEE 212

RESULT 22  
 Q43488 PRELIMINARY; PRT; 255 AA.  
 AC Q43488;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE PAF93. PROTEIN.  
 GN PAF93.  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_Taxid=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. GEORGIE; TISSUE=GREEN LEAF;  
 RA Grossi M., Gullit M., Stanca A.M., Cattivelli L.;  
 RT "Characterization of two barley genes that respond rapidly to  
 RT dehydration stress.";  
 RL Plant Sci. 105:71-80(1995).  
 DR EMBL: X84056; CA58875.1; -.  
 DR InterPro: IPR000167; Dehydrin.  
 DR Pfam: PF00257; dehydrin; 2.  
 DR PROSITE: PS00823; DEHYDRIN\_2; 2.  
 SQ SEQUENCE 255 AA; 27666 MW; 49C4618BC95A77FD CRC64;

Query Match  
 Best Local Similarity 3.0%; Score 7; DB 10; Length 255;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 PAPAEE 155  
 |||||||  
 Db 206 PAPAEE 212

RESULT 23  
 Q9VV71 PRELIMINARY; PRT; 256 AA.  
 AC Q9VV71;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE CG4229. PROTEIN (LD44179P).  
 GN CG4229.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_Taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY.  
 RX MEDLINE=20196006; Pubmed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang O., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fouts C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,  
 RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kenisnon J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasro P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mlshina N.V., Moberry C., Morris J., Mostrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazolo M., Piltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Sinden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svltkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Welschbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Y, CN BW SP;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Change M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuncio J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AE003527; AAF49451.1; -;  
 DR EMBL: AT061476; AAL29024.1; -;  
 DR FLYbase: FBgn0036639; CG4229.  
 DR InterPro: IPR004011; GYR.  
 DR InterPro: IPR004019; YLP.  
 DR Pfam: PF02757; GYR: 3.  
 DR Pfam: PF02757; YLP: 5.  
 SQ SEQUENCE 256 AA; 27418 MW; 10712DB970A13F5D CRC64;

Query Match 3.0%; Score 7; DB 5; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 150 AAPAEE 156  
 Db 165 AAPAEE 171  
 RESULT 24  
 Q9PD13 PRELIMINARY; PRT; 256 AA.  
 AC Q9PD13;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE HYPOTHETICAL PROTEIN XF1591.

GN XF1591.  
 OS Xylella fastidiosa.  
 OC Bacteria: Proteobacteria: gamma subdivision: Xanthomonas group;  
 OC Xylella.  
 OX NCBI\_TaxID=2371;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9A5C;  
 RX MEDLINE=20365717; PubMed=10910347;  
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,  
 RA Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,  
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,  
 RA Barrios M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,  
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,  
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,  
 RA Paciniani A.P., Ferreira A.J.S., Ferreira V.C.A., Fetto J.A.,  
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,  
 RA Garner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,  
 RA Ho P.L., Hohnsbeil J.D., Junqueira M.L., Kemper E.L., Kitaajima J.P.,  
 RA Krieger J.E., Kuramae E.E., Laligret F., Lambais M.R., Leite L.C.C.,  
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,  
 RA Machado M.A., Madeira A.M.B.N., Martins H.M.P., Martino C.L.,  
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,  
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,  
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,  
 RA Nhani A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,  
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,  
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A.Jr., Pesquero J.B.,  
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,  
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,  
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,  
 RA da Silveira J.F., Silvestri M.L.Z., Silveira W.J., de Souza A.A.,  
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuchiko M.H.,  
 RA Valada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,  
 RA Zago M.A., Zatz M., Zeldanis J., Zetubel J.C.;  
 RT "The genome sequence of the plant pathogen *Xylella fastidiosa*.";  
 RL Nature 406:151-159(2000).  
 DR EMBL: AE003987; AAF84400.1; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 256 AA; 27888 MW; E38B51ERDD82010 CRC64;

Query Match 3.0%; Score 7; DB 16; Length 256;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 149 PAPAAE 155  
 Db 65 PAPAAE 71  
 RESULT 25  
 Q9PCT1 PRELIMINARY; PRT; 256 AA.  
 AC Q9PCT1;  
 DT 01-OCT-2000 (TReMBLrel. 15, Created)  
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE HYPOTHETICAL PROTEIN XF1697.  
 GN XF1697.  
 OS Xylella fastidiosa.  
 OC Bacteria: Proteobacteria: gamma subdivision: Xanthomonas group;  
 OC Xylella.  
 OX NCBI\_TaxID=2371;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9A5C;  
 RX MEDLINE=20365717; PubMed=10910347;  
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,  
 RA Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,  
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,  
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,  
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,





RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RA WASHU;  
 RT "The A. thaliana Genome Sequencing Project."  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RA Kallicki J., Elliott G., Cloud J.;  
 RT "The sequence of A. thaliana T14P8."  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RA Waterston R.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Lamar B., Stoneking T., Stumpf J., Mewes H.W., Lemcke K.,  
 RA Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF069298; AAC19287.1; -;  
 DR EMBL: AL61494; CAB80738.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 262 AA; 27944 MW; 67BBF89EEF6625D6 CRC64;

Query Match 3.0%; Score 7; DB 10; Length 262;  
 Best Local Similarity 100.0%; Pred. No. 49;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 PAPAEE 156  
 Db 249 APAEE 255

RESULT 29  
 Q17806 PRELIMINARY; PRT; 263 AA.  
 AC Q17806;  
 DT 01-NOV-1996 (TREMUREL. 01, Created)  
 DT 01-NOV-1996 (TREMUREL. 01, Last sequence update)  
 DE 01-DEC-2001 (TREMUREL. 19, Last annotation update)  
 GN C08A9.3.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
 RA Gardiner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,  
 RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,  
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,  
 RA Smalton N., Smith A., Sonhammer E., Staden A., Sulston J.,  
 RA Thelery-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,  
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans."  
 RL Nature 368:32-38(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;  
 RA Latreille P.;  
 RT "The sequence of C. elegans cosmid C08A9."  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Waterston R.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U42844; AAB53817.1; -;  
 SQ SEQUENCE 263 AA; 30460 MW; EDF6EA44080AD135 CRC64;

Query Match 3.0%; Score 7; DB 5; Length 263;  
 Best Local Similarity 100.0%; Pred. No. 49;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 VLIIVLI 230  
 Db 116 VLIIVLI 122

RESULT 30  
 Q9ZFB0 PRELIMINARY; PRT; 266 AA.  
 AC Q9ZFB0;  
 DT 01-MAY-1999 (TREMUREL. 10, Created)  
 DT 01-MAY-1999 (TREMUREL. 10, Last sequence update)  
 DE 01-DEC-2001 (TREMUREL. 19, Last annotation update)  
 GN Y1B0.  
 OS Rhodospirillum rubrum (Rhodospirillum rubrum).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillum group;  
 OC Rhodospirillum;  
 OX NCBI\_TaxID=1063;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-2.4.1;  
 RX MEDLINE=94442363; PubMed=10511537;  
 RA Mackenzie C., Simmons A.E., Kaplan S.;  
 RT "Multiple Chromosomes in Bacteria: The Yin and Yang of trp Gene  
 Localization in Rhodospirillum rubrum 2.4.1.";  
 RL Genetics 153:525-538(1999).  
 DR EMBL: AF108766; AAD09126.1; -;  
 SQ SEQUENCE 266 AA; 27988 MW; D45992B6BE77215D CRC64;

Query Match 3.0%; Score 7; DB 2; Length 266;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 PAPAEE 155  
 Db 37 PAPAEE 43

RESULT 31  
 P93607 PRELIMINARY; PRT; 268 AA.  
 AC P93607;  
 DT 01-MAY-1997 (TREMUREL. 03, Created)  
 DT 01-MAY-1997 (TREMUREL. 03, Last sequence update)  
 DE 01-DEC-2001 (TREMUREL. 19, Last annotation update)  
 GN WCO410B.  
 OS Triticum aestivum (wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticaceae; Triticum.  
 OX NCBI\_TaxID=4565;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. NORSTAR; TISSUE=SHOOT;

RA Danyluk J., Sarhan F.;  
 RT "Identification of a gene encoding an acidic dehydrin in wheat."  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U73210; AAB18201.1; -;  
 DR InterPro: IPR000167; Dehydrin.  
 DR Pfam: PF00257; dehydrin; 2;  
 DR PROSITE: PS00823; DEHYDRIN\_2; 1.  
 SQ SEQUENCE 268 AA; 28837 MW; BA8AFE7C17D1D631 CRC64;

Query Match 3.0%; Score 7; DB 10; Length 268;  
 Best Local Similarity 100.0%; Pred. No. 50;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 PAPAAEE 155  
 |||||  
 Db 219 PAPAAEE 225

RESULT 32  
 Q988Y8 PRELIMINARY; PRT; 272 AA.  
 AC Q988Y8:  
 DT 01-OCT-2001 (TREMBLrel. 18, Created)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
 DE ABC TRANSPORTER, POLYAMINE TRANSPORT PROTEIN, PERMEASE  
 DE PROTEIN.  
 GN MLR6537.  
 OS Rhizobium loti (Mesorhizobium loti)  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Phyllobacteriaceae; Mesorhizobium.  
 OX NCBI\_TaxID=381;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MAFF303099;  
 RX MEDLINE=21082930; PubMed=11214968;  
 RA Kaneo T., Nakamura Y., Sato S., Asamiu E., Kato T., Sasamoto S.,  
 RA Watanabe A., Idegawa K., Ishikawa K., Kimura T.,  
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno M.,  
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpō S., Sugimoto M.,  
 RA Takeuchi C., Yamada M., Tabata S.;  
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
 Mesorhizobium loti."  
 RL DNA Res. 7:331-338(2000).  
 DR EMBL: AP003009; BAB52809.1; -;  
 DR InterPro: IPR000515; BPD\_transp.  
 DR Pfam: PF00528; BPD\_transp; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 272 AA; 29561 MW; 7B023F194CEA5DE8 CRC64;

Query Match 3.0%; Score 7; DB 16; Length 272;  
 Best Local Similarity 100.0%; Pred. No. 51;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 IVLLIVF 232  
 |||||  
 Db 24 IVLLIVF 30

RESULT 33  
 ID 032850 PRELIMINARY; PRT; 295 AA.  
 AC 032850:  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE HYPOTHETICAL 29.4 KDA PROTEIN (FRAGMENT).  
 GN MBE4863A.  
 OS Mycobacterium bovis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriidae;  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI\_TaxID=1765;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BCG\_FRENCH;  
 RA Kim J.K., Choe Y.K.;  
 RT "Mycobacterium bovis BCG clone E4863."  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF009829; AAB63811.1; -;  
 DR InterPro: IPR002965; P-rich\_extensn.  
 DR PRINTS: PR01217; PRICHEXTENS.  
 KW Hypothetical protein.  
 FT NON\_TER  
 SQ SEQUENCE 295 AA; 29421 MW; 04E68DF13B9A7EEC CRC64;

Query Match 3.0%; Score 7; DB 2; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 54;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QQTVAPO 16  
 |||||  
 Db 264 QQTVAPO 270

RESULT 34  
 Q93D93 PRELIMINARY; PRT; 299 AA.  
 ID Q93D93  
 AC Q93D93:  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE PROTEINASE HTPX-LIKE PROTEIN.  
 DE HTPX.  
 GN Streptococcus mutans.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1309;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT11;  
 RA Tao L., Tanzer J.M.;  
 RT "Novel sucrose-dependent adhesion cofactors (sdc) in Streptococcus  
 mutans."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF397166; AAL04088.1; -;  
 SQ SEQUENCE 299 AA; 32725 MW; 6409CB04766D9F8B CRC64;

Query Match 3.0%; Score 7; DB 2; Length 299;  
 Best Local Similarity 100.0%; Pred. No. 55;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 IVLLIVF 232  
 |||||  
 Db 14 IVLLIVF 20

RESULT 35  
 ID 050268 PRELIMINARY; PRT; 313 AA.  
 AC 050268:  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 GN KOAB.  
 OS Agrobacterium tumefaciens.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Rhizobium.  
 OX NCBI\_TaxID=358;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=99141607; PubMed=9987134;  
 RA Lyi S.M., Jafri S., Winans S.C.;  
 RT "Mannoplic acid and agrodinic acid catabolism region of the octopine-  
 RT type Ti plasmid pT15955";  
 RL Mol. Microbiol. 31:339-347(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Winans S.C., Zhu J., Oger P.M., Schrammeyer B., Hooykaas P.J.,  
 RA Farand S.K.;  
 RT "Octopine-type Ti plasmid sequence";  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF242881; AAB8473.1; -;  
 DR InterPro: IPR000515; BPD\_transp.  
 DR Pfam: PF00528; BPD\_transp.1.  
 KM Plasmid.  
 SQ SEQUENCE 313 AA; 34078 MW; 28B6D54AE94BE6C2 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 313;  
 Best Local Similarity 100.0%; Pred. No. 57;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 IVLLIVF 232  
 DB 149 IVLLIVF 155

RESULT 36  
 Q9BVC4 PRELIMINARY; PRT; 326 AA.  
 AC Q9BVC4;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE SIMILAR TO G BETA-LIKE PROTEIN (HYPOTHETICAL 35.9 KDA PROTEIN).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA, CHORIOCARCINOMA;  
 RA Strausberg R.;  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=UTERUS, LEIOMYOSARCOMA;  
 RA Strausberg R.;  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 CC -; SIMILARITY: CONTAINS 6 WD REPEATS (TRP-ASP DOMAINS).  
 DR EMBL: BC001313; AAH01313.1; -;  
 DR EMBL: BC017119; AAH17119.1; -;  
 DR InterPro: IPR001680; WD40.  
 DR Pfam: PF00400; WD40; 6.  
 DR PRINTS: PR00320; GPROTEINBRPT.  
 DR SMART: SM00320; WD40; 6.  
 DR PROSITE: PS00678; WD\_REPEATS\_1; UNKNOWN\_1.  
 DR PROSITE: PS00682; WD\_REPEATS\_2; 3.  
 DR PROSITE: PS02924; WD\_REPEATS\_REGION; 1.  
 KW Repeat; WD repeat; Hypothetical protein.  
 SQ SEQUENCE 326 AA; 35876 MW; 43A600DAEF2B6543 CRC64;

Query Match 3.0%; Score 7; DB 4; Length 326;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 MNTSPGT 148  
 DB 1 MNTSPGT 7

RESULT 37

Q96S05  
 ID Q96S05 PRELIMINARY; PRT; 330 AA.  
 AC Q96S05;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE CDNA FLJ14627 FIS, CLONE NT2RP2000289.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,  
 RA Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,  
 RA Nakamura Y., Nagahari K., Masuno Y., Sasaki N.;  
 RT "NEDO human cDNA sequencing project";  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK027533; BAB55182.1; -;  
 SQ SEQUENCE 330 AA; 36563 MW; 831A04E0693C131 CRC64;

Query Match 3.0%; Score 7; DB 4; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 60;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 PGTAPA 152  
 DB 56 PGTAPA 62

RESULT 38  
 Q98TD7 PRELIMINARY; PRT; 346 AA.  
 AC Q98TD7;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE CCAAT/ENHANCER BINDING PROTEIN BETA.  
 GN JRC/EBBP.  
 OS Paralicthys olivaceus (Flounder).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
 OC Pleuronectoidae; Paralicthyidae; Paralicthys.  
 OX NCBI\_TaxID=8255;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tucker C.S., Hirono I., Aoki T.;  
 RT "Molecular cloning of CCAAT/enhancer binding proteins in Japanese  
 RT flounder Paralicthys olivaceus, a first report of C/EBP in fish.";  
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB049813; BAB40971.1; -;  
 DR InterPro: IPR001871; bZIP.  
 DR SMART: SM00338; BRLZ; 1.  
 SQ SEQUENCE 346 AA; 39086 MW; 2772CF80D59BEC05 CRC64;

Query Match 3.0%; Score 7; DB 13; Length 346;  
 Best Local Similarity 100.0%; Pred. No. 62;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 PGTAPA 152  
 DB 241 PGTAPA 247

RESULT 39  
 Q9JY60 PRELIMINARY; PRT; 365 AA.  
 ID Q9JY60  
 AC Q9JY60;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)

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DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE CYTOCHROME C OXIDASE, SUBUNIT III.
GN NMB1723.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
ON NCB1_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tetelin H., Saunders N.J., Heidberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.U.,
RA Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Cifton H., Clark E.B.,
RA Cotton M.D., Uterback T.R., Khouri H., Qin H., Yamaherhan J.,
RA Gill J., Scalato V., Massignani V., Pizzo M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.";
RL Science 287:1809-1815(2000).
DR EMBL; AF002522; AAF42068.1; -.
DR TIGR; NMB1723; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR003088; Cyt.CI.
DR InterPro; IPR002329; Cyt.CIC.
DR Pfam; PF000034; cytochrome_c; 2.
DR PRINTS; PR00605; CYTOCHROME.CIC.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 365 AA; 40039 MW; AF344435A51EB4A2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 16; Length 365;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 TPAPAE 154
    |||||
Db 321 TPAPAE 327

RESULT 40
Q9J744 PRELIMINARY; PRT; 365 AA.
ID Q9J744;
AC Q9J744;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE PUTATIVE CYTOCHROME C.
GN NMA1977.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
ON NCB1_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-22491 / SEROGROUP A / SEROTYPE 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltham T., Hamlin N., Holtroyd S.,
RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Ralstead M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whithead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis 22491.";
RL Nature 404:502-506(2000).
DR EMBL; AL162757; CAB85197.1; -.
DR InterPro; IPR000345; CytC_heme_bind.
DR InterPro; IPR003088; Cyt.CI.
DR InterPro; IPR002329; Cyt.CIC.
DR Pfam; PF000034; cytochrome_c; 2.

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DR PRINTS; PR00605; CYTOCHROME.CIC.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 365 AA; 40011 MW; AF223552A51EB4A2 CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 16; Length 365;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 TPAPAE 154
    |||||
Db 321 TPAPAE 327

RESULT 41
ID 080413 PRELIMINARY; PRT; 366 AA.
AC 080413;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MITOCHONDRIAL PHOSPHATE TRANSPORTER.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoidae; Andropogoneae; Zea.
ON NCB1_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H84; TISSUE=ROOT;
RX MEDLINE=99364542; PubMed=10437831;
RA Takabatake R., Hata S., Taniguchi M., Kouchi H., Sugiyama T., Izui K.;
RT "Isolation and characterization of cDNAs encoding mitochondrial
RT phosphate transporters in soybean, maize, rice, and Arabidopsis.";
RL Plant Mol. Biol. 40:479-486(1999).
DR EMBL; AB016064; BAA31583.1; -.
DR InterPro; IPR001993; Mitoch-carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
SQ SEQUENCE 366 AA; 38658 MW; 7A372332D8D416CE CRC64;

Query Match
Best Local Similarity 100.0%; Score 7; DB 10; Length 366;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 TPAPAE 154
    |||||
Db 353 TPAPAE 359

RESULT 42
O79658 PRELIMINARY; PRT; 380 AA.
ID O79658;
AC O79658;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE CYTOCHROME B.
GN CytB.
OS Pucrasia macrolopha (Koklass pheasant).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Pucrasia.
ON NCB1_TaxID=9061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99184957; PubMed=10082609;
RA Kimball R.T., Braun E.L., Zwartjes P.W., Crowe T.M., Lyon J.D.;
RT "A molecular phylogeny of the pheasants and partridges suggests that
RT these lineages are not monophyletic.";

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RL Mol. Phylogenet. Evol. 11:38-54(1999).  
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE  
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A  
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL  
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).  
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B565) WHICH ARE NOT COVALENTLY  
CC BOUND TO THE PROTEIN (BY SIMILARITY).  
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,  
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.  
DR EMBL: AF028800; AAC62190.1; -  
DR InterPro: IPR000179; Cyt\_b\_b6.  
DR Pfam: PF00033; cytochrome\_b\_n; 1.  
DR PROSITE: PS00192; CYTOCHROME\_B\_HEME; 1.  
DR PROSITE: PS00193; CYTOCHROME\_B\_OO; UNKNOWN.1.  
DR Electron transport; Heme; Mitochondrion; Respiratory chain;  
KW Transmembrane.  
SQ SEQUENCE 380 AA; 42568 MW; EF9224EALIC491C3 CRC64;

Query Match 3.0%; Score 7; DB 8; Length 380;  
Best Local Similarity 100.0%; Pred. No. 68;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 VLIYVLI 230  
|111111|  
DB 299 VLIYVLI 305

RESULT 43  
O9RK28 ID O9RK28 PRELIMINARY; PRT; 390 AA.  
AC O9RK28;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
DE HYPOTHETICAL 42.3 KDA PROTEIN.  
GN SCF15.09.  
OS Streptomyces coelicolor.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RA Oliver K., Harris D.;  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RX MEDLINE=97000351; PubMed=8843436;  
RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,  
RA Kinashi H., Hopwood D.A.;  
RT "A set of ordered cosmids and a detailed genetic and physical map for  
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
RL M01. Microbiol. 21:77-96(1996).  
DR EMBL: AL132856; CAB60469.1; -  
KM Hypothetical protein.  
SQ SEQUENCE 390 AA; 42349 MW; A21C43451B84B92 CRC64;

Query Match 3.0%; Score 7; DB 2; Length 390;  
Best Local Similarity 100.0%; Pred. No. 69;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 146 PGTPAPA 152  
|111111|

DB 227 PGTPAPA 233

RESULT 44  
O58434 ID O58434 PRELIMINARY; PRT; 397 AA.  
AC O58434;  
DT 01-AUG-1998 (TREMBLrel. 07, Created)  
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE HYPOTHETICAL 43.6 KDA PROTEIN PH0703.  
GN PH0703.  
OS Pyrococcus horikoshii.  
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.  
OX NCBI\_TaxID=53953;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-OT3;  
RX MEDLINE=98344137; PubMed=9679194;  
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,  
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,  
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,  
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Koshida N., Oguchi A.,  
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,  
RA Masuchi Y., Shizuya H., Kikuchi H.;  
RT "Complete sequence and gene organization of the genome of a hyper-  
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";  
RL DNA Res. 5:55-76(1998).  
DR EMBL: AF000003; BAA29794.1; -  
DR InterPro: IPR00265; MgtE.  
DR Pfam: PF01769; MgtE; 2.  
KM Hypothetical protein; Complete proteome.  
SQ SEQUENCE 397 AA; 43585 MW; FD4B7456F42F8BA6 CRC64;

Query Match 3.0%; Score 7; DB 17; Length 397;  
Best Local Similarity 100.0%; Pred. No. 70;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 227 VLIYFV 233  
|111111|  
DB 133 VLIYFV 139

RESULT 45  
O9BJM3 ID O9BJM3 PRELIMINARY; PRT; 401 AA.  
AC O9BJM3;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE CATHERSIN L-LIKE CYSTEINE PROTEINASE.  
OS Onchocerca volvulus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
OC Onchocercidae; Onchocerca.  
OX NCBI\_TaxID=6282;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Guilliano D.B., Blaxter M.L., Williams S.A., Lustigman S.;  
RT "Characterization of a Novel Developmentally Regulated Family of  
RT Cysteine Proteinases from Filarial Nematodes.";  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF331036; AAK16514.1; -  
DR HSSP: O17473; 1BMU.  
DR MEROPS: C01.055; -  
DR InterPro: IPR000668; Peptidase\_C1.  
DR InterPro: IPR000169; Thiolprol\_act\_site.  
DR Pfam: PF00112; Peptidase\_C1; 1.  
DR PRINTS: PR00705; PAPA1N.  
DR PROSITE: PS00139; THIOL\_PROTEASE\_CYS; 1.  
DR PROSITE: PS00639; THIOL\_PROTEASE\_HIS; 1.  
KM Hydrolyase; Thiol protease.  
SQ SEQUENCE 401 AA; 45511 MW; 58E10CE3913A3F66 CRC64;

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Query Match          3.0%; Score 7; DB 5; Length 401;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 LIVLIVF 232
|||||
Db 5 LIVLIVF 11

RESULT 46
Q9CRR2 PRELIMINARY; PRT; 405 AA.
AC Q9CRR2;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ADRENERGIC RECEPTOR, BETA 1 (FRAGMENT).
GN ADREB1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC LUNG;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arai K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Katsukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno K., Kono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustlincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC - - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC - - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AK018378; BAB31185.1; -.
DR MGD; MGI:87937; Adrb1.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT NON TER 1
SQ SEQUENCE 405 AA; 44741 MW; 4F0F3FBB956FEF24 CRC64;

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ID Q9FN24 PRELIMINARY; PRT; 419 AA.
AC Q9FN24;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE SIMILARITY TO GTP-RICH ZINC FINGER PROTEIN.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98162728; PubMed=9501997;
RA Nakamura Y., Sato S., Kaneko T., Kötani H., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
RT Sequence features of the regions of 1,191,918 bp covered by seventeen
RT physically assigned P1 clones.";
RL DNA Res. 4:401-414(1997).
DR EMBL; AB007644; BAB10733.1; -.
DR InterPro; IPR002219; DAG_PE_bind.
DR InterPro; IPR000215; Serpin.
DR SMART; SM00109; C1; 4.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN.1.
SQ SEQUENCE 419 AA; 48481 MW; B38F1A57A45645C5 CRC64;

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Query Match          3.0%; Score 7; DB 10; Length 419;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 KCSCRPS 107
|||||
Db 227 KCSCRPS 233

RESULT 48
Q17854 PRELIMINARY; PRT; 450 AA.
AC Q17854;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE F28G4.4 PROTEIN.
GN F28G4.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Wall M.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z93381; CAB07607.1; -.
SQ SEQUENCE 450 AA; 52757 MW; 498F8D992865FBF1 CRC64;

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Query Match          3.0%; Score 7; DB 11; Length 405;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 LIVLIV 231
|||||
Db 6 LIVLIV 12

RESULT 47
Q9FN24

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Query Match          3.0%; Score 7; DB 5; Length 450;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 VLVVLI 230
|||||

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Db 11 VLIVLLI 17

RESULT 49

Q9H7M8 ID Q9H7M8 PRELIMINARY; PRT; 452 AA.  
 AC Q9H7M8;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE FLJ00042 PROTEIN (FRAGMENT).  
 GN FLJ00042.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SPLEN;  
 RA Ohara O., Nagase T., Kikuno R., Okumura K.;  
 RT "The nucleotide sequence of a long cDNA clone isolated from human  
 spleen."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK024450; BAB15740.1; -;  
 DR InterPro: IPR001806; Ras\_transfing.  
 DR InterPro: IPR003575; Small\_GTPase.  
 DR PRINTS: PRO0449; RASTRNSFRMG.  
 DR SMART: SM00010; small\_GTPase; 1.  
 KM CTP-binding.  
 FT NON\_TER  
 SQ SEQUENCE 452 AA; 48320 MW; FD10D8A4EA1652B7 CRC64;

Query Match 3.0%; Score 7; DB 4; Length 452;  
 Best Local Similarity 100.0%; Pred. No. 79;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQOQRHS 21  
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 Db 39 PQOQRHS 45

RESULT 50  
 Q9AY47 ID Q9AY47 PRELIMINARY; PRT; 458 AA.  
 AC Q9AY47;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE PUTATIVE NUCLEIC ACID BINDING PROTEIN.  
 GN OSJNBA0027P10.5.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. NIPPONBARE;  
 RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Hsiao J.,  
 RA Zisman V., Pal G., Bowman C.L., Fujii C.Y., Vanaken S.E., Craven B.,  
 RA Khalak H., Feldblum T.V., Quackenbush J., White O., Salzberg S.L.,  
 RA Fraser C.M.;  
 RT "Oryza sativa chromosome 10 BAC OSJNBA0027P10 genomic sequence."  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC084763; AAC60186.1; -;  
 DR InterPro: IPR004087; KH.  
 DR InterPro: IPR004088; KH\_type\_1.  
 DR Pfam; PF00013; KH-domain; 3.  
 DR SMART; SM00322; KH; 3.  
 DR PROSITE; PSS0084; KH\_type\_1; 3.  
 SQ SEQUENCE 458 AA; 48410 MW; 671AAACD8E75446D CRC64;

Query Match 3.0%; Score 7; DB 10; Length 458;  
 Best Local Similarity 100.0%; Pred. No. 80;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 PAPAEE 155  
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 Db 20 PAPAEE 26

Search completed: August 13, 2002, 08:42:13  
 Job time: 231 sec

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